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(54) Title: METHODS OF DIAGNOSIS OF PROSTATE CANCER, COMPOSITIONS AND METHODS OF SCREENING FOR MODULATORS OF PROSTATE CANCER

(57) Abstract: Described herein are genes whose expression are up-regulated or down-regulated in prostate cancer. Also described are such genes whose expression is further up-regulated or down-regulated in drug-resistant prostate cancer cells. Related methods and compositions that can be used for diagnosis and treatment of prostate cancer are disclosed. Also described herein are methods that can be used to identify modulators of prostate cancer.

**METHODS OF DIAGNOSIS OF PROSTATE CANCER,
COMPOSITIONS AND METHODS OF SCREENING FOR
MODULATORS OF PROSTATE CANCER**

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CROSS-REFERENCES TO RELATED APPLICATIONS

This application claims priority from the following applications: USSN 09/687,576 filed October 13, 2000, USSN 60/276,791 filed March 16, 2001; USSN 60/288,589, filed May 4, 2001; USSN 09/733,742, filed December 8, 2000; USSN
10 09/733,288, filed December 8, 2000; USSN 09/847,046, filed April 30, 2001; USSN 60/276,888, filed March 16, 2001; USSN 60/286,214, filed April 24, 2001; USSN 60/281,922, filed April 6, 2001; USSN 60/263,957, filed January 24, 2001, which are incorporated herein by reference in their entirety.

15

FIELD OF THE INVENTION

The invention relates to the identification of nucleic acid and protein expression profiles and nucleic acids, products, and antibodies thereto that are involved in prostate cancer; and to the use of such expression profiles and compositions in the diagnosis, prognosis and therapy of prostate cancer. The invention further relates to methods for
20 identifying and using agents and/or targets that inhibit prostate cancer.

BACKGROUND OF THE INVENTION

Prostate cancer is the most commonly diagnosed internal malignancy and second most common cause of cancer death in men in the U.S., resulting in approximately
25 40,000 deaths each year (Landis et al., *CA Cancer J. Clin.* 48:6-29 (1998); Greenlee et al., *CA Cancer J. Clin.* 50(1):7-13 (2000)), and incidence of prostate cancer has been increasing rapidly over the past 20 years in many parts of the world (Nakata et al., *Int. J. Urol.* 7(7):254-257 (2000); Majeed et al., *BJU Int.* 85(9):1058-1062 (2000)). It develops as the

result of a pathologic transformation of normal prostate cells. In tumorigenesis, the cancer cell undergoes initiation, proliferation and loss of contact inhibition, culminating in invasion of surrounding tissue and, ultimately, metastasis.

Deaths from prostate cancer are a result of metastasis of a prostate tumor.

5 Therefore, early detection of the development of prostate cancer is critical in reducing mortality from this disease. Measuring levels of prostate-specific antigen (PSA) has become a very common method for early detection and screening, and may have contributed to the slight decrease in the mortality rate from prostate cancer in recent years (Nowroozi et al., *Cancer Control* 5(6):522-531 (1998)). However, many cases are not diagnosed until the
10 disease has progressed to an advanced stage.

Treatments such as surgery (prostatectomy) , radiation therapy, and cryotherapy are potentially curative when the cancer remains localized to the prostate. Therefore, early detection of prostate cancer is important for a positive prognosis for treatment. Systemic treatment for metastatic prostate cancer is limited to hormone therapy
15 and chemotherapy. Chemical or surgical castration has been the primary treatment for symptomatic metastatic prostate cancer for over 50 years. This testicular androgen deprivation therapy usually results in stabilization or regression of the disease (in 80% of patients), but progression of metastatic prostate cancer eventually develops (Panvichian et al., *Cancer Control* 3(6):493-500 (1996)). Metastatic disease is currently considered incurable,
20 and the primary goals of treatment are to prolong survival and improve quality of life (Rago, *Cancer Control* 5(6):513-521 (1998)).

Thus, methods that can be used for diagnosis and prognosis of prostate cancer and effective treatment of prostate cancer, and including particularly metastatic prostate cancer, would be desirable. Accordingly, provided herein are methods that can be used in
25 diagnosis and prognosis of prostate cancer. Further provided are methods that can be used to screen candidate bioactive agents for the ability to modulate, e.g., treat, prostate cancer. Additionally, provided herein are molecular targets and compositions for therapeutic intervention in prostate cancer and other cancers.

SUMMARY OF THE INVENTION

The present invention therefore provides nucleotide sequences of genes that are up- and down-regulated in prostate cancer cells. Such genes are useful for diagnostic purposes, and also as targets for screening for therapeutic compounds that modulate prostate cancer, such as hormones or antibodies. Other aspects of the invention will become apparent to the skilled artisan by the following description of the invention.

In one aspect, the present invention provides a method of detecting a prostate cancer-associated transcript in a cell from a patient, the method comprising contacting a biological sample from the patient with a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1-16.

In one embodiment, the present invention provides a method of determining the level of a prostate cancer associated transcript in a cell from a patient.

In one embodiment, the present invention provides a method of detecting a prostate cancer-associated transcript in a cell from a patient, the method comprising contacting a biological sample from the patient with a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1-16.

In one embodiment, the polynucleotide selectively hybridizes to a sequence at least 95% identical to a sequence as shown in Tables 1-16. In another embodiment, the polynucleotide comprises a sequence as shown in Tables 1-16.

In one embodiment, the biological sample is a tissue sample. In another embodiment, the biological sample comprises isolated nucleic acids, e.g., mRNA.

In one embodiment, the polynucleotide is labeled, e.g., with a fluorescent label.

In one embodiment, the polynucleotide is immobilized on a solid surface.

In one embodiment, the patient is undergoing a therapeutic regimen to treat prostate cancer. In another embodiment, the patient is suspected of having metastatic prostate cancer.

In one embodiment, the patient is a human.

In one embodiment, the patient is suspected of having a taxol-resistant cancer.

In one embodiment, the prostate cancer associated transcript is mRNA.

In one embodiment, the method further comprises the step of amplifying nucleic acids before the step of contacting the biological sample with the polynucleotide.

In another aspect, the present invention provides a method of monitoring the efficacy of a therapeutic treatment of prostate cancer, the method comprising the steps of: (i) providing a biological sample from a patient undergoing the therapeutic treatment; and (ii) determining the level of a prostate cancer-associated transcript in the biological sample by contacting the biological sample with a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1-16, thereby monitoring the efficacy of the therapy. In a further embodiment, the patient has metastatic prostate cancer. In a further embodiment, the patient has a drug resistant (e.g., taxol resistant) form of prostate cancer.

In one embodiment, the method further comprises the step of: (iii) comparing the level of the prostate cancer-associated transcript to a level of the prostate cancer-associated transcript in a biological sample from the patient prior to, or earlier in, the therapeutic treatment.

Additionally, provided herein is a method of evaluating the effect of a candidate prostate cancer drug comprising administering the drug to a patient and removing a cell sample from the patient. The expression profile of the cell is then determined. This method may further comprise comparing the expression profile to an expression profile of a healthy individual. In a preferred embodiment, said expression profile includes a gene of Tables 1-16.

In one aspect, the present invention provides an isolated nucleic acid molecule consisting of a polynucleotide sequence as shown in Tables 1-16.

In one embodiment, an expression vector or cell comprises the isolated nucleic acid.

In one aspect, the present invention provides an isolated polypeptide which is encoded by a nucleic acid molecule having polynucleotide sequence as shown in Tables 1-16.

In another aspect, the present invention provides an antibody that specifically binds to an isolated polypeptide which is encoded by a nucleic acid molecule having polynucleotide sequence as shown in Tables 1-16.

In one embodiment, the antibody is conjugated to an effector component, e.g., a fluorescent label, a radioisotope or a cytotoxic chemical.

In one embodiment, the antibody is an antibody fragment. In another embodiment, the antibody is humanized.

5 In one aspect, the present invention provides a method of detecting a prostate cancer cell in a biological sample from a patient, the method comprising contacting the biological sample with an antibody as described herein.

In another aspect, the present invention provides a method of detecting antibodies specific to prostate cancer in a patient, the method comprising contacting a
10 biological sample from the patient with a polypeptide encoded by a nucleic acid comprising a sequence from Tables 1-16.

In another aspect, the present invention provides a method for identifying a compound that modulates a prostate cancer-associated polypeptide, the method comprising the steps of: (i) contacting the compound with a prostate cancer-associated polypeptide, the
15 polypeptide encoded by a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1-16; and (ii) determining the functional effect of the compound upon the polypeptide.

In one embodiment, the functional effect is a physical effect, an enzymatic effect, or a chemical effect.

20 In one embodiment, the polypeptide is expressed in a eukaryotic host cell or cell membrane. In another embodiment, the polypeptide is recombinant.

In one embodiment, the functional effect is determined by measuring ligand binding to the polypeptide.

In another aspect, the present invention provides a method of inhibiting
25 proliferation of a prostate cancer-associated cell to treat prostate cancer in a patient, the method comprising the step of administering to the subject a therapeutically effective amount of a compound identified as described herein.

In one embodiment, the compound is an antibody.

In another aspect, the present invention provides a drug screening assay
30 comprising the steps of: (i) administering a test compound to a mammal having prostate cancer or to a cell sample isolated therefrom; (ii) comparing the level of gene expression of a

polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1-16 in a treated cell or mammal with the level of gene expression of the polynucleotide in a control cell sample or mammal, wherein a test compound that modulates the level of expression of the polynucleotide is a candidate for the treatment of prostate cancer.

In one embodiment, the control is a mammal with prostate cancer or a cell sample therefrom that has not been treated with the test compound. In another embodiment, the control is a normal cell or mammal.

In one embodiment, the test compound is administered in varying amounts or concentrations. In another embodiment, the test compound is administered for varying time periods. In another embodiment, the comparison can occur after addition or removal of the drug candidate.

In one embodiment, the levels of a plurality of polynucleotides that selectively hybridize to a sequence at least 80% identical to a sequence as shown in Tables 1-16 are individually compared to their respective levels in a control cell sample or mammal. In a preferred embodiment the plurality of polynucleotides is from three to ten.

In another aspect, the present invention provides a method for treating a mammal having prostate cancer comprising administering a compound identified by the assay described herein.

In another aspect, the present invention provides a pharmaceutical composition for treating a mammal having prostate cancer, the composition comprising a compound identified by the assay described herein and a physiologically acceptable excipient.

In one aspect, the present invention provides a method of screening drug candidates by providing a cell expressing a gene that is up- and down-regulated as in a prostate cancer. In one embodiment, a gene is selected from Tables 1-16. The method further includes adding a drug candidate to the cell and determining the effect of the drug candidate on the expression of the expression profile gene.

In one embodiment, the method of screening drug candidates includes comparing the level of expression in the absence of the drug candidate to the level of expression in the presence of the drug candidate, wherein the concentration of the drug

candidate can vary when present, and wherein the comparison can occur after addition or removal of the drug candidate. In a preferred embodiment, the cell expresses at least two expression profile genes. The profile genes may show an increase or decrease.

Also provided is a method of evaluating the effect of a candidate prostate cancer drug comprising administering the drug to a transgenic animal expressing or
5 over-expressing the prostate cancer modulatory protein, or an animal lacking the prostate cancer modulatory protein, for example as a result of a gene knockout.

Moreover, provided herein is a biochip comprising one or more nucleic acid segments of Tables 1-16, wherein the biochip comprises fewer than 1000 nucleic acid probes.
10 Preferably, at least two nucleic acid segments are included. More preferably, at least three nucleic acid segments are included.

Furthermore, a method of diagnosing a disorder associated with prostate cancer is provided. The method comprises determining the expression of a gene of Tables 1-16, in a first tissue type of a first individual, and comparing the distribution to the expression
15 of the gene from a second normal tissue type from the first individual or a second unaffected individual. A difference in the expression indicates that the first individual has a disorder associated with prostate cancer.

In a further embodiment, the biochip also includes a polynucleotide sequence of a gene that is not up- and down-regulated in prostate cancer.

20 In one embodiment a method for screening for a bioactive agent capable of interfering with the binding of a prostate cancer modulating protein (prostate cancer modulatory protein) or a fragment thereof and an antibody which binds to said prostate cancer modulatory protein or fragment thereof. In a preferred embodiment, the method comprises combining a prostate cancer modulatory protein or fragment thereof, a candidate
25 bioactive agent and an antibody which binds to said prostate cancer modulatory protein or fragment thereof. The method further includes determining the binding of said prostate cancer modulatory protein or fragment thereof and said antibody. Wherein there is a change in binding, an agent is identified as an interfering agent. The interfering agent can be an agonist or an antagonist. Preferably, the agent inhibits prostate cancer.

30 Also provided herein are methods of eliciting an immune response in an individual. In one embodiment a method provided herein comprises administering to an

individual a composition comprising a prostate cancer modulating protein, or a fragment thereof. In another embodiment, the protein is encoded by a nucleic acid selected from those of Tables 1-16.

Further provided herein are compositions capable of eliciting an immune response in an individual. In one embodiment, a composition provided herein comprises a prostate cancer modulating protein, preferably encoded by a nucleic acid of Tables 1-16, or a fragment thereof, and a pharmaceutically acceptable carrier. In another embodiment, said composition comprises a nucleic acid comprising a sequence encoding a prostate cancer modulating protein, preferably selected from the nucleic acids of Tables 1-16, and a pharmaceutically acceptable carrier.

Also provided are methods of neutralizing the effect of a prostate cancer protein, or a fragment thereof, comprising contacting an agent specific for said protein with said protein in an amount sufficient to effect neutralization. In another embodiment, the protein is encoded by a nucleic acid selected from those of Tables 1-16.

In another aspect of the invention, a method of treating an individual for prostate cancer is provided. In one embodiment, the method comprises administering to said individual an inhibitor of a prostate cancer modulating protein. In another embodiment, the method comprises administering to a patient having prostate cancer an antibody to a prostate cancer modulating protein conjugated to a therapeutic moiety. Such a therapeutic moiety can be a cytotoxic agent or a radioisotope.

DETAILED DESCRIPTION OF THE INVENTION

In accordance with the objects outlined above, the present invention provides novel methods for diagnosis and prognosis evaluation for prostate cancer (PC), including metastatic prostate cancer, as well as methods for screening for compositions which modulate prostate cancer. Also provided are methods for treating prostate cancer.

In addition to the other nucleic acid and peptide sequences, the present invention also relates to the identification of PAA2 as a gene that is highly over expressed in prostate cancer patient tissues. PAA2 sequence is identical to the zinc transporter ZNT4. Results presented herein demonstrate that PAA2/ZNT4 is highly expressed in prostate cancer cells. The prostate gland is unique in that it has the highest capacity of any organ in the body

to accumulate zinc. Zinc uptake is regulated by prolactin and testosterone, which induce the expression of a member of the ZIP family of zinc transporters (Costello et al., 1999, J. Biol. Chem. 274:17499-17504). Zinc accumulation in the prostate functions to inhibit citrate oxidation, which results in a decrease in cellular ATP production (Costello and Franklin, 1998, Prostate 35:285-296). Cancer cells are more sensitive to decreased ATP production and have evolved to prevent zinc accumulation. Without wishing to be bound by theory, the up-regulation of ZNT4 in prostate cancer cells may result in protection of the cells from high zinc levels by its ability to pump accumulated zinc out of the cells.

The present invention also relates to nucleic acid sequences encoding PBH1. PBH1 is related to human TRPC7 (transient receptor potential-related channels, NP_003298), a putative calcium channel highly expressed in brain (Nagamine et al., Genomics 54:124-131 (1998)). Trp is related to melastatin, a gene down-regulated in metastatic melanomas (Duncan et al., Cancer Res. 58:1515-1520 (1998)), and MTR1, a gene localized to within the Beckwith-Wiedemann syndrome/Wilm's tumor susceptibility region (Prawitt et al., Hum. Mol. Genet. 9:203-216 (2000)). Without wishing to be bound by theory, it is believed that PBH1 functions as a calcium channel.

As a calcium channel, PBH1 is an ideal target for a small molecule therapeutic, or a therapeutic antibody that disrupts channel function. CD20, the target of Rituximab in non-Hodgkin's lymphoma (Maloney et al., Blood 90:2188-2195 (1997); Leget and Czuczman, Curr. Opin. Oncol. 10:548-551 (1998)), is a plasma membrane calcium channel expressed in B cells (Tedder and Engel, Immunol. Today 15:450-454 (1994)). Similarly, a small molecule, or antibody that inhibits or alters a calcium signal mediated by PBH1, will result in the death of prostate cancer cells.

PBH1, and other genes of the invention, are also be useful as targets for cytotoxic T-lymphocytes. Genes that are tumor specific, or that are expressed in immune-privileged organs, are currently being used as potential vaccine targets (Van den Eynde and Boon, Int. J. Clin. Lab. Res. 27:81-86 (1997)). The expression pattern of PBH1 indicates that it is an ideal target for cytotoxic T-lymphocytes. Thus, therapies that utilize PBH1-specific cytotoxic T-lymphocytes to induce prostate cancer cell death are also provided by this invention. See, e.g., U.S. Patent No. 6,051,227 and WO 00/32231, the disclosures of which are herein incorporated by reference.

The present invention is also related to the identification of PAA3 as a gene that is important in the modulation of prostate cancer and or breast cancer.

Tables 1-16 provide unigene cluster identification numbers, exemplar accession numbers, or genomic nucleotide position numbers for the nucleotide sequence of
5 genes that exhibit increased or decreased expression in prostate cancer samples.

Definitions

The term "prostate cancer protein" or "prostate cancer polynucleotide" or "prostate cancer-associated transcript" refers to nucleic acid and polypeptide polymorphic
10 variants, alleles, mutants, and interspecies homologues that: (1) have a nucleotide sequence that has greater than about 60% nucleotide sequence identity, 65%, 70%, 75%, 80%, 85%, 90%, preferably 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% or greater nucleotide sequence identity, preferably over a region of over a region of at least about 25, 50, 100, 200,
15 500, 1000, or more nucleotides, to a nucleotide sequence of or associated with a unigene cluster of Tables 1-16; (2) bind to antibodies, e.g., polyclonal antibodies, raised against an immunogen comprising an amino acid sequence encoded by a nucleotide sequence of or associated with a unigene cluster of Tables 1-16, and conservatively modified variants thereof; (3) specifically hybridize under stringent hybridization conditions to a nucleic acid sequence, or the complement thereof of Tables 1-16 and conservatively modified variants
20 thereof or (4) have an amino acid sequence that has greater than about 60% amino acid sequence identity, 65%, 70%, 75%, 80%, 85%, 90%, preferably 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% or greater amino sequence identity, preferably over a region of over a region of at least about 25, 50, 100, 200, 500, 1000, or more amino acid, to an amino acid sequence encoded by a nucleotide sequence of or associated with a unigene cluster of Tables
25 1-16. A polynucleotide or polypeptide sequence is typically from a mammal including, but not limited to, primate, e.g., human; rodent, e.g., rat, mouse, hamster; cow, pig, horse, sheep, or other mammal. A "prostate cancer polypeptide" and a "prostate cancer polynucleotide," include both naturally occurring or recombinant forms.

A "full length" prostate cancer protein or nucleic acid refers to a prostate
30 cancer polypeptide or polynucleotide sequence, or a variant thereof, that contains all of the elements normally contained in one or more naturally occurring, wild type prostate cancer

polynucleotide or polypeptide sequences. For example, a full length prostate cancer nucleic acid will typically comprise all of the exons that encode for the full length, naturally occurring protein. The "full length" may be prior to, or after, various stages of post-translation processing or splicing, including alternative splicing.

5 "Biological sample" as used herein is a sample of biological tissue or fluid that contains nucleic acids or polypeptides, e.g., of a prostate cancer protein, polynucleotide or transcript. Such samples include, but are not limited to, tissue isolated from primates, e.g., humans, or rodents, e.g., mice, and rats. Biological samples may also include sections of tissues such as biopsy and autopsy samples, frozen sections taken for histologic purposes,
10 blood, plasma, serum, sputum, stool, tears, mucus, hair, skin, etc. Biological samples also include explants and primary and/or transformed cell cultures derived from patient tissues. A biological sample is typically obtained from a eukaryotic organism, most preferably a mammal such as a primate e.g., chimpanzee or human; cow; dog; cat; a rodent, e.g., guinea pig, rat, mouse; rabbit; or a bird; reptile; or fish.

15 "Providing a biological sample" means to obtain a biological sample for use in methods described in this invention. Most often, this will be done by removing a sample of cells from an animal, but can also be accomplished by using previously isolated cells (e.g., isolated by another person, at another time, and/or for another purpose), or by performing the methods of the invention *in vivo*. Archival tissues, having treatment or outcome history, will
20 be particularly useful.

 The terms "identical" or percent "identity," in the context of two or more nucleic acids or polypeptide sequences, refer to two or more sequences or subsequences that are the same or have a specified percentage of amino acid residues or nucleotides that are the same (i.e., about 60% identity, preferably 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%,
25 95%, 96%, 97%, 98%, 99%, or higher identity over a specified region, when compared and aligned for maximum correspondence over a comparison window or designated region) as measured using a BLAST or BLAST 2.0 sequence comparison algorithms with default parameters described below, or by manual alignment and visual inspection (*see, e.g.,* NCBI web site <http://www.ncbi.nlm.nih.gov/BLAST/> or the like). Such sequences are then said to
30 be "substantially identical." This definition also refers to, or may be applied to, the complement of a test sequence. The definition also includes sequences that have deletions

and/or additions, as well as those that have substitutions, as well as naturally occurring, e.g., polymorphic or allelic variants, and man-made variants. As described below, the preferred algorithms can account for gaps and the like. Preferably, identity exists over a region that is at least about 25 amino acids or nucleotides in length, or more preferably over a region that is
5 50-100 amino acids or nucleotides in length.

For sequence comparison, typically one sequence acts as a reference sequence, to which test sequences are compared. When using a sequence comparison algorithm, test and reference sequences are entered into a computer, subsequence coordinates are designated, if necessary, and sequence algorithm program parameters are designated. Preferably, default
10 program parameters can be used, or alternative parameters can be designated. The sequence comparison algorithm then calculates the percent sequence identities for the test sequences relative to the reference sequence, based on the program parameters.

A "comparison window", as used herein, includes reference to a segment of one of the number of contiguous positions selected from the group consisting typically of
15 from 20 to 600, usually about 50 to about 200, more usually about 100 to about 150 in which a sequence may be compared to a reference sequence of the same number of contiguous positions after the two sequences are optimally aligned. Methods of alignment of sequences for comparison are well-known in the art. Optimal alignment of sequences for comparison can be conducted, e.g., by the local homology algorithm of Smith & Waterman, *Adv. Appl. Math.* 2:482 (1981), by the homology alignment algorithm of Needleman & Wunsch, *J. Mol. Biol.* 48:443 (1970), by the search for similarity method of Pearson & Lipman, *Proc. Nat'l. Acad. Sci. USA* 85:2444 (1988), by computerized implementations of these algorithms (GAP, BESTFIT, FASTA, and TFASTA in the Wisconsin Genetics Software Package, Genetics Computer Group, 575 Science Dr., Madison, WI), or by manual alignment and
20 visual inspection (*see, e.g., Current Protocols in Molecular Biology* (Ausubel *et al.*, eds. 1995 supplement)).

Preferred examples of algorithms that are suitable for determining percent sequence identity and sequence similarity include the BLAST and BLAST 2.0 algorithms, which are described in Altschul *et al.*, *Nuc. Acids Res.* 25:3389-3402 (1977) and Altschul *et al.*, *J. Mol. Biol.* 215:403-410 (1990). BLAST and BLAST 2.0 are used, with the parameters
30 described herein, to determine percent sequence identity for the nucleic acids and proteins of

the invention. Software for performing BLAST analyses is publicly available through the National Center for Biotechnology Information (<http://www.ncbi.nlm.nih.gov/>). This algorithm involves first identifying high scoring sequence pairs (HSPs) by identifying short words of length W in the query sequence, which either match or satisfy some positive-valued threshold score T when aligned with a word of the same length in a database sequence. T is referred to as the neighborhood word score threshold (Altschul *et al.*, *supra*). These initial neighborhood word hits act as seeds for initiating searches to find longer HSPs containing them. The word hits are extended in both directions along each sequence for as far as the cumulative alignment score can be increased. Cumulative scores are calculated using, e.g., for nucleotide sequences, the parameters M (reward score for a pair of matching residues; always > 0) and N (penalty score for mismatching residues; always < 0). For amino acid sequences, a scoring matrix is used to calculate the cumulative score. Extension of the word hits in each direction are halted when: the cumulative alignment score falls off by the quantity X from its maximum achieved value; the cumulative score goes to zero or below, due to the accumulation of one or more negative-scoring residue alignments; or the end of either sequence is reached. The BLAST algorithm parameters W , T , and X determine the sensitivity and speed of the alignment. The BLASTN program (for nucleotide sequences) uses as defaults a wordlength (W) of 11, an expectation (E) of 10, $M=5$, $N=-4$ and a comparison of both strands. For amino acid sequences, the BLASTP program uses as defaults a wordlength of 3, and expectation (E) of 10, and the BLOSUM62 scoring matrix (see Henikoff & Henikoff, *Proc. Natl. Acad. Sci. USA* 89:10915 (1989)) alignments (B) of 50, expectation (E) of 10, $M=5$, $N=-4$, and a comparison of both strands.

The BLAST algorithm also performs a statistical analysis of the similarity between two sequences (see, e.g., Karlin & Altschul, *Proc. Nat'l. Acad. Sci. USA* 90:5873-5787 (1993)). One measure of similarity provided by the BLAST algorithm is the smallest sum probability ($P(N)$), which provides an indication of the probability by which a match between two nucleotide or amino acid sequences would occur by chance. For example, a nucleic acid is considered similar to a reference sequence if the smallest sum probability in a comparison of the test nucleic acid to the reference nucleic acid is less than about 0.2, more preferably less than about 0.01, and most preferably less than about 0.001. Log values may be large negative numbers, e.g., 5, 10, 20, 30, 40, 40, 70, 90, 110, 150, 170, etc.

An indication that two nucleic acid sequences or polypeptides are substantially identical is that the polypeptide encoded by the first nucleic acid is immunologically cross reactive with the antibodies raised against the polypeptide encoded by the second nucleic acid, as described below. Thus, a polypeptide is typically substantially identical to a second polypeptide, e.g., where the two peptides differ only by conservative substitutions. Another indication that two nucleic acid sequences are substantially identical is that the two molecules or their complements hybridize to each other under stringent conditions, as described below. Yet another indication that two nucleic acid sequences are substantially identical is that the same primers can be used to amplify the sequences.

A "host cell" is a naturally occurring cell or a transformed cell that contains an expression vector and supports the replication or expression of the expression vector. Host cells may be cultured cells, explants, cells *in vivo*, and the like. Host cells may be prokaryotic cells such as *E. coli*, or eukaryotic cells such as yeast, insect, amphibian, or mammalian cells such as CHO, HeLa, and the like (*see, e.g.*, the American Type Culture Collection catalog or web site, www.atcc.org).

The terms "isolated," "purified," or "biologically pure" refer to material that is substantially or essentially free from components that normally accompany it as found in its native state. Purity and homogeneity are typically determined using analytical chemistry techniques such as polyacrylamide gel electrophoresis or high performance liquid chromatography. A protein or nucleic acid that is the predominant species present in a preparation is substantially purified. In particular, an isolated nucleic acid is separated from some open reading frames that naturally flank the gene and encode proteins other than protein encoded by the gene. The term "purified" in some embodiments denotes that a nucleic acid or protein gives rise to essentially one band in an electrophoretic gel. Preferably, it means that the nucleic acid or protein is at least 85% pure, more preferably at least 95% pure, and most preferably at least 99% pure. "Purify" or "purification" in other embodiments means removing at least one contaminant from the composition to be purified. In this sense, purification does not require that the purified compound be homogenous, e.g., 100% pure.

The terms "polypeptide," "peptide" and "protein" are used interchangeably herein to refer to a polymer of amino acid residues. The terms apply to amino acid polymers in which one or more amino acid residue is an artificial chemical mimetic of a corresponding

naturally occurring amino acid, as well as to naturally occurring amino acid polymers, those containing modified residues, and non-naturally occurring amino acid polymer.

The term "amino acid" refers to naturally occurring and synthetic amino acids, as well as amino acid analogs and amino acid mimetics that function similarly to the naturally occurring amino acids. Naturally occurring amino acids are those encoded by the genetic code, as well as those amino acids that are later modified, e.g., hydroxyproline, γ -carboxyglutamate, and O-phosphoserine. Amino acid analogs refers to compounds that have the same basic chemical structure as a naturally occurring amino acid, e.g., an α carbon that is bound to a hydrogen, a carboxyl group, an amino group, and an R group, e.g., homoserine, norleucine, methionine sulfoxide, methionine methyl sulfonium. Such analogs may have modified R groups (e.g., norleucine) or modified peptide backbones, but retain the same basic chemical structure as a naturally occurring amino acid. Amino acid mimetics refers to chemical compounds that have a structure that is different from the general chemical structure of an amino acid, but that functions similarly to a naturally occurring amino acid.

Amino acids may be referred to herein by either their commonly known three letter symbols or by the one-letter symbols recommended by the IUPAC-IUB Biochemical Nomenclature Commission. Nucleotides, likewise, may be referred to by their commonly accepted single-letter codes.

"Conservatively modified variants" applies to both amino acid and nucleic acid sequences. With respect to particular nucleic acid sequences, conservatively modified variants refers to those nucleic acids which encode identical or essentially identical amino acid sequences, or where the nucleic acid does not encode an amino acid sequence, to essentially identical or associated, e.g., naturally contiguous, sequences. Because of the degeneracy of the genetic code, a large number of functionally identical nucleic acids encode most proteins. For instance, the codons GCA, GCC, GCG and GCU all encode the amino acid alanine. Thus, at every position where an alanine is specified by a codon, the codon can be altered to another of the corresponding codons described without altering the encoded polypeptide. Such nucleic acid variations are "silent variations," which are one species of conservatively modified variations. Every nucleic acid sequence herein which encodes a polypeptide also describes silent variations of the nucleic acid. One of skill will recognize that in certain contexts each codon in a nucleic acid (except AUG, which is ordinarily the

only codon for methionine, and TGG, which is ordinarily the only codon for tryptophan) can be modified to yield a functionally identical molecule. Accordingly, often silent variations of a nucleic acid which encodes a polypeptide is implicit in a described sequence with respect to the expression product, but not with respect to actual probe sequences.

- 5 As to amino acid sequences, one of skill will recognize that individual substitutions, deletions or additions to a nucleic acid, peptide, polypeptide, or protein sequence which alters, adds or deletes a single amino acid or a small percentage of amino acids in the encoded sequence is a "conservatively modified variant" where the alteration results in the substitution of an amino acid with a chemically similar amino acid.
- 10 Conservative substitution tables providing functionally similar amino acids are well known in the art. Such conservatively modified variants are in addition to and do not exclude polymorphic variants, interspecies homologs, and alleles of the invention. typically conservative substitutions for one another: 1) Alanine (A), Glycine (G); 2) Aspartic acid (D), Glutamic acid (E); 3) Asparagine (N), Glutamine (Q); 4) Arginine (R), Lysine (K); 5)
- 15 Isoleucine (I), Leucine (L), Methionine (M), Valine (V); 6) Phenylalanine (F), Tyrosine (Y), Tryptophan (W); 7) Serine (S), Threonine (T); and 8) Cysteine (C), Methionine (M) (*see, e.g., Creighton, Proteins* (1984)).

- Macromolecular structures such as polypeptide structures can be described in terms of various levels of organization. For a general discussion of this organization, *see,*
- 20 *e.g., Alberts et al., Molecular Biology of the Cell* (3rd ed., 1994) and Cantor & Schimmel, *Biophysical Chemistry Part I: The Conformation of Biological Macromolecules* (1980). "Primary structure" refers to the amino acid sequence of a particular peptide. "Secondary structure" refers to locally ordered, three dimensional structures within a polypeptide. These structures are commonly known as domains. Domains are portions of a polypeptide that
- 25 often form a compact unit of the polypeptide and are typically 25 to approximately 500 amino acids long. Typical domains are made up of sections of lesser organization such as stretches of β -sheet and α -helices. "Tertiary structure" refers to the complete three dimensional structure of a polypeptide monomer. "Quaternary structure" refers to the three dimensional structure formed, usually by the noncovalent association of independent tertiary
- 30 units. Anisotropic terms are also known as energy terms.

"Nucleic acid" or "oligonucleotide" or "polynucleotide" or grammatical equivalents used herein means at least two nucleotides covalently linked together. Oligonucleotides are typically from about 5, 6, 7, 8, 9, 10, 12, 15, 25, 30, 40, 50 or more nucleotides in length, up to about 100 nucleotides in length. Nucleic acids and

5 polynucleotides are a polymers of any length, including longer lengths, e.g., 200, 300, 500, 1000, 2000, 3000, 5000, 7000, 10,000, etc. A nucleic acid of the present invention will generally contain phosphodiester bonds, although in some cases, nucleic acid analogs are included that may have alternate backbones, comprising, e.g., phosphoramidate, phosphorothioate, phosphorodithioate, or O-methylphosphoroamidite linkages (see Eckstein,

10 Oligonucleotides and Analogues: A Practical Approach, Oxford University Press); and peptide nucleic acid backbones and linkages. Other analog nucleic acids include those with positive backbones; non-ionic backbones, and non-ribose backbones, including those described in U.S. Patent Nos. 5,235,033 and 5,034,506, and Chapters 6 and 7, ASC Symposium Series 580, *Carbohydrate Modifications in Antisense Research*, Sanghui &

15 Cook, eds.. Nucleic acids containing one or more carbocyclic sugars are also included within one definition of nucleic acids. Modifications of the ribose-phosphate backbone may be done for a variety of reasons, e.g. to increase the stability and half-life of such molecules in physiological environments or as probes on a biochip. Mixtures of naturally occurring nucleic acids and analogs can be made; alternatively, mixtures of different nucleic acid

20 analogs, and mixtures of naturally occurring nucleic acids and analogs may be made.

A variety of references disclose such nucleic acid analogs, including, for example, phosphoramidate (Beaucage et al., *Tetrahedron* 49(10):1925 (1993) and references therein; Letsinger, *J. Org. Chem.* 35:3800 (1970); Sprinzl et al., *Eur. J. Biochem.* 81:579 (1977); Letsinger et al., *Nucl. Acids Res.* 14:3487 (1986); Sawai et al., *Chem. Lett.* 805

25 (1984), Letsinger et al., *J. Am. Chem. Soc.* 110:4470 (1988); and Pauwels et al., *Chemica Scripta* 26:141 (1986)), phosphorothioate (Mag et al., *Nucleic Acids Res.* 19:1437 (1991); and U.S. Patent No. 5,644,048), phosphorodithioate (Briu et al., *J. Am. Chem. Soc.* 111:2321 (1989), O-methylphosphoroamidite linkages (see Eckstein, *Oligonucleotides and Analogues: A Practical Approach*, Oxford University Press), and peptide nucleic acid backbones and

30 linkages (see Egholm, *J. Am. Chem. Soc.* 114:1895 (1992); Meier et al., *Chem. Int. Ed. Engl.* 31:1008 (1992); Nielsen, *Nature*, 365:566 (1993); Carlsson et al., *Nature* 380:207 (1996), all

of which are incorporated by reference). Other analog nucleic acids include those with positive backbones (Denpcy et al., Proc. Natl. Acad. Sci. USA 92:6097 (1995); non-ionic backbones (U.S. Patent Nos. 5,386,023, 5,637,684, 5,602,240, 5,216,141 and 4,469,863; Kiedrowski et al., Angew. Chem. Intl. Ed. English 30:423 (1991); Letsinger et al., J. Am. Chem. Soc. 110:4470 (1988); Letsinger et al., Nucleoside & Nucleotide 13:1597 (1994); Chapters 2 and 3, ASC Symposium Series 580, "Carbohydrate Modifications in Antisense Research", Ed. Y.S. Sanghui and P. Dan Cook; Mesmaeker et al., Bioorganic & Medicinal Chem. Lett. 4:395 (1994); Jeffs et al., J. Biomolecular NMR 34:17 (1994); Tetrahedron Lett. 37:743 (1996)) and non-ribose backbones, including those described in U.S. Patent Nos. 5,235,033 and 5,034,506, and Chapters 6 and 7, ASC Symposium Series 580, "Carbohydrate Modifications in Antisense Research", Ed. Y.S. Sanghui and P. Dan Cook. Nucleic acids containing one or more carbocyclic sugars are also included within one definition of nucleic acids (see Jenkins et al., Chem. Soc. Rev. (1995) pp 169-176). Several nucleic acid analogs are described in Rawls, C & E News June 2, 1997 page 35. All of these references are hereby expressly incorporated by reference.

Particularly preferred are peptide nucleic acids (PNA) which includes peptide nucleic acid analogs. These backbones are substantially non-ionic under neutral conditions, in contrast to the highly charged phosphodiester backbone of naturally occurring nucleic acids. This results in two advantages. First, the PNA backbone exhibits improved hybridization kinetics. PNAs have larger changes in the melting temperature (T_m) for mismatched versus perfectly matched basepairs. DNA and RNA typically exhibit a 2-4°C drop in T_m for an internal mismatch. With the non-ionic PNA backbone, the drop is closer to 7-9°C. Similarly, due to their non-ionic nature, hybridization of the bases attached to these backbones is relatively insensitive to salt concentration. In addition, PNAs are not degraded by cellular enzymes, and thus can be more stable.

The nucleic acids may be single stranded or double stranded, as specified, or contain portions of both double stranded or single stranded sequence. As will be appreciated by those in the art, the depiction of a single strand also defines the sequence of the complementary strand; thus the sequences described herein also provide the complement of the sequence. The nucleic acid may be DNA, both genomic and cDNA, RNA or a hybrid, where the nucleic acid may contain combinations of deoxyribo- and ribo-nucleotides, and

combinations of bases, including uracil, adenine, thymine, cytosine, guanine, inosine, xanthine hypoxanthine, isocytosine, isoguanine, etc. "Transcript" typically refers to a naturally occurring RNA, e.g., a pre-mRNA, hnRNA, or mRNA. As used herein, the term "nucleoside" includes nucleotides and nucleoside and nucleotide analogs, and modified
5 nucleosides such as amino modified nucleosides. In addition, "nucleoside" includes non-naturally occurring analog structures. Thus, e.g. the individual units of a peptide nucleic acid, each containing a base, are referred to herein as a nucleoside.

A "label" or a "detectable moiety" is a composition detectable by spectroscopic, photochemical, biochemical, immunochemical, chemical, or other physical
10 means. For example, useful labels include fluorescent dyes, electron-dense reagents, enzymes (e.g., as commonly used in an ELISA), biotin, digoxigenin, or haptens and proteins or other entities which can be made detectable, e.g., by incorporating a radiolabel into the peptide or used to detect antibodies specifically reactive with the peptide. The radioisotope may be, for example, ³H, ¹⁴C, ³²P, ³⁵S, or ¹²⁵I. In some cases, particularly using antibodies against the
15 proteins of the invention, the radioisotopes are used as toxic moieties, as described below. The labels may be incorporated into the prostate cancer nucleic acids, proteins and antibodies at any position. Any method known in the art for conjugating the antibody to the label may be employed, including those methods described by Hunter et al., *Nature*, 144:945 (1962); David et al., *Biochemistry*, 13:1014 (1974); Pain et al., *J. Immunol. Meth.*, 40:219 (1981);
20 and Nygren, *J. Histochem. and Cytochem.*, 30:407 (1982). The lifetime of radiolabeled peptides or radiolabeled antibody compositions may extended by the addition of substances that stabilize the radiolabeled peptide or antibody and protect it from degradation. Any substance or combination of substances that stabilize the radiolabeled peptide or antibody may be used including those substances disclosed in US Patent No. 5,961,955.

25 An "effector" or "effector moiety" or "effector component" is a molecule that is bound (or linked, or conjugated), either covalently, through a linker or a chemical bond, or noncovalently, through ionic, van der Waals, electrostatic, or hydrogen bonds, to an antibody. The "effector" can be a variety of molecules including, e.g., detection moieties including radioactive compounds, fluorescent compounds, an enzyme or substrate, tags such as epitope
30 tags, a toxin; activatable moieties, a chemotherapeutic agent; a lipase; an antibiotic; or a radioisotope emitting "hard" e.g., beta radiation.

A "labeled nucleic acid probe or oligonucleotide" is one that is bound, either covalently, through a linker or a chemical bond, or noncovalently, through ionic, van der Waals, electrostatic, or hydrogen bonds to a label such that the presence of the probe may be detected by detecting the presence of the label bound to the probe. Alternatively, method
5 using high affinity interactions may achieve the same results where one of a pair of binding partners binds to the other, e.g., biotin, streptavidin.

As used herein a "nucleic acid probe or oligonucleotide" is defined as a nucleic acid capable of binding to a target nucleic acid of complementary sequence through one or more types of chemical bonds, usually through complementary base pairing, usually
10 through hydrogen bond formation. As used herein, a probe may include natural (i.e., A, G, C, or T) or modified bases (7-deazaguanosine, inosine, etc.). In addition, the bases in a probe may be joined by a linkage other than a phosphodiester bond, so long as it does not functionally interfere with hybridization. Thus, e.g., probes may be peptide nucleic acids in which the constituent bases are joined by peptide bonds rather than phosphodiester linkages.
15 It will be understood by one of skill in the art that probes may bind target sequences lacking complete complementarity with the probe sequence depending upon the stringency of the hybridization conditions. The probes are preferably directly labeled as with isotopes, chromophores, lumiphores, chromogens, or indirectly labeled such as with biotin to which a streptavidin complex may later bind. By assaying for the presence or absence of the probe,
20 one can detect the presence or absence of the select sequence or subsequence. Diagnosis or prognosis may be based at the genomic level, or at the level of RNA or protein expression.

The term "recombinant" when used with reference, e.g., to a cell, or nucleic acid, protein, or vector, indicates that the cell, nucleic acid, protein or vector, has been modified by the introduction of a heterologous nucleic acid or protein or the alteration of a
25 native nucleic acid or protein, or that the cell is derived from a cell so modified. Thus, e.g., recombinant cells express genes that are not found within the native (non-recombinant) form of the cell or express native genes that are otherwise abnormally expressed, under expressed or not expressed at all. By the term "recombinant nucleic acid" herein is meant nucleic acid, originally formed *in vitro*, in general, by the manipulation of nucleic acid, e.g., using
30 polymerases and endonucleases, in a form not normally found in nature. In this manner, operably linkage of different sequences is achieved. Thus an isolated nucleic acid, in a linear

form, or an expression vector formed *in vitro* by ligating DNA molecules that are not normally joined, are both considered recombinant for the purposes of this invention. It is understood that once a recombinant nucleic acid is made and reintroduced into a host cell or organism, it will replicate non-recombinantly, i.e., using the *in vivo* cellular machinery of the host cell rather than *in vitro* manipulations; however, such nucleic acids, once produced recombinantly, although subsequently replicated non-recombinantly, are still considered recombinant for the purposes of the invention. Similarly, a "recombinant protein" is a protein made using recombinant techniques, i.e., through the expression of a recombinant nucleic acid as depicted above.

The term "heterologous" when used with reference to portions of a nucleic acid indicates that the nucleic acid comprises two or more subsequences that are not normally found in the same relationship to each other in nature. For instance, the nucleic acid is typically recombinantly produced, having two or more sequences, e.g., from unrelated genes arranged to make a new functional nucleic acid, e.g., a promoter from one source and a coding region from another source. Similarly, a heterologous protein will often refer to two or more subsequences that are not found in the same relationship to each other in nature (e.g., a fusion protein).

A "promoter" is defined as an array of nucleic acid control sequences that direct transcription of a nucleic acid. As used herein, a promoter includes necessary nucleic acid sequences near the start site of transcription, such as, in the case of a polymerase II type promoter, a TATA element. A promoter also optionally includes distal enhancer or repressor elements, which can be located as much as several thousand base pairs from the start site of transcription. A "constitutive" promoter is a promoter that is active under most environmental and developmental conditions. An "inducible" promoter is a promoter that is active under environmental or developmental regulation. The term "operably linked" refers to a functional linkage between a nucleic acid expression control sequence (such as a promoter, or array of transcription factor binding sites) and a second nucleic acid sequence, wherein the expression control sequence directs transcription of the nucleic acid corresponding to the second sequence.

An "expression vector" is a nucleic acid construct, generated recombinantly or synthetically, with a series of specified nucleic acid elements that permit transcription of a

particular nucleic acid in a host cell. The expression vector can be part of a plasmid, virus, or nucleic acid fragment. Typically, the expression vector includes a nucleic acid to be transcribed operably linked to a promoter.

5 The phrase "selectively (or specifically) hybridizes to" refers to the binding, duplexing, or hybridizing of a molecule only to a particular nucleotide sequence that is determinative of the presence of the nucleotide sequence, in a heterogeneous population of nucleic acids and other biologics (e.g., total cellular or library DNA or RNA). Similarly, the phrase "specifically (or selectively) binds" to an antibody or "specifically (or selectively) immunoreactive with," when referring to a protein or peptide, refers to a binding reaction that
10 is determinative of the presence of the protein, in a heterogeneous population of proteins and other biologics. Thus, under designated immunoassay or nucleic acid hybridization conditions, the specified antibodies or nucleic acid probes bind to a particular protein nucleotide sequences at least two times the background and more typically more than 10 to 100 times background.

15 Specific binding to an antibody under such conditions requires an antibody that is selected for its specificity for a particular protein. For example, polyclonal antibodies raised to a particular protein, polymorphic variants, alleles, orthologs, and conservatively modified variants, or splice variants, or portions thereof, can be selected to obtain only those polyclonal antibodies that are specifically immunoreactive with the desired prostate cancer
20 protein and not with other proteins. This selection may be achieved by subtracting out antibodies that cross-react with other molecules. A variety of immunoassay formats may be used to select antibodies specifically immunoreactive with a particular protein. For example, solid-phase ELISA immunoassays are routinely used to select antibodies specifically immunoreactive with a protein (*see, e.g., Harlow & Lane, Antibodies, A Laboratory Manual*
25 (1988) for a description of immunoassay formats and conditions that can be used to determine specific immunoreactivity).

The phrase "stringent hybridization conditions" refers to conditions under which a probe will hybridize to its target subsequence, typically in a complex mixture of nucleic acids, but to no other sequences. Stringent conditions are sequence-dependent and
30 will be different in different circumstances. Longer sequences hybridize specifically at higher temperatures. An extensive guide to the hybridization of nucleic acids is found in

Tijssen, *Techniques in Biochemistry and Molecular Biology--Hybridization with Nucleic Probes*, "Overview of principles of hybridization and the strategy of nucleic acid assays" (1993). Generally, stringent conditions are selected to be about 5-10°C lower than the thermal melting point (T_m) for the specific sequence at a defined ionic strength pH. The T_m is the temperature (under defined ionic strength, pH, and nucleic concentration) at which 50% of the probes complementary to the target hybridize to the target sequence at equilibrium (as the target sequences are present in excess, at T_m , 50% of the probes are occupied at equilibrium). Stringent conditions will be those in which the salt concentration is less than about 1.0 M sodium ion, typically about 0.01 to 1.0 M sodium ion concentration (or other salts) at pH 7.0 to 8.3 and the temperature is at least about 30°C for short probes (e.g., 10 to 50 nucleotides) and at least about 60°C for long probes (e.g., greater than 50 nucleotides). Stringent conditions may also be achieved with the addition of destabilizing agents such as formamide. For selective or specific hybridization, a positive signal is at least two times background; preferably 10 times background hybridization. Exemplary stringent hybridization conditions can be as following: 50% formamide, 5x SSC, and 1% SDS, incubating at 42°C, or, 5x SSC, 1% SDS, incubating at 65°C, with wash in 0.2x SSC, and 0.1% SDS at 65°C. For PCR, a temperature of about 36°C is typical for low stringency amplification, although annealing temperatures may vary between about 32°C and 48°C depending on primer length. For high stringency PCR amplification, a temperature of about 62°C is typical, although high stringency annealing temperatures can range from about 50°C to about 65°C, depending on the primer length and specificity. Typical cycle conditions for both high and low stringency amplifications include a denaturation phase of 90°C - 95°C for 30 sec - 2 min., an annealing phase lasting 30 sec. - 2 min., and an extension phase of about 72°C for 1 - 2 min. Protocols and guidelines for low and high stringency amplification reactions are provided, e.g., in Innis *et al.* (1990) *PCR Protocols, A Guide to Methods and Applications*, Academic Press, Inc. N.Y.).

Nucleic acids that do not hybridize to each other under stringent conditions are still substantially identical if the polypeptides which they encode are substantially identical. This occurs, e.g., when a copy of a nucleic acid is created using the maximum codon degeneracy permitted by the genetic code. In such cases, the nucleic acids typically hybridize

under moderately stringent hybridization conditions. Exemplary "moderately stringent hybridization conditions" include a hybridization in a buffer of 40% formamide, 1 M NaCl, 1% SDS at 37°C, and a wash in 1X SSC at 45°C. A positive hybridization is at least twice background. Those of ordinary skill will readily recognize that alternative hybridization and wash conditions can be utilized to provide conditions of similar stringency. Additional guidelines for determining hybridization parameters are provided in numerous reference, e.g., and Current Protocols in Molecular Biology, ed. Ausubel, *et al.*

The phrase "functional effects" in the context of assays for testing compounds that modulate activity of a prostate cancer protein includes the determination of a parameter that is indirectly or directly under the influence of the prostate cancer protein or nucleic acid, e.g., a functional, physical, or chemical effect, such as the ability to decrease prostate cancer. It includes ligand binding activity; cell growth on soft agar; anchorage dependence; contact inhibition and density limitation of growth; cellular proliferation; cellular transformation; growth factor or serum dependence; tumor specific marker levels; invasiveness into Matrigel; tumor growth and metastasis *in vivo*; mRNA and protein expression in cells undergoing metastasis, and other characteristics of prostate cancer cells. "Functional effects" include *in vitro*, *in vivo*, and *ex vivo* activities.

By "determining the functional effect" is meant assaying for a compound that increases or decreases a parameter that is indirectly or directly under the influence of a prostate cancer protein sequence, e.g., functional, enzymatic, physical and chemical effects. Such functional effects can be measured by any means known to those skilled in the art, e.g., changes in spectroscopic characteristics (e.g., fluorescence, absorbance, refractive index), hydrodynamic (e.g., shape), chromatographic, or solubility properties for the protein, measuring inducible markers or transcriptional activation of the prostate cancer protein; measuring binding activity or binding assays, e.g. binding to antibodies or other ligands, and measuring cellular proliferation. Determination of the functional effect of a compound on prostate cancer can also be performed using prostate cancer assays known to those of skill in the art such as an *in vitro* assays, e.g., cell growth on soft agar; anchorage dependence; contact inhibition and density limitation of growth; cellular proliferation; cellular transformation; growth factor or serum dependence; tumor specific marker levels; invasiveness into Matrigel; tumor growth and metastasis *in vivo*; mRNA and protein

expression in cells undergoing metastasis, and other characteristics of prostate cancer cells. The functional effects can be evaluated by many means known to those skilled in the art, e.g., microscopy for quantitative or qualitative measures of alterations in morphological features, measurement of changes in RNA or protein levels for prostate cancer-associated sequences, measurement of RNA stability, identification of downstream or reporter gene expression (CAT, luciferase, β -gal, GFP and the like), e.g., via chemiluminescence, fluorescence, colorimetric reactions, antibody binding, inducible markers, and ligand binding assays.

“Inhibitors”, “activators”, and “modulators” of prostate cancer polynucleotide and polypeptide sequences are used to refer to activating, inhibitory, or modulating molecules or compounds identified using *in vitro* and *in vivo* assays of prostate cancer polynucleotide and polypeptide sequences. Inhibitors are compounds that, e.g., bind to, partially or totally block activity, decrease, prevent, delay activation, inactivate, desensitize, or down regulate the activity or expression of prostate cancer proteins, e.g., antagonists. Antisense nucleic acids may seem to inhibit expression and subsequent function of the protein. “Activators” are compounds that increase, open, activate, facilitate, enhance activation, sensitize, agonize, or up regulate prostate cancer protein activity. Inhibitors, activators, or modulators also include genetically modified versions of prostate cancer proteins, e.g., versions with altered activity, as well as naturally occurring and synthetic ligands, antagonists, agonists, antibodies, small chemical molecules and the like. Such assays for inhibitors and activators include, e.g., expressing the prostate cancer protein *in vitro*, in cells, or cell membranes, applying putative modulator compounds, and then determining the functional effects on activity, as described above. Activators and inhibitors of prostate cancer can also be identified by incubating prostate cancer cells with the test compound and determining increases or decreases in the expression of 1 or more prostate cancer proteins, e.g., 1; 2, 3, 4, 5, 10, 15, 20, 25, 30, 40, 50 or more prostate cancer proteins, such as prostate cancer proteins encoded by the sequences set out in Tables 1-16.

Samples or assays comprising prostate cancer proteins that are treated with a potential activator, inhibitor, or modulator are compared to control samples without the inhibitor, activator, or modulator to examine the extent of inhibition. Control samples (untreated with inhibitors) are assigned a relative protein activity value of 100%. Inhibition of a polypeptide is achieved when the activity value relative to the control is about 80%,

preferably 50%, more preferably 25-0%. Activation of a prostate cancer polypeptide is achieved when the activity value relative to the control (untreated with activators) is 110%, more preferably 150%, more preferably 200-500% (i.e., two to five fold higher relative to the control), more preferably 1000-3000% higher.

5 The phrase "changes in cell growth" refers to any change in cell growth and proliferation characteristics *in vitro* or *in vivo*, such as formation of foci, anchorage independence, semi-solid or soft agar growth, changes in contact inhibition and density limitation of growth, loss of growth factor or serum requirements, changes in cell morphology, gaining or losing immortalization, gaining or losing tumor specific markers, 10 ability to form or suppress tumors when injected into suitable animal hosts, and/or immortalization of the cell. *See, e.g., Freshney, Culture of Animal Cells a Manual of Basic Technique* pp. 231-241 (3rd ed. 1994).

"Tumor cell" refers to precancerous, cancerous, and normal cells in a tumor.

"Cancer cells," "transformed" cells or "transformation" in tissue culture, refers 15 to spontaneous or induced phenotypic changes that do not necessarily involve the uptake of new genetic material. Although transformation can arise from infection with a transforming virus and incorporation of new genomic DNA, or uptake of exogenous DNA, it can also arise spontaneously or following exposure to a carcinogen, thereby mutating an endogenous gene. Transformation is associated with phenotypic changes, such as immortalization of cells, 20 aberrant growth control, nonmorphological changes, and/or malignancy (*see, Freshney, Culture of Animal Cells a Manual of Basic Technique* (3rd ed. 1994)).

"Antibody" refers to a polypeptide comprising a framework region from an immunoglobulin gene or fragments thereof that specifically binds and recognizes an antigen. The recognized immunoglobulin genes include the kappa, lambda, alpha, gamma, delta, 25 epsilon, and mu constant region genes, as well as the myriad immunoglobulin variable region genes. Light chains are classified as either kappa or lambda. Heavy chains are classified as gamma, mu, alpha, delta, or epsilon, which in turn define the immunoglobulin classes, IgG, IgM, IgA, IgD and IgE, respectively. Typically, the antigen-binding region of an antibody or its functional equivalent will be most critical in specificity and affinity of binding. *See Paul,* 30 *Fundamental Immunology.*

An exemplary immunoglobulin (antibody) structural unit comprises a tetramer. Each tetramer is composed of two identical pairs of polypeptide chains, each pair having one "light" (about 25 kD) and one "heavy" chain (about 50-70 kD). The N-terminus of each chain defines a variable region of about 100 to 110 or more amino acids primarily responsible for antigen recognition. The terms variable light chain (V_L) and variable heavy chain (V_H) refer to these light and heavy chains respectively.

Antibodies exist, e.g., as intact immunoglobulins or as a number of well-characterized fragments produced by digestion with various peptidases. Thus, e.g., pepsin digests an antibody below the disulfide linkages in the hinge region to produce $F(ab)'_2$, a dimer of Fab which itself is a light chain joined to V_H-C_H1 by a disulfide bond. The $F(ab)'_2$ may be reduced under mild conditions to break the disulfide linkage in the hinge region, thereby converting the $F(ab)'_2$ dimer into an Fab' monomer. The Fab' monomer is essentially Fab with part of the hinge region (*see Fundamental Immunology* (Paul ed., 3d ed. 1993)). While various antibody fragments are defined in terms of the digestion of an intact antibody, one of skill will appreciate that such fragments may be synthesized *de novo* either chemically or by using recombinant DNA methodology. Thus, the term antibody, as used herein, also includes antibody fragments either produced by the modification of whole antibodies, or those synthesized *de novo* using recombinant DNA methodologies (e.g., single chain Fv) or those identified using phage display libraries (*see, e.g., McCafferty et al., Nature* 348:552-554 (1990)).

For preparation of antibodies, e.g., recombinant, monoclonal, or polyclonal antibodies, many technique known in the art can be used (*see, e.g., Kohler & Milstein, Nature* 256:495-497 (1975); Kozbor *et al., Immunology Today* 4:72 (1983); Cole *et al.*, pp. 77-96 in *Monoclonal Antibodies and Cancer Therapy* (1985); Coligan, *Current Protocols in Immunology* (1991); Harlow & Lane, *Antibodies, A Laboratory Manual* (1988); and Goding, *Monoclonal Antibodies: Principles and Practice* (2d ed. 1986)). Techniques for the production of single chain antibodies (U.S. Patent 4,946,778) can be adapted to produce antibodies to polypeptides of this invention. Also, transgenic mice, or other organisms such as other mammals, may be used to express humanized antibodies. Alternatively, phage display technology can be used to identify antibodies and heteromeric Fab fragments that

specifically bind to selected antigens (*see, e.g., McCafferty et al., Nature* 348:552-554 (1990); Marks *et al., Biotechnology* 10:779-783 (1992)).

A "chimeric antibody" is an antibody molecule in which (a) the constant region, or a portion thereof, is altered, replaced or exchanged so that the antigen binding site (variable region) is linked to a constant region of a different or altered class, effector function and/or species, or an entirely different molecule which confers new properties to the chimeric antibody, *e.g.,* an enzyme, toxin, hormone, growth factor, drug, etc.; or (b) the variable region, or a portion thereof, is altered, replaced or exchanged with a variable region having a different or altered antigen specificity.

Identification of prostate cancer-associated sequences

In one aspect, the expression levels of genes are determined in different patient samples for which diagnosis information is desired, to provide expression profiles. An expression profile of a particular sample is essentially a "fingerprint" of the state of the sample; while two states may have any particular gene similarly expressed, the evaluation of a number of genes simultaneously allows the generation of a gene expression profile that is characteristic of the state of the cell. That is, normal tissue (*e.g.,* normal prostate or other tissue) may be distinguished from cancerous or metastatic cancerous tissue of the prostate, or prostate cancer tissue or metastatic prostate cancerous tissue can be compared with tissue samples of prostate and other tissues from surviving cancer patients. By comparing expression profiles of tissue in known different prostate cancer states, information regarding which genes are important (including both up- and down-regulation of genes) in each of these states is obtained.

The identification of sequences that are differentially expressed in prostate cancer versus non-prostate cancer tissue allows the use of this information in a number of ways. For example, a particular treatment regime may be evaluated: does a chemotherapeutic drug act to down-regulate prostate cancer, and thus tumor growth or recurrence, in a particular patient. Similarly, diagnosis and treatment outcomes may be done or confirmed by comparing patient samples with the known expression profiles. Metastatic tissue can also be analyzed to determine the stage of prostate cancer in the tissue. Furthermore, these gene expression profiles (or individual genes) allow screening of drug candidates with an eye to

mimicking or altering a particular expression profile; e.g., screening can be done for drugs that suppress the prostate cancer expression profile. This may be done by making biochips comprising sets of the important prostate cancer genes, which can then be used in these screens. These methods can also be done on the protein basis; that is, protein expression levels of the prostate cancer proteins can be evaluated for diagnostic purposes or to screen candidate agents. In addition, the prostate cancer nucleic acid sequences can be administered for gene therapy purposes, including the administration of antisense nucleic acids, or the prostate cancer proteins (including antibodies and other modulators thereof) administered as therapeutic drugs.

Thus the present invention provides nucleic acid and protein sequences that are differentially expressed in prostate cancer, herein termed "prostate cancer sequences." As outlined below, prostate cancer sequences include those that are up-regulated (i.e., expressed at a higher level) in prostate cancer, as well as those that are down-regulated (i.e., expressed at a lower level). In a preferred embodiment, the prostate cancer sequences are from humans; however, as will be appreciated by those in the art, prostate cancer sequences from other organisms may be useful in animal models of disease and drug evaluation; thus, other prostate cancer sequences are provided, from vertebrates, including mammals, including rodents (rats, mice, hamsters, guinea pigs, etc.), primates, farm animals (including sheep, goats, pigs, cows, horses, etc.) and pets, e.g., (dogs, cats, etc.). Prostate cancer sequences from other organisms may be obtained using the techniques outlined below.

Prostate cancer sequences can include both nucleic acid and amino acid sequences. As will be appreciated by those in the art and is more fully outlined below, prostate cancer nucleic acid sequences are useful in a variety of applications, including diagnostic applications, which will detect naturally occurring nucleic acids, as well as screening applications; e.g., biochips comprising nucleic acid probes or PCR microtiter plates with selected probes to the prostate cancer sequences can be generated.

A prostate cancer sequence can be initially identified by substantial nucleic acid and/or amino acid sequence homology to the prostate cancer sequences outlined herein. Such homology can be based upon the overall nucleic acid or amino acid sequence, and is generally determined as outlined below, using either homology programs or hybridization conditions.

For identifying prostate cancer-associated sequences, the prostate cancer screen typically includes comparing genes identified in different tissues, e.g., normal and cancerous tissues, or tumor tissue samples from patients who have metastatic disease vs. non metastatic tissue. Other suitable tissue comparisons include comparing prostate cancer samples with metastatic cancer samples from other cancers, such as lung, breast, gastrointestinal cancers, ovarian, etc. Samples of different stages of prostate cancer, e.g., survivor tissue, drug resistant states, and tissue undergoing metastasis, are applied to biochips comprising nucleic acid probes. The samples are first microdissected, if applicable, and treated as is known in the art for the preparation of mRNA. Suitable biochips are commercially available, e.g. from Affymetrix. Gene expression profiles as described herein are generated and the data analyzed.

In one embodiment, the genes showing changes in expression as between normal and disease states are compared to genes expressed in other normal tissues, preferably normal prostate, but also including, and not limited to lung, heart, brain, liver, breast, kidney, muscle, colon, small intestine, large intestine, spleen, bone and placenta. In a preferred embodiment, those genes identified during the prostate cancer screen that are expressed in any significant amount in other tissues are removed from the profile, although in some embodiments, this is not necessary. That is, when screening for drugs, it is usually preferable that the target be disease specific, to minimize possible side effects.

In a preferred embodiment, prostate cancer sequences are those that are up-regulated in prostate cancer; that is, the expression of these genes is higher in the prostate cancer tissue as compared to non-cancerous tissue. "Up-regulation" as used herein often means at least about a two-fold change, preferably at least about a three fold change, with at least about five-fold or higher being preferred. All unigene cluster identification numbers and accession numbers herein are for the GenBank sequence database and the sequences of the accession numbers are hereby expressly incorporated by reference. GenBank is known in the art, *see, e.g.*, Benson, DA, *et al.*, Nucleic Acids Research 26:1-7 (1998) and <http://www.ncbi.nlm.nih.gov/>. Sequences are also available in other databases, e.g., European Molecular Biology Laboratory (EMBL) and DNA Database of Japan (DDBJ).

In another preferred embodiment, prostate cancer sequences are those that are down-regulated in prostate cancer; that is, the expression of these genes is lower in prostate

cancer tissue as compared to non-cancerous tissue (*see, e.g.*, Tables 8, 12 and 14). "Down-regulation" as used herein often means at least about a 1.5-fold change more preferably a two-fold change, preferably at least about a three fold change, with at least about five-fold or higher being most preferred.

5

Informatics

The ability to identify genes that are over or under expressed in prostate cancer can additionally provide high-resolution, high-sensitivity datasets which can be used in the areas of diagnostics, therapeutics, drug development, pharmacogenetics, protein structure, biosensor development, and other related areas. For example, the expression profiles can be used in diagnostic or prognostic evaluation of patients with prostate cancer. Or as another example, subcellular toxicological information can be generated to better direct drug structure and activity correlation (*see* Anderson, *Pharmaceutical Proteomics: Targets, Mechanism, and Function*, paper presented at the IBC Proteomics conference, Coronado, CA (June 11-12, 1998)). Subcellular toxicological information can also be utilized in a biological sensor device to predict the likely toxicological effect of chemical exposures and likely tolerable exposure thresholds (*see* U.S. Patent No. 5,811,231). Similar advantages accrue from datasets relevant to other biomolecules and bioactive agents (e.g., nucleic acids, saccharides, lipids, drugs, and the like).

Thus, in another embodiment, the present invention provides a database that includes at least one set of assay data. The data contained in the database is acquired, e.g., using array analysis either singly or in a library format. The database can be in substantially any form in which data can be maintained and transmitted, but is preferably an electronic database. The electronic database of the invention can be maintained on any electronic device allowing for the storage of and access to the database, such as a personal computer, but is preferably distributed on a wide area network, such as the World Wide Web.

The focus of the present section on databases that include peptide sequence data is for clarity of illustration only. It will be apparent to those of skill in the art that similar databases can be assembled for any assay data acquired using an assay of the invention.

30

The compositions and methods for identifying and/or quantitating the relative and/or absolute abundance of a variety of molecular and macromolecular species from a biological sample undergoing prostate cancer, i.e., the identification of prostate cancer-associated sequences described herein, provide an abundance of information, which can be correlated with pathological conditions, predisposition to disease, drug testing, therapeutic monitoring, gene-disease causal linkages, identification of correlates of immunity and physiological status, among others. Although the data generated from the assays of the invention is suited for manual review and analysis, in a preferred embodiment, prior data processing using high-speed computers is utilized.

An array of methods for indexing and retrieving biomolecular information is known in the art. For example, U.S. Patents 6,023,659 and 5,966,712 disclose a relational database system for storing biomolecular sequence information in a manner that allows sequences to be catalogued and searched according to one or more protein function hierarchies. U.S. Patent 5,953,727 discloses a relational database having sequence records containing information in a format that allows a collection of partial-length DNA sequences to be catalogued and searched according to association with one or more sequencing projects for obtaining full-length sequences from the collection of partial length sequences. U.S. Patent 5,706,498 discloses a gene database retrieval system for making a retrieval of a gene sequence similar to a sequence data item in a gene database based on the degree of similarity between a key sequence and a target sequence. U.S. Patent 5,538,897 discloses a method using mass spectroscopy fragmentation patterns of peptides to identify amino acid sequences in computer databases by comparison of predicted mass spectra with experimentally-derived mass spectra using a closeness-of-fit measure. U.S. Patent 5,926,818 discloses a multi-dimensional database comprising a functionality for multi-dimensional data analysis described as on-line analytical processing (OLAP), which entails the consolidation of projected and actual data according to more than one consolidation path or dimension. U.S. Patent 5,295,261 reports a hybrid database structure in which the fields of each database record are divided into two classes, navigational and informational data, with navigational fields stored in a hierarchical topological map which can be viewed as a tree structure or as the merger of two or more such tree structures.

See also Mount *et al.*, *Bioinformatics* (2001); *Biological Sequence Analysis: Probabilistic Models of Proteins and Nucleic Acids* (Durbin *et al.*, eds., 1999); *Bioinformatics: A Practical Guide to the Analysis of Genes and Proteins* (Baxevanis & Ouellette eds., 1998)); Rashidi & Buehler, *Bioinformatics: Basic Applications in Biological Science and Medicine* (1999); *Introduction to Computational Molecular Biology* (Setubal *et al.*, eds 1997); *Bioinformatics: Methods and Protocols* (Misener & Krawetz, eds, 2000); *Bioinformatics: Sequence, Structure, and Databanks: A Practical Approach* (Higgins & Taylor, eds., 2000); Brown, *Bioinformatics: A Biologist's Guide to Biocomputing and the Internet* (2001); Han & Kamber, *Data Mining: Concepts and Techniques* (2000); and
10 Waterman, *Introduction to Computational Biology: Maps, Sequences, and Genomes* (1995).

The present invention provides a computer database comprising a computer and software for storing in computer-retrievable form assay data records cross-tabulated, e.g., with data specifying the source of the target-containing sample from which each sequence specificity record was obtained.

15 In an exemplary embodiment, at least one of the sources of target-containing sample is from a control tissue sample known to be free of pathological disorders. In a variation, at least one of the sources is a known pathological tissue specimen, e.g., a neoplastic lesion or another tissue specimen to be analyzed for prostate cancer. In another variation, the assay records cross-tabulate one or more of the following parameters for each
20 target species in a sample: (1) a unique identification code, which can include, e.g., a target molecular structure and/or characteristic separation coordinate (e.g., electrophoretic coordinates); (2) sample source; and (3) absolute and/or relative quantity of the target species present in the sample.

The invention also provides for the storage and retrieval of a collection of
25 target data in a computer data storage apparatus, which can include magnetic disks, optical disks, magneto-optical disks, DRAM, SRAM, SGRAM, SDRAM, RDRAM, DDR RAM, magnetic bubble memory devices, and other data storage devices, including CPU registers and on-CPU data storage arrays. Typically, the target data records are stored as a bit pattern in an array of magnetic domains on a magnetizable medium or as an array of charge states or
30 transistor gate states, such as an array of cells in a DRAM device (e.g., each cell comprised of a transistor and a charge storage area, which may be on the transistor). In one embodiment,

the invention provides such storage devices, and computer systems built therewith, comprising a bit pattern encoding a protein expression fingerprint record comprising unique identifiers for at least 10 target data records cross-tabulated with target source.

When the target is a peptide or nucleic acid, the invention preferably provides
5 a method for identifying related peptide or nucleic acid sequences, comprising performing a computerized comparison between a peptide or nucleic acid sequence assay record stored in or retrieved from a computer storage device or database and at least one other sequence. The comparison can include a sequence analysis or comparison algorithm or computer program embodiment thereof (e.g., FASTA, TFASTA, GAP, BESTFIT) and/or the comparison may
10 be of the relative amount of a peptide or nucleic acid sequence in a pool of sequences determined from a polypeptide or nucleic acid sample of a specimen.

The invention also preferably provides a magnetic disk, such as an IBM-compatible (DOS, Windows, Windows95/98/2000, Windows NT, OS/2) or other format (e.g., Linux, SunOS, Solaris, AIX, SCO Unix, VMS, MV, Macintosh, etc.) floppy diskette or
15 hard (fixed, Winchester) disk drive, comprising a bit pattern encoding data from an assay of the invention in a file format suitable for retrieval and processing in a computerized sequence analysis, comparison, or relative quantitation method.

The invention also provides a network, comprising a plurality of computing devices linked via a data link, such as an Ethernet cable (coax or 10BaseT), telephone line,
20 ISDN line, wireless network, optical fiber, or other suitable signal transmission medium, whereby at least one network device (e.g., computer, disk array, etc.) comprises a pattern of magnetic domains (e.g., magnetic disk) and/or charge domains (e.g., an array of DRAM cells) composing a bit pattern encoding data acquired from an assay of the invention.

The invention also provides a method for transmitting assay data that includes
25 generating an electronic signal on an electronic communications device, such as a modem, ISDN terminal adapter, DSL, cable modem, ATM switch, or the like, wherein the signal includes (in native or encrypted format) a bit pattern encoding data from an assay or a database comprising a plurality of assay results obtained by the method of the invention.

In a preferred embodiment, the invention provides a computer system for
30 comparing a query target to a database containing an array of data structures, such as an assay result obtained by the method of the invention, and ranking database targets based on the

degree of identity and gap weight to the target data. A central processor is preferably initialized to load and execute the computer program for alignment and/or comparison of the assay results. Data for a query target is entered into the central processor via an I/O device. Execution of the computer program results in the central processor retrieving the assay data
5 from the data file, which comprises a binary description of an assay result.

The target data or record and the computer program can be transferred to secondary memory, which is typically random access memory (e.g., DRAM, SRAM, SGRAM, or SDRAM). Targets are ranked according to the degree of correspondence between a selected assay characteristic (e.g., binding to a selected affinity moiety) and the
10 same characteristic of the query target and results are output via an I/O device. For example, a central processor can be a conventional computer (e.g., Intel Pentium, PowerPC, Alpha, PA-8000, SPARC, MIPS 4400, MIPS 10000, VAX, etc.); a program can be a commercial or public domain molecular biology software package (e.g., UWGCG Sequence Analysis Software, Darwin); a data file can be an optical or magnetic disk, a data server, a memory
15 device (e.g., DRAM, SRAM, SGRAM, SDRAM, EPROM, bubble memory, flash memory, etc.); an I/O device can be a terminal comprising a video display and a keyboard, a modem, an ISDN terminal adapter, an Ethernet port, a punched card reader, a magnetic strip reader, or other suitable I/O device.

The invention also preferably provides the use of a computer system, such as
20 that described above, which comprises: (1) a computer; (2) a stored bit pattern encoding a collection of peptide sequence specificity records obtained by the methods of the invention, which may be stored in the computer; (3) a comparison target, such as a query target; and (4) a program for alignment and comparison, typically with rank-ordering of comparison results on the basis of computed similarity values.

25

Characteristics of prostate cancer-associated proteins

Prostate cancer proteins of the present invention may be classified as secreted proteins, transmembrane proteins or intracellular proteins. In one embodiment, the prostate cancer protein is an intracellular protein. Intracellular proteins may be found in the
30 cytoplasm and/or in the nucleus. Intracellular proteins are involved in all aspects of cellular function and replication (including, e.g., signaling pathways); aberrant expression of such

proteins often results in unregulated or disregulated cellular processes (*see, e.g., Molecular Biology of the Cell* (Alberts, ed., 3rd ed., 1994). For example, many intracellular proteins have enzymatic activity such as protein kinase activity, protein phosphatase activity, protease activity, nucleotide cyclase activity, polymerase activity and the like. Intracellular proteins
5 also serve as docking proteins that are involved in organizing complexes of proteins, or targeting proteins to various subcellular localizations, and are involved in maintaining the structural integrity of organelles.

An increasingly appreciated concept in characterizing proteins is the presence in the proteins of one or more motifs for which defined functions have been attributed. In
10 addition to the highly conserved sequences found in the enzymatic domain of proteins, highly conserved sequences have been identified in proteins that are involved in protein-protein interaction. For example, Src-homology-2 (SH2) domains bind tyrosine-phosphorylated targets in a sequence dependent manner. PTB domains, which are distinct from SH2 domains, also bind tyrosine phosphorylated targets. SH3 domains bind to proline-rich
15 targets. In addition, PH domains, tetratricopeptide repeats and WD domains to name only a few, have been shown to mediate protein-protein interactions. Some of these may also be involved in binding to phospholipids or other second messengers. As will be appreciated by one of ordinary skill in the art, these motifs can be identified on the basis of primary sequence; thus, an analysis of the sequence of proteins may provide insight into both the
20 enzymatic potential of the molecule and/or molecules with which the protein may associate. One useful database is Pfam (protein families), which is a large collection of multiple sequence alignments and hidden Markov models covering many common protein domains. Versions are available via the internet from Washington University in St. Louis, the Sanger Center in England, and the Karolinska Institute in Sweden (*see, e.g., Bateman et al., Nuc.*
25 *Acids Res.* 28:263-266 (2000); Sonnhammer *et al., Proteins* 28:405-420 (1997); Bateman *et al., Nuc. Acids Res.* 27:260-262 (1999); and Sonnhammer *et al., Nuc. Acids Res.* 26:320-322- (1998)).

In another embodiment, the prostate cancer sequences are transmembrane proteins. Transmembrane proteins are molecules that span a phospholipid bilayer of a cell.
30 They may have an intracellular domain, an extracellular domain, or both. The intracellular domains of such proteins may have a number of functions including those already described

for intracellular proteins. For example, the intracellular domain may have enzymatic activity and/or may serve as a binding site for additional proteins. Frequently the intracellular domain of transmembrane proteins serves both roles. For example certain receptor tyrosine kinases have both protein kinase activity and SH2 domains. In addition, autophosphorylation of tyrosines on the receptor molecule itself, creates binding sites for additional SH2 domain containing proteins.

Transmembrane proteins may contain from one to many transmembrane domains. For example, receptor tyrosine kinases, certain cytokine receptors, receptor guanylyl cyclases and receptor serine/threonine protein kinases contain a single transmembrane domain. However, various other proteins including channels and adenylyl cyclases contain numerous transmembrane domains. Many important cell surface receptors such as G protein coupled receptors (GPCRs) are classified as "seven transmembrane domain" proteins, as they contain 7 membrane spanning regions. Characteristics of transmembrane domains include approximately 20 consecutive hydrophobic amino acids that may be followed by charged amino acids. Therefore, upon analysis of the amino acid sequence of a particular protein, the localization and number of transmembrane domains within the protein may be predicted (*see, e.g.* PSORT web site <http://psort.nibb.ac.jp/>). Important transmembrane protein receptors include, but are not limited to the insulin receptor, insulin-like growth factor receptor, human growth hormone receptor, glucose transporters, transferrin receptor, epidermal growth factor receptor, low density lipoprotein receptor, epidermal growth factor receptor, leptin receptor, interleukin receptors, e.g. IL-1 receptor, IL-2 receptor,

The extracellular domains of transmembrane proteins are diverse; however, conserved motifs are found repeatedly among various extracellular domains. Conserved structure and/or functions have been ascribed to different extracellular motifs. Many extracellular domains are involved in binding to other molecules. In one aspect, extracellular domains are found on receptors. Factors that bind the receptor domain include circulating ligands, which may be peptides, proteins, or small molecules such as adenosine and the like. For example, growth factors such as EGF, FGF and PDGF are circulating growth factors that bind to their cognate receptors to initiate a variety of cellular responses. Other factors include cytokines, mitogenic factors, neurotrophic factors and the like. Extracellular domains also

bind to cell-associated molecules. In this respect, they mediate cell-cell interactions. Cell-associated ligands can be tethered to the cell, e.g., via a glycosylphosphatidylinositol (GPI) anchor, or may themselves be transmembrane proteins. Extracellular domains also associate with the extracellular matrix and contribute to the maintenance of the cell structure.

5 Prostate cancer proteins that are transmembrane are particularly preferred in the present invention as they are readily accessible targets for immunotherapeutics, as are described herein. In addition, as outlined below, transmembrane proteins can be also useful in imaging modalities. Antibodies may be used to label such readily accessible proteins *in situ*. Alternatively, antibodies can also label intracellular proteins, in which case samples are
10 typically permeabilized to provide access to intracellular proteins.

It will also be appreciated by those in the art that a transmembrane protein can be made soluble by removing transmembrane sequences, e.g., through recombinant methods. Furthermore, transmembrane proteins that have been made soluble can be made to be secreted through recombinant means by adding an appropriate signal sequence.

15 In another embodiment, the prostate cancer proteins are secreted proteins; the secretion of which can be either constitutive or regulated. These proteins have a signal peptide or signal sequence that targets the molecule to the secretory pathway. Secreted proteins are involved in numerous physiological events; by virtue of their circulating nature, they serve to transmit signals to various other cell types. The secreted protein may function in
20 an autocrine manner (acting on the cell that secreted the factor), a paracrine manner (acting on cells in close proximity to the cell that secreted the factor) or an endocrine manner (acting on cells at a distance). Thus secreted molecules find use in modulating or altering numerous aspects of physiology. Prostate cancer proteins that are secreted proteins are particularly preferred in the present invention as they serve as good targets for diagnostic markers, e.g.,
25 for blood, plasma, serum, or stool tests.

Use of prostate cancer nucleic acids

As described above, prostate cancer sequence is initially identified by substantial nucleic acid and/or amino acid sequence homology or linkage to the prostate
30 cancer sequences outlined herein. Such homology can be based upon the overall nucleic acid or amino acid sequence, and is generally determined as outlined below, using either

homology programs or hybridization conditions. Typically, linked sequences on a mRNA are found on the same molecule.

The prostate cancer nucleic acid sequences of the invention, e.g., the sequences in Tables 1-16, can be fragments of larger genes, i.e., they are nucleic acid segments. "Genes" in this context includes coding regions, non-coding regions, and mixtures of coding and non-coding regions. Accordingly, as will be appreciated by those in the art, using the sequences provided herein, extended sequences, in either direction, of the prostate cancer genes can be obtained, using techniques well known in the art for cloning either longer sequences or the full length sequences; see Ausubel, *et al.*, *supra*. Much can be done by informatics and many sequences can be clustered to include multiple sequences corresponding to a single gene, e.g., systems such as UniGene (see, <http://www.ncbi.nlm.nih.gov/UniGene/>).

Once the prostate cancer nucleic acid is identified, it can be cloned and, if necessary, its constituent parts recombined to form the entire prostate cancer nucleic acid coding regions or the entire mRNA sequence. Once isolated from its natural source, e.g., contained within a plasmid or other vector or excised therefrom as a linear nucleic acid segment, the recombinant prostate cancer nucleic acid can be further-used as a probe to identify and isolate other prostate cancer nucleic acids, e.g., extended coding regions. It can also be used as a "precursor" nucleic acid to make modified or variant prostate cancer nucleic acids and proteins.

The prostate cancer nucleic acids of the present invention are used in several ways. In a first embodiment, nucleic acid probes to the prostate cancer nucleic acids are made and attached to biochips to be used in screening and diagnostic methods, as outlined below, or for administration, e.g., for gene therapy, vaccine, and/or antisense applications. Alternatively, the prostate cancer nucleic acids that include coding regions of prostate cancer proteins can be put into expression vectors for the expression of prostate cancer proteins, again for screening purposes or for administration to a patient.

In a preferred embodiment, nucleic acid probes to prostate cancer nucleic acids (both the nucleic acid sequences outlined in the figures and/or the complements thereof) are made. The nucleic acid probes attached to the biochip are designed to be substantially complementary to the prostate cancer nucleic acids, i.e. the target sequence (either the target

sequence of the sample or to other probe sequences, e.g., in sandwich assays), such that hybridization of the target sequence and the probes of the present invention occurs. As outlined below, this complementarity need not be perfect; there may be any number of base pair mismatches which will interfere with hybridization between the target sequence and the single stranded nucleic acids of the present invention. However, if the number of mutations is so great that no hybridization can occur under even the least stringent of hybridization conditions, the sequence is not a complementary target sequence. Thus, by "substantially complementary" herein is meant that the probes are sufficiently complementary to the target sequences to hybridize under normal reaction conditions, particularly high stringency conditions, as outlined herein.

A nucleic acid probe is generally single stranded but can be partially single and partially double stranded. The strandedness of the probe is dictated by the structure, composition, and properties of the target sequence. In general, the nucleic acid probes range from about 8 to about 100 bases long, with from about 10 to about 80 bases being preferred, and from about 30 to about 50 bases being particularly preferred. That is, generally whole genes are not used. In some embodiments, much longer nucleic acids can be used, up to hundreds of bases.

In a preferred embodiment, more than one probe per sequence is used, with either overlapping probes or probes to different sections of the target being used. That is, two, three, four or more probes, with three being preferred, are used to build in a redundancy for a particular target. The probes can be overlapping (i.e., have some sequence in common), or separate. In some cases, PCR primers may be used to amplify signal for higher sensitivity.

As will be appreciated by those in the art, nucleic acids can be attached or immobilized to a solid support in a wide variety of ways. By "immobilized" and grammatical equivalents herein is meant the association or binding between the nucleic acid probe and the solid support is sufficient to be stable under the conditions of binding, washing, analysis, and removal as outlined below. The binding can typically be covalent or non-covalent. By "non-covalent binding" and grammatical equivalents herein is meant one or more of electrostatic, hydrophilic, and hydrophobic interactions. Included in non-covalent binding is the covalent attachment of a molecule, such as, streptavidin to the support and the non-covalent binding of the biotinylated probe to the streptavidin. By "covalent binding" and grammatical

equivalents herein is meant that the two moieties, the solid support and the probe, are attached by at least one bond, including sigma bonds, pi bonds and coordination bonds. Covalent bonds can be formed directly between the probe and the solid support or can be formed by a cross linker or by inclusion of a specific reactive group on either the solid support or the probe or both molecules. Immobilization may also involve a combination of covalent and non-covalent interactions.

In general, the probes are attached to the biochip in a wide variety of ways, as will be appreciated by those in the art. As described herein, the nucleic acids can either be synthesized first, with subsequent attachment to the biochip, or can be directly synthesized on the biochip.

The biochip comprises a suitable solid substrate. By "substrate" or "solid support" or other grammatical equivalents herein is meant a material that can be modified to contain discrete individual sites appropriate for the attachment or association of the nucleic acid probes and is amenable to at least one detection method. As will be appreciated by those in the art, the number of possible substrates are very large, and include, but are not limited to, glass and modified or functionalized glass, plastics (including acrylics, polystyrene and copolymers of styrene and other materials, polypropylene, polyethylene, polybutylene, polyurethanes, Teflon, etc.), polysaccharides, nylon or nitrocellulose, resins, silica or silica-based materials including silicon and modified silicon, carbon, metals, inorganic glasses, plastics, etc. In general, the substrates allow optical detection and do not appreciably fluoresce. A preferred substrate is described in copending application entitled Reusable Low Fluorescent Plastic Biochip, U.S. Application Serial No. 09/270,214, filed March 15, 1999, herein incorporated by reference in its entirety.

Generally the substrate is planar, although as will be appreciated by those in the art, other configurations of substrates may be used as well. For example, the probes may be placed on the inside surface of a tube, for flow-through sample analysis to minimize sample volume. Similarly, the substrate may be flexible, such as a flexible foam, including closed cell foams made of particular plastics.

In a preferred embodiment, the surface of the biochip and the probe may be derivatized with chemical functional groups for subsequent attachment of the two. Thus, e.g., the biochip is derivatized with a chemical functional group including, but not limited to,

amino groups, carboxy groups, oxo groups and thiol groups, with amino groups being particularly preferred. Using these functional groups, the probes can be attached using functional groups on the probes. For example, nucleic acids containing amino groups can be attached to surfaces comprising amino groups, e.g. using linkers as are known in the art; e.g.,
5 homo-or hetero-bifunctional linkers as are well known (*see* 1994 Pierce Chemical Company catalog, technical section on cross-linkers, pages 155-200). In addition, in some cases, additional linkers, such as alkyl groups (including substituted and heteroalkyl groups) may be used.

In this embodiment, oligonucleotides are synthesized as is known in the art,
10 and then attached to the surface of the solid support. As will be appreciated by those skilled in the art, either the 5' or 3' terminus may be attached to the solid support, or attachment may be via an internal nucleoside.

In another embodiment, the immobilization to the solid support may be very strong, yet non-covalent. For example, biotinylated oligonucleotides can be made, which
15 bind to surfaces covalently coated with streptavidin, resulting in attachment.

Alternatively, the oligonucleotides may be synthesized on the surface, as is known in the art. For example, photoactivation techniques utilizing photopolymerization compounds and techniques are used. In a preferred embodiment, the nucleic acids can be synthesized in situ, using well known photolithographic techniques, such as those described
20 in WO 95/25116; WO 95/35505; U.S. Patent Nos. 5,700,637 and 5,445,934; and references cited within, all of which are expressly incorporated by reference; these methods of attachment form the basis of the Affimetrix GeneChip™ technology.

Often, amplification-based assays are performed to measure the expression level of prostate cancer-associated sequences. These assays are typically performed in
25 conjunction with reverse transcription. In such assays, a prostate cancer-associated nucleic acid sequence acts as a template in an amplification reaction (e.g., Polymerase Chain Reaction, or PCR). In a quantitative amplification, the amount of amplification product will be proportional to the amount of template in the original sample. Comparison to appropriate controls provides a measure of the amount of prostate cancer-associated RNA. Methods of
30 quantitative amplification are well known to those of skill in the art. Detailed protocols for

quantitative PCR are provided, e.g., in Innis *et al.*, *PCR Protocols, A Guide to Methods and Applications* (1990).

In some embodiments, a TaqMan based assay is used to measure expression. TaqMan based assays use a fluorogenic oligonucleotide probe that contains a 5' fluorescent dye and a 3' quenching agent. The probe hybridizes to a PCR product, but cannot itself be extended due to a blocking agent at the 3' end. When the PCR product is amplified in subsequent cycles, the 5' nuclease activity of the polymerase, e.g., AmpliTaq, results in the cleavage of the TaqMan probe. This cleavage separates the 5' fluorescent dye and the 3' quenching agent, thereby resulting in an increase in fluorescence as a function of amplification (see, e.g., literature provided by Perkin-Elmer, e.g., www2.perkin-elmer.com).

Other suitable amplification methods include, but are not limited to, ligase chain reaction (LCR) (see Wu & Wallace, *Genomics* 4:560 (1989), Landegren *et al.*, *Science* 241:1077 (1988), and Barringer *et al.*, *Gene* 89:117 (1990)), transcription amplification (Kwoh *et al.*, *Proc. Natl. Acad. Sci. USA* 86:1173 (1989)), self-sustained sequence replication (Guatelli *et al.*, *Proc. Nat. Acad. Sci. USA* 87:1874 (1990)), dot PCR, and linker adapter PCR, etc.

Expression of prostate cancer proteins from nucleic acids

In a preferred embodiment, prostate cancer nucleic acids, e.g., encoding prostate cancer proteins are used to make a variety of expression vectors to express prostate cancer proteins which can then be used in screening assays, as described below. Expression vectors and recombinant DNA technology are well known to those of skill in the art (see, e.g., Ausubel, *supra*, and *Gene Expression Systems* (Fernandez & Hoeffler, eds, 1999)) and are used to express proteins. The expression vectors may be either self-replicating extrachromosomal vectors or vectors which integrate into a host genome. Generally, these expression vectors include transcriptional and translational regulatory nucleic acid operably linked to the nucleic acid encoding the prostate cancer protein. The term "control sequences" refers to DNA sequences used for the expression of an operably linked coding sequence in a particular host organism. Control sequences that are suitable for prokaryotes, e.g., include a promoter, optionally an operator sequence, and a ribosome binding site. Eukaryotic cells are known to utilize promoters, polyadenylation signals, and enhancers.

Nucleic acid is "operably linked" when it is placed into a functional relationship with another nucleic acid sequence. For example, DNA for a presequence or secretory leader is operably linked to DNA for a polypeptide if it is expressed as a preprotein that participates in the secretion of the polypeptide; a promoter or enhancer is operably linked to a coding sequence if it affects the transcription of the sequence; or a ribosome binding site is operably linked to a coding sequence if it is positioned so as to facilitate translation. Generally, "operably linked" means that the DNA sequences being linked are contiguous, and, in the case of a secretory leader, contiguous and in reading phase. However, enhancers do not have to be contiguous. Linking is typically accomplished by ligation at convenient restriction sites. If such sites do not exist, synthetic oligonucleotide adaptors or linkers are used in accordance with conventional practice. Transcriptional and translational regulatory nucleic acid will generally be appropriate to the host cell used to express the prostate cancer protein. Numerous types of appropriate expression vectors, and suitable regulatory sequences are known in the art for a variety of host cells.

In general, transcriptional and translational regulatory sequences may include, but are not limited to, promoter sequences, ribosomal binding sites, transcriptional start and stop sequences, translational start and stop sequences, and enhancer or activator sequences. In a preferred embodiment, the regulatory sequences include a promoter and transcriptional start and stop sequences.

Promoter sequences encode either constitutive or inducible promoters. The promoters may be either naturally occurring promoters or hybrid promoters. Hybrid promoters, which combine elements of more than one promoter, are also known in the art, and are useful in the present invention.

In addition, an expression vector may comprise additional elements. For example, the expression vector may have two replication systems, thus allowing it to be maintained in two organisms, e.g. in mammalian or insect cells for expression and in a procaryotic host for cloning and amplification. Furthermore, for integrating expression vectors, the expression vector contains at least one sequence homologous to the host cell genome, and preferably two homologous sequences which flank the expression construct. The integrating vector may be directed to a specific locus in the host cell by selecting the

appropriate homologous sequence for inclusion in the vector. Constructs for integrating vectors are well known in the art (e.g., Fernandez & Hoeffler, *supra*).

In addition, in a preferred embodiment, the expression vector contains a selectable marker gene to allow the selection of transformed host cells. Selection genes are well known in the art and will vary with the host cell used.

The prostate cancer proteins of the present invention are produced by culturing a host cell transformed with an expression vector containing nucleic acid encoding a prostate cancer protein, under the appropriate conditions to induce or cause expression of the prostate cancer protein. Conditions appropriate for prostate cancer protein expression will vary with the choice of the expression vector and the host cell, and will be easily ascertained by one skilled in the art through routine experimentation or optimization. For example, the use of constitutive promoters in the expression vector will require optimizing the growth and proliferation of the host cell, while the use of an inducible promoter requires the appropriate growth conditions for induction. In addition, in some embodiments, the timing of the harvest is important. For example, the baculoviral systems used in insect cell expression are lytic viruses, and thus harvest time selection can be crucial for product yield.

Appropriate host cells include yeast, bacteria, archaeobacteria, fungi, and insect and animal cells, including mammalian cells. Of particular interest are *Saccharomyces cerevisiae* and other yeasts, *E. coli*, *Bacillus subtilis*, Sf9 cells, C129 cells, 293 cells, *Neurospora*, BHK, CHO, COS, HeLa cells, HUVEC (human umbilical vein endothelial cells), THP1 cells (a macrophage cell line) and various other human cells and cell lines.

In a preferred embodiment, the prostate cancer proteins are expressed in mammalian cells. Mammalian expression systems are also known in the art, and include retroviral and adenoviral systems. One expression vector system is a retroviral vector system such as is generally described in PCT/US97/01019 and PCT/US97/01048, both of which are hereby expressly incorporated by reference. Of particular use as mammalian promoters are the promoters from mammalian viral genes, since the viral genes are often highly expressed and have a broad host range. Examples include the SV40 early promoter, mouse mammary tumor virus LTR promoter, adenovirus major late promoter, herpes simplex virus promoter, and the CMV promoter (*see, e.g.*, Fernandez & Hoeffler, *supra*). Typically, transcription termination and polyadenylation sequences recognized by mammalian cells are regulatory

regions located 3' to the translation stop codon and thus, together with the promoter elements, flank the coding sequence. Examples of transcription terminator and polyadenylation signals include those derived from SV40.

The methods of introducing exogenous nucleic acid into mammalian hosts, as well as other hosts, is well known in the art, and will vary with the host cell used. Techniques include dextran-mediated transfection, calcium phosphate precipitation, polybrene mediated transfection, protoplast fusion, electroporation, viral infection, encapsulation of the polynucleotide(s) in liposomes, and direct microinjection of the DNA into nuclei.

In a preferred embodiment, prostate cancer proteins are expressed in bacterial systems. Bacterial expression systems are well known in the art. Promoters from bacteriophage may also be used and are known in the art. In addition, synthetic promoters and hybrid promoters are also useful; e.g., the tac promoter is a hybrid of the trp and lac promoter sequences. Furthermore, a bacterial promoter can include naturally occurring promoters of non-bacterial origin that have the ability to bind bacterial RNA polymerase and initiate transcription. In addition to a functioning promoter sequence, an efficient ribosome binding site is desirable. The expression vector may also include a signal peptide sequence that provides for secretion of the prostate cancer protein in bacteria. The protein is either secreted into the growth media (gram-positive bacteria) or into the periplasmic space, located between the inner and outer membrane of the cell (gram-negative bacteria). The bacterial expression vector may also include a selectable marker gene to allow for the selection of bacterial strains that have been transformed. Suitable selection genes include genes which render the bacteria resistant to drugs such as ampicillin, chloramphenicol, erythromycin, kanamycin, neomycin and tetracycline. Selectable markers also include biosynthetic genes, such as those in the histidine, tryptophan and leucine biosynthetic pathways. These components are assembled into expression vectors. Expression vectors for bacteria are well known in the art, and include vectors for *Bacillus subtilis*, *E. coli*, *Streptococcus cremoris*, and *Streptococcus lividans*, among others (e.g., Fernandez & Hoeffler, *supra*). The bacterial expression vectors are transformed into bacterial host cells using techniques well known in the art, such as calcium chloride treatment, electroporation, and others.

In one embodiment, prostate cancer proteins are produced in insect cells. Expression vectors for the transformation of insect cells, and in particular, baculovirus-based expression vectors, are well known in the art.

In a preferred embodiment, prostate cancer protein is produced in yeast cells.

- 5 Yeast expression systems are well known in the art, and include expression vectors for *Saccharomyces cerevisiae*, *Candida albicans* and *C. maltosa*, *Hansenula polymorpha*, *Kluyveromyces fragilis* and *K. lactis*, *Pichia guillerimondii* and *P. pastoris*, *Schizosaccharomyces pombe*, and *Yarrowia lipolytica*.

- 10 The prostate cancer protein may also be made as a fusion protein, using techniques well known in the art. Thus, e.g., for the creation of monoclonal antibodies, if the desired epitope is small, the prostate cancer protein may be fused to a carrier protein to form an immunogen. Alternatively, the prostate cancer protein may be made as a fusion protein to increase expression, or for other reasons. For example, when the prostate cancer protein is a prostate cancer peptide, the nucleic acid encoding the peptide may be linked to other nucleic acid for expression purposes.

- 15 In a preferred embodiment, the prostate cancer protein is purified or isolated after expression. Prostate cancer proteins may be isolated or purified in a variety of ways known to those skilled in the art depending on what other components are present in the sample. Standard purification methods include electrophoretic, molecular, immunological and chromatographic techniques, including ion exchange, hydrophobic, affinity, and reverse-phase HPLC chromatography, and chromatofocusing. For example, the prostate cancer protein may be purified using a standard anti-prostate cancer protein antibody column. Ultrafiltration and diafiltration techniques, in conjunction with protein concentration, are also useful. For general guidance in suitable purification techniques, see Scopes, *Protein Purification* (1982). The degree of purification necessary will vary depending on the use of the prostate cancer protein. In some instances no purification will be necessary.

- 25 Once expressed and purified if necessary, the prostate cancer proteins and nucleic acids are useful in a number of applications. They may be used as immunoselection reagents, as vaccine reagents, as screening agents, etc.

30

Variants of prostate cancer proteins

In one embodiment, the prostate cancer proteins are derivative or variant prostate cancer proteins as compared to the wild-type sequence. That is, as outlined more fully below, the derivative prostate cancer peptide will often contain at least one amino acid substitution, deletion or insertion, with amino acid substitutions being particularly preferred. The amino acid substitution, insertion or deletion may occur at any residue within the prostate cancer peptide.

Also included within one embodiment of prostate cancer proteins of the present invention are amino acid sequence variants. These variants typically fall into one or more of three classes: substitutional, insertional or deletional variants. These variants ordinarily are prepared by site specific mutagenesis of nucleotides in the DNA encoding the prostate cancer protein, using cassette or PCR mutagenesis or other techniques well known in the art, to produce DNA encoding the variant, and thereafter expressing the DNA in recombinant cell culture as outlined above. However, variant prostate cancer protein fragments having up to about 100-150 residues may be prepared by in vitro synthesis using established techniques. Amino acid sequence variants are characterized by the predetermined nature of the variation, a feature that sets them apart from naturally occurring allelic or interspecies variation of the prostate cancer protein amino acid sequence. The variants typically exhibit the same qualitative biological activity as the naturally occurring analogue, although variants can also be selected which have modified characteristics as will be more fully outlined below.

While the site or region for introducing an amino acid sequence variation is predetermined, the mutation per se need not be predetermined. For example, in order to optimize the performance of a mutation at a given site, random mutagenesis may be conducted at the target codon or region and the expressed prostate cancer variants screened for the optimal combination of desired activity. Techniques for making substitution mutations at predetermined sites in DNA having a known sequence are well known, e.g., M13 primer mutagenesis and PCR mutagenesis. Screening of the mutants is done using assays of prostate cancer protein activities.

Amino acid substitutions are typically of single residues; insertions usually will be on the order of from about 1 to 20 amino acids, although considerably larger

insertions may be tolerated. Deletions range from about 1 to about 20 residues, although in some cases deletions may be much larger.

Substitutions, deletions, insertions or any combination thereof may be used to arrive at a final derivative. Generally these changes are done on a few amino acids to
5 minimize the alteration of the molecule. However, larger changes may be tolerated in certain circumstances. When small alterations in the characteristics of the prostate cancer protein are desired, substitutions are generally made in accordance with the amino acid substitution relationships provided in the definition section.

The variants typically exhibit the same qualitative biological activity and will
10 elicit the same immune response as the naturally-occurring analog, although variants also are selected to modify the characteristics of the prostate cancer proteins as needed. Alternatively, the variant may be designed such that the biological activity of the prostate cancer protein is altered. For example, glycosylation sites may be altered or removed.

Substantial changes in function or immunological identity are made by
15 selecting substitutions that are less conservative than those described above. For example, substitutions may be made which more significantly affect: the structure of the polypeptide backbone in the area of the alteration, for example the alpha-helical or beta-sheet structure; the charge or hydrophobicity of the molecule at the target site; or the bulk of the side chain. The substitutions which in general are expected to produce the greatest changes in the
20 polypeptide's properties are those in which (a) a hydrophilic residue, e.g. seryl or threonyl is substituted for (or by) a hydrophobic residue, e.g. leucyl, isoleucyl, phenylalanyl, valyl or alanyl; (b) a cysteine or proline is substituted for (or by) any other residue; (c) a residue having an electropositive side chain, e.g. lysyl, arginyl, or histidyl, is substituted for (or by) an electronegative residue, e.g. glutamyl or aspartyl; or (d) a residue having a bulky side
25 chain, e.g. phenylalanine, is substituted for (or by) one not having a side chain, e.g. glycine.

Covalent modifications of prostate cancer polypeptides are included within the scope of this invention. One type of covalent modification includes reacting targeted amino acid residues of a prostate cancer polypeptide with an organic derivatizing agent that is
30 capable of reacting with selected side chains or the N-or C-terminal residues of a prostate cancer polypeptide. Derivatization with bifunctional agents is useful, for instance, for crosslinking prostate cancer polypeptides to a water-insoluble support matrix or surface for

use in the method for purifying anti-prostate cancer polypeptide antibodies or screening assays, as is more fully described below. Commonly used crosslinking agents include, e.g., 1,1-bis(diazoacetyl)-2-phenylethane, glutaraldehyde, N-hydroxysuccinimide esters, e.g., esters with 4-azidosalicylic acid, homobifunctional imidoesters, including disuccinimidyl
5 esters such as 3,3'-dithiobis(succinimidylpropionate), bifunctional maleimides such as bis-N-maleimido-1,8-octane and agents such as methyl-3-((p-azidophenyl)dithio)propioimide.

Other modifications include deamidation of glutamyl and asparaginy residues to the corresponding glutamyl and aspartyl residues, respectively, hydroxylation of proline and lysine, phosphorylation of hydroxyl groups of seryl, threonyl or tyrosyl residues,
10 methylation of the amino groups of the lysine, arginine, and histidine side chains (Creighton, *Proteins: Structure and Molecular Properties*, pp. 79-86 (1983)), acetylation of the N-terminal amine, and amidation of any C-terminal carboxyl group.

Another type of covalent modification of the prostate cancer polypeptide included within the scope of this invention comprises altering the native glycosylation pattern
15 of the polypeptide. "Altering the native glycosylation pattern" is intended for purposes herein to mean deleting one or more carbohydrate moieties found in native sequence prostate cancer polypeptide, and/or adding one or more glycosylation sites that are not present in the native sequence prostate cancer polypeptide. Glycosylation patterns can be altered in many ways. For example the use of different cell types to express prostate cancer-associated
20 sequences can result in different glycosylation patterns.

Addition of glycosylation sites to prostate cancer polypeptides may also be accomplished by altering the amino acid sequence thereof. The alteration may be made, e.g., by the addition of, or substitution by, one or more serine or threonine residues to the native sequence prostate cancer polypeptide (for O-linked glycosylation sites). The prostate cancer
25 amino acid sequence may optionally be altered through changes at the DNA level, particularly by mutating the DNA encoding the prostate cancer polypeptide at preselected bases such that codons are generated that will translate into the desired amino acids.

Another means of increasing the number of carbohydrate moieties on the prostate cancer polypeptide is by chemical or enzymatic coupling of glycosides to the
30 polypeptide. Such methods are described in the art, e.g., in WO 87/05330, and in Aplin & Wriston, *CRC Crit. Rev. Biochem.*, pp. 259-306 (1981).

Removal of carbohydrate moieties present on the prostate cancer polypeptide may be accomplished chemically or enzymatically or by mutational substitution of codons encoding for amino acid residues that serve as targets for glycosylation. Chemical deglycosylation techniques are known in the art and described, for instance, by Hakimuddin, *et al.*, *Arch. Biochem. Biophys.*, 259:52 (1987) and by Edge *et al.*, *Anal. Biochem.*, 118:131 (1981). Enzymatic cleavage of carbohydrate moieties on polypeptides can be achieved by the use of a variety of endo- and exo-glycosidases as described by Thotakura *et al.*, *Meth. Enzymol.*, 138:350 (1987).

Another type of covalent modification of prostate cancer comprises linking the prostate cancer polypeptide to one of a variety of nonproteinaceous polymers, e.g., polyethylene glycol, polypropylene glycol, or polyoxyalkylenes, in the manner set forth in U.S. Patent Nos. 4,640,835; 4,496,689; 4,301,144; 4,670,417; 4,791,192 or 4,179,337.

Prostate cancer polypeptides of the present invention may also be modified in a way to form chimeric molecules comprising a prostate cancer polypeptide fused to another, heterologous polypeptide or amino acid sequence. In one embodiment, such a chimeric molecule comprises a fusion of a prostate cancer polypeptide with a tag polypeptide which provides an epitope to which an anti-tag antibody can selectively bind. The epitope tag is generally placed at the amino- or carboxyl-terminus of the prostate cancer polypeptide. The presence of such epitope-tagged forms of a prostate cancer polypeptide can be detected using an antibody against the tag polypeptide. Also, provision of the epitope tag enables the prostate cancer polypeptide to be readily purified by affinity purification using an anti-tag antibody or another type of affinity matrix that binds to the epitope tag. In an alternative embodiment, the chimeric molecule may comprise a fusion of a prostate cancer polypeptide with an immunoglobulin or a particular region of an immunoglobulin. For a bivalent form of the chimeric molecule, such a fusion could be to the Fc region of an IgG molecule.

Various tag polypeptides and their respective antibodies are well known in the art. Examples include poly-histidine (poly-his) or poly-histidine-glycine (poly-his-gly) tags; HIS6 and metal chelation tags, the flu HA tag polypeptide and its antibody 12CA5 (Field *et al.*, *Mol. Cell. Biol.* 8:2159-2165 (1988)); the c-myc tag and the 8F9, 3C7, 6E10, G4, B7 and 9E10 antibodies thereto (Evan *et al.*, *Molecular and Cellular Biology* 5:3610-3616 (1985)); and the Herpes Simplex virus glycoprotein D (gD) tag and its antibody (Paborsky *et al.*,

5 *Protein Engineering* 3(6):547-553 (1990)). Other tag polypeptides include the Flag-peptide (Hopp *et al.*, *BioTechnology* 6:1204-1210 (1988)); the KT3 epitope peptide (Martin *et al.*, *Science* 255:192-194 (1992)); tubulin epitope peptide (Skinner *et al.*, *J. Biol. Chem.* 266:15163-15166 (1991)); and the T7 gene 10 protein peptide tag (Lutz-Freyermuth *et al.*, *Proc. Natl. Acad. Sci. USA* 87:6393-6397 (1990)).

Also included are other prostate cancer proteins of the prostate cancer family, and prostate cancer proteins from other organisms, which are cloned and expressed as outlined below. Thus, probe or degenerate polymerase chain reaction (PCR) primer sequences may be used to find other related prostate cancer proteins from humans or other
10 organisms. As will be appreciated by those in the art, particularly useful probe and/or PCR primer sequences include the unique areas of the prostate cancer nucleic acid sequence. As is generally known in the art, preferred PCR primers are from about 15 to about 35 nucleotides in length, with from about 20 to about 30 being preferred, and may contain inosine as needed. The conditions for the PCR reaction are well known in the art (e.g., Innis, PCR Protocols,
15 *supra*).

Antibodies to prostate cancer proteins

In a preferred embodiment, when the prostate cancer protein is to be used to generate antibodies, e.g., for immunotherapy or immunodiagnosis, the prostate cancer protein
20 should share at least one epitope or determinant with the full length protein. By "epitope" or "determinant" herein is typically meant a portion of a protein which will generate and/or bind an antibody or T-cell receptor in the context of MHC. Thus, in most instances, antibodies made to a smaller prostate cancer protein will be able to bind to the full-length protein, particularly linear epitopes. In a preferred embodiment, the epitope is unique; that is,
25 antibodies generated to a unique epitope show little or no cross-reactivity.

Methods of preparing polyclonal antibodies are known to the skilled artisan (e.g., Coligan, *supra*; and Harlow & Lane, *supra*). Polyclonal antibodies can be raised in a mammal, e.g., by one or more injections of an immunizing agent and, if desired, an adjuvant. Typically, the immunizing agent and/or adjuvant will be injected in the mammal by multiple
30 subcutaneous or intraperitoneal injections. The immunizing agent may include a protein encoded by a nucleic acid of the figures or fragment thereof or a fusion protein thereof. It

may be useful to conjugate the immunizing agent to a protein known to be immunogenic in the mammal being immunized. Examples of such immunogenic proteins include but are not limited to keyhole limpet hemocyanin, serum albumin, bovine thyroglobulin, and soybean trypsin inhibitor. Examples of adjuvants which may be employed include Freund's complete
5 adjuvant and MPL-TDM adjuvant (monophosphoryl Lipid A, synthetic trehalose dicorynomycolate). The immunization protocol may be selected by one skilled in the art without undue experimentation.

The antibodies may, alternatively, be monoclonal antibodies. Monoclonal antibodies may be prepared using hybridoma methods, such as those described by Kohler &
10 Milstein, *Nature* 256:495 (1975). In a hybridoma method, a mouse, hamster, or other appropriate host animal, is typically immunized with an immunizing agent to elicit lymphocytes that produce or are capable of producing antibodies that will specifically bind to the immunizing agent. Alternatively, the lymphocytes may be immunized in vitro. The immunizing agent will typically include a polypeptide encoded by a nucleic acid of Tables 1-
15 16 fragment thereof, or a fusion protein thereof. Generally, either peripheral blood lymphocytes ("PBLs") are used if cells of human origin are desired, or spleen cells or lymph node cells are used if non-human mammalian sources are desired. The lymphocytes are then fused with an immortalized cell line using a suitable fusing agent, such as polyethylene glycol, to form a hybridoma cell (Goding, *Monoclonal Antibodies: Principles and Practice*,
20 pp. 59-103 (1986)). Immortalized cell lines are usually transformed mammalian cells, particularly myeloma cells of rodent, bovine and human origin. Usually, rat or mouse myeloma cell lines are employed. The hybridoma cells may be cultured in a suitable culture medium that preferably contains one or more substances that inhibit the growth or survival of the unfused, immortalized cells. For example, if the parental cells lack the enzyme
25 hypoxanthine guanine phosphoribosyl transferase (HGPRT or HPRT), the culture medium for the hybridomas typically will include hypoxanthine, aminopterin, and thymidine ("HAT medium"), which substances prevent the growth of HGPRT-deficient cells.

In one embodiment, the antibodies are bispecific antibodies. Bispecific antibodies are monoclonal, preferably human or humanized, antibodies that have binding
30 specificities for at least two different antigens or that have binding specificities for two epitopes on the same antigen. In one embodiment, one of the binding specificities is for a

protein encoded by a nucleic acid Tables 1-16 or a fragment thereof, the other one is for any other antigen, and preferably for a cell-surface protein or receptor or receptor subunit, preferably one that is tumor specific. Alternatively, tetramer-type technology may create multivalent reagents.

5 In a preferred embodiment, the antibodies to prostate cancer protein are capable of reducing or eliminating a biological function of a prostate cancer protein, as is described below. That is, the addition of anti-prostate cancer protein antibodies (either polyclonal or preferably monoclonal) to prostate cancer tissue (or cells containing prostate cancer) may reduce or eliminate the prostate cancer. Generally, at least a 25% decrease in
10 activity, growth, size or the like is preferred, with at least about 50% being particularly preferred and about a 95-100% decrease being especially preferred.

 In a preferred embodiment the antibodies to the prostate cancer proteins are humanized antibodies (e.g., Xenerex Biosciences, Mederex, Inc., Abgenix, Inc., Protein Design Labs, Inc.) Humanized forms of non-human (e.g., murine) antibodies are chimeric
15 molecules of immunoglobulins, immunoglobulin chains or fragments thereof (such as Fv, Fab, Fab', F(ab')₂ or other antigen-binding subsequences of antibodies) which contain minimal sequence derived from non-human immunoglobulin. Humanized antibodies include human immunoglobulins (recipient antibody) in which residues from a complementary determining region (CDR) of the recipient are replaced by residues from a CDR of a non-
20 human species (donor antibody) such as mouse, rat or rabbit having the desired specificity, affinity and capacity. In some instances, Fv framework residues of the human immunoglobulin are replaced by corresponding non-human residues. Humanized antibodies may also comprise residues which are found neither in the recipient antibody nor in the imported CDR or framework sequences. In general, a humanized antibody will comprise
25 substantially all of at least one, and typically two, variable domains, in which all or substantially all of the CDR regions correspond to those of a non-human immunoglobulin and all or substantially all of the framework (FR) regions are those of a human immunoglobulin consensus sequence. The humanized antibody optimally also will comprise at least a portion of an immunoglobulin constant region (Fc), typically that of a human
30 immunoglobulin (Jones *et al.*, *Nature* 321:522-525 (1986); Riechmann *et al.*, *Nature* 332:323-329 (1988); and Presta, *Curr. Op. Struct. Biol.* 2:593-596 (1992)). Humanization

can be essentially performed following the method of Winter and co-workers (Jones *et al.*, *Nature* 321:522-525 (1986); Riechmann *et al.*, *Nature* 332:323-327 (1988); Verhoeyen *et al.*, *Science* 239:1534-1536 (1988)), by substituting rodent CDRs or CDR sequences for the corresponding sequences of a human antibody. Accordingly, such humanized antibodies are chimeric antibodies (U.S. Patent No. 4,816,567), wherein substantially less than an intact human variable domain has been substituted by the corresponding sequence from a non-human species.

Human antibodies can also be produced using various techniques known in the art, including phage display libraries (Hoogenboom & Winter, *J. Mol. Biol.* 227:381 (1991); Marks *et al.*, *J. Mol. Biol.* 222:581 (1991)). The techniques of Cole *et al.* and Boerner *et al.* are also available for the preparation of human monoclonal antibodies (Cole *et al.*, *Monoclonal Antibodies and Cancer Therapy*, p. 77 (1985) and Boerner *et al.*, *J. Immunol.* 147(1):86-95 (1991)). Similarly, human antibodies can be made by introducing of human immunoglobulin loci into transgenic animals, e.g., mice in which the endogenous immunoglobulin genes have been partially or completely inactivated. Upon challenge, human antibody production is observed, which closely resembles that seen in humans in all respects, including gene rearrangement, assembly, and antibody repertoire. This approach is described, e.g., in U.S. Patent Nos. 5,545,807; 5,545,806; 5,569,825; 5,625,126; 5,633,425; 5,661,016, and in the following scientific publications: Marks *et al.*, *Bio/Technology* 10:779-783 (1992); Lonberg *et al.*, *Nature* 368:856-859 (1994); Morrison, *Nature* 368:812-13 (1994); Fishwild *et al.*, *Nature Biotechnology* 14:845-51 (1996); Neuberger, *Nature Biotechnology* 14:826 (1996); Lonberg & Huszar, *Intern. Rev. Immunol.* 13:65-93 (1995).

By immunotherapy is meant treatment of prostate cancer with an antibody raised against prostate cancer proteins. As used herein, immunotherapy can be passive or active. Passive immunotherapy as defined herein is the passive transfer of antibody to a recipient (patient). Active immunization is the induction of antibody and/or T-cell responses in a recipient (patient). Induction of an immune response is the result of providing the recipient with an antigen to which antibodies are raised. As appreciated by one of ordinary skill in the art, the antigen may be provided by injecting a polypeptide against which antibodies are desired to be raised into a recipient, or contacting the recipient with a nucleic

acid capable of expressing the antigen and under conditions for expression of the antigen, leading to an immune response.

In a preferred embodiment the prostate cancer proteins against which antibodies are raised are secreted proteins as described above. Without being bound by theory, antibodies used for treatment, bind and prevent the secreted protein from binding to its receptor, thereby inactivating the secreted prostate cancer protein.

In another preferred embodiment, the prostate cancer protein to which antibodies are raised is a transmembrane protein. Without being bound by theory, antibodies used for treatment, bind the extracellular domain of the prostate cancer protein and prevent it from binding to other proteins, such as circulating ligands or cell-associated molecules. The antibody may cause down-regulation of the transmembrane prostate cancer protein. As will be appreciated by one of ordinary skill in the art, the antibody may be a competitive, non-competitive or uncompetitive inhibitor of protein binding to the extracellular domain of the prostate cancer protein. The antibody is also an antagonist of the prostate cancer protein. Further, the antibody prevents activation of the transmembrane prostate cancer protein. In one aspect, when the antibody prevents the binding of other molecules to the prostate cancer protein, the antibody prevents growth of the cell. The antibody may also be used to target or sensitize the cell to cytotoxic agents, including, but not limited to TNF- α , TNF- β , IL-1, INF- γ and IL-2, or chemotherapeutic agents including 5FU, vinblastine, actinomycin D, cisplatin, methotrexate, and the like. In some instances the antibody belongs to a sub-type that activates serum complement when complexed with the transmembrane protein thereby mediating cytotoxicity or antigen-dependent cytotoxicity (ADCC). Thus, prostate cancer is treated by administering to a patient antibodies directed against the transmembrane prostate cancer protein. Antibody-labeling may activate a co-toxin, localize a toxin payload, or otherwise provide means to locally ablate cells.

In another preferred embodiment, the antibody is conjugated to an effector moiety. The effector moiety can be any number of molecules, including labelling moieties such as radioactive labels or fluorescent labels, or can be a therapeutic moiety. In one aspect the therapeutic moiety is a small molecule that modulates the activity of the prostate cancer protein. In another aspect the therapeutic moiety modulates the activity of molecules associated with or in close proximity to the prostate cancer protein. The therapeutic moiety

may inhibit enzymatic activity such as protease or collagenase or protein kinase activity associated with prostate cancer.

In a preferred embodiment, the therapeutic moiety can also be a cytotoxic agent. In this method, targeting the cytotoxic agent to prostate cancer tissue or cells, results in a reduction in the number of afflicted cells, thereby reducing symptoms associated with prostate cancer. Cytotoxic agents are numerous and varied and include, but are not limited to, cytotoxic drugs or toxins or active fragments of such toxins. Suitable toxins and their corresponding fragments include diphtheria A chain, exotoxin A chain, ricin A chain, abrin A chain, curcin, crotin, phenomycin, enomycin and the like. Cytotoxic agents also include radiochemicals made by conjugating radioisotopes to antibodies raised against prostate cancer proteins, or binding of a radionuclide to a chelating agent that has been covalently attached to the antibody. Targeting the therapeutic moiety to transmembrane prostate cancer proteins not only serves to increase the local concentration of therapeutic moiety in the prostate cancer afflicted area, but also serves to reduce deleterious side effects that may be associated with the therapeutic moiety.

In another preferred embodiment, the prostate cancer protein against which the antibodies are raised is an intracellular protein. In this case, the antibody may be conjugated to a protein which facilitates entry into the cell. In one case, the antibody enters the cell by endocytosis. In another embodiment, a nucleic acid encoding the antibody is administered to the individual or cell. Moreover, wherein the prostate cancer protein can be targeted within a cell, i.e., the nucleus, an antibody thereto contains a signal for that target localization, i.e., a nuclear localization signal.

The prostate cancer antibodies of the invention specifically bind to prostate cancer proteins. By "specifically bind" herein is meant that the antibodies bind to the protein with a K_d of at least about 0.1 mM, more usually at least about 1 μ M, preferably at least about 0.1 μ M or better, and most preferably, 0.01 μ M or better. Selectivity of binding is also important.

Detection of prostate cancer sequence for diagnostic and therapeutic applications

In one aspect, the RNA expression levels of genes are determined for different cellular states in the prostate cancer phenotype. Expression levels of genes in normal tissue

(i.e., not undergoing prostate cancer) and in prostate cancer tissue (and in some cases, for varying severities of prostate cancer that relate to prognosis, as outlined below) are evaluated to provide expression profiles. An expression profile of a particular cell state or point of development is essentially a "fingerprint" of the state. While two states may have any particular gene similarly expressed, the evaluation of a number of genes simultaneously allows the generation of a gene expression profile that is reflective of the state of the cell. By comparing expression profiles of cells in different states, information regarding which genes are important (including both up- and down-regulation of genes) in each of these states is obtained. Then, diagnosis may be performed or confirmed to determine whether a tissue sample has the gene expression profile of normal or cancerous tissue. This will provide for molecular diagnosis of related conditions.

"Differential expression," or grammatical equivalents as used herein, refers to qualitative or quantitative differences in the temporal and/or cellular gene expression patterns within and among cells and tissue. Thus, a differentially expressed gene can qualitatively have its expression altered, including an activation or inactivation, in, e.g., normal versus prostate cancer tissue. Genes may be turned on or turned off in a particular state, relative to another state thus permitting comparison of two or more states. A qualitatively regulated gene will exhibit an expression pattern within a state or cell type which is detectable by standard techniques. Some genes will be expressed in one state or cell type, but not in both. Alternatively, the difference in expression may be quantitative, e.g., in that expression is increased or decreased; i.e., gene expression is either upregulated, resulting in an increased amount of transcript, or downregulated, resulting in a decreased amount of transcript. The degree to which expression differs need only be large enough to quantify via standard characterization techniques as outlined below, such as by use of Affymetrix GeneChip™ expression arrays, Lockhart, *Nature Biotechnology* 14:1675-1680 (1996), hereby expressly incorporated by reference. Other techniques include, but are not limited to, quantitative reverse transcriptase PCR, northern analysis and RNase protection. As outlined above, preferably the change in expression (i.e., upregulation or downregulation) is at least about 50%, more preferably at least about 100%, more preferably at least about 150%, more preferably at least about 200%, with from 300 to at least 1000% being especially preferred.

Evaluation may be at the gene transcript, or the protein level. The amount of gene expression may be monitored using nucleic acid probes to the DNA or RNA equivalent of the gene transcript, and the quantification of gene expression levels, or, alternatively, the final gene product itself (protein) can be monitored, e.g., with antibodies to the prostate cancer protein and standard immunoassays (ELISAs, etc.) or other techniques, including mass spectroscopy assays, 2D gel electrophoresis assays, etc. Proteins corresponding to prostate cancer genes, i.e., those identified as being important in a prostate cancer phenotype, can be evaluated in a prostate cancer diagnostic test.

In a preferred embodiment, gene expression monitoring is performed simultaneously on a number of genes. Multiple protein expression monitoring can be performed as well. Similarly, these assays may be performed on an individual basis as well.

In this embodiment, the prostate cancer nucleic acid probes are attached to biochips as outlined herein for the detection and quantification of prostate cancer sequences in a particular cell. The assays are further described below in the example. PCR techniques can be used to provide greater sensitivity.

In a preferred embodiment nucleic acids encoding the prostate cancer protein are detected. Although DNA or RNA encoding the prostate cancer protein may be detected, of particular interest are methods wherein an mRNA encoding a prostate cancer protein is detected. Probes to detect mRNA can be a nucleotide/deoxynucleotide probe that is complementary to and hybridizes with the mRNA and includes, but is not limited to, oligonucleotides, cDNA or RNA. Probes also should contain a detectable label, as defined herein. In one method the mRNA is detected after immobilizing the nucleic acid to be examined on a solid support such as nylon membranes and hybridizing the probe with the sample. Following washing to remove the non-specifically bound probe, the label is detected. In another method detection of the mRNA is performed in situ. In this method permeabilized cells or tissue samples are contacted with a detectably labeled nucleic acid probe for sufficient time to allow the probe to hybridize with the target mRNA. Following washing to remove the non-specifically bound probe, the label is detected. For example a digoxigenin labeled riboprobe (RNA probe) that is complementary to the mRNA encoding a prostate cancer protein is detected by binding the digoxigenin with an anti-digoxigenin

secondary antibody and developed with nitro blue tetrazolium and 5-bromo-4-chloro-3-indoyl phosphate.

5 In a preferred embodiment, various proteins from the three classes of proteins as described herein (secreted, transmembrane or intracellular proteins) are used in diagnostic assays. The prostate cancer proteins, antibodies, nucleic acids, modified proteins and cells containing prostate cancer sequences are used in diagnostic assays. This can be performed on an individual gene or corresponding polypeptide level. In a preferred embodiment, the expression profiles are used, preferably in conjunction with high throughput screening techniques to allow monitoring for expression profile genes and/or corresponding
10 polypeptides.

As described and defined herein, prostate cancer proteins, including intracellular, transmembrane or secreted proteins, find use as markers of prostate cancer. Detection of these proteins in putative prostate cancer tissue allows for detection or diagnosis of prostate cancer. In one embodiment, antibodies are used to detect prostate cancer proteins.
15 A preferred method separates proteins from a sample by electrophoresis on a gel (typically a denaturing and reducing protein gel, but may be another type of gel, including isoelectric focusing gels and the like). Following separation of proteins, the prostate cancer protein is detected, e.g., by immunoblotting with antibodies raised against the prostate cancer protein. Methods of immunoblotting are well known to those of ordinary skill in the art.

20 In another preferred method, antibodies to the prostate cancer protein find use in *in situ* imaging techniques, e.g., in histology (e.g., *Methods in Cell Biology: Antibodies in Cell Biology*, volume 37 (Asai, ed. 1993)). In this method cells are contacted with from one to many antibodies to the prostate cancer protein(s). Following washing to remove non-specific antibody binding, the presence of the antibody or antibodies is detected. In one
25 embodiment the antibody is detected by incubating with a secondary antibody that contains a detectable label. In another method the primary antibody to the prostate cancer protein(s) contains a detectable label, e.g. an enzyme marker that can act on a substrate. In another preferred embodiment each one of multiple primary antibodies contains a distinct and detectable label. This method finds particular use in simultaneous screening for a plurality of
30 prostate cancer proteins. As will be appreciated by one of ordinary skill in the art, many other histological imaging techniques are also provided by the invention.

In a preferred embodiment the label is detected in a fluorometer which has the ability to detect and distinguish emissions of different wavelengths. In addition, a fluorescence activated cell sorter (FACS) can be used in the method.

In another preferred embodiment, antibodies find use in diagnosing prostate cancer from blood, serum, plasma, stool, and other samples. Such samples, therefore, are useful as samples to be probed or tested for the presence of prostate cancer proteins. Antibodies can be used to detect a prostate cancer protein by previously described immunoassay techniques including ELISA, immunoblotting (western blotting), immunoprecipitation, BIACORE technology and the like. Conversely, the presence of antibodies may indicate an immune response against an endogenous prostate cancer protein.

In a preferred embodiment, *in situ* hybridization of labeled prostate cancer nucleic acid probes to tissue arrays is done. For example, arrays of tissue samples, including prostate cancer tissue and/or normal tissue, are made. *In situ* hybridization (*see, e.g., Ausubel, supra*) is then performed. When comparing the fingerprints between an individual and a standard, the skilled artisan can make a diagnosis, a prognosis, or a prediction based on the findings. It is further understood that the genes which indicate the diagnosis may differ from those which indicate the prognosis and molecular profiling of the condition of the cells may lead to distinctions between responsive or refractory conditions or may be predictive of outcomes.

In a preferred embodiment, the prostate cancer proteins, antibodies, nucleic acids, modified proteins and cells containing prostate cancer sequences are used in prognosis assays. As above, gene expression profiles can be generated that correlate to prostate cancer, in terms of long term prognosis. Again, this may be done on either a protein or gene level, with the use of genes being preferred. As above, prostate cancer probes may be attached to biochips for the detection and quantification of prostate cancer sequences in a tissue or patient. The assays proceed as outlined above for diagnosis. PCR method may provide more sensitive and accurate quantification.

Assays for therapeutic compounds

In a preferred embodiment members of the proteins, nucleic acids, and antibodies as described herein are used in drug screening assays. The prostate cancer

proteins, antibodies, nucleic acids, modified proteins and cells containing prostate cancer sequences are used in drug screening assays or by evaluating the effect of drug candidates on a "gene expression profile" or expression profile of polypeptides. In a preferred embodiment, the expression profiles are used, preferably in conjunction with high throughput screening techniques to allow monitoring for expression profile genes after treatment with a candidate agent (e.g., Zlokarnik, *et al.*, *Science* 279:84-8 (1998); Heid, *Genome Res* 6:986-94, 1996).

In a preferred embodiment, the prostate cancer proteins, antibodies, nucleic acids, modified proteins and cells containing the native or modified prostate cancer proteins are used in screening assays. That is, the present invention provides novel methods for screening for compositions which modulate the prostate cancer phenotype or an identified physiological function of a prostate cancer protein. As above, this can be done on an individual gene level or by evaluating the effect of drug candidates on a "gene expression profile". In a preferred embodiment, the expression profiles are used, preferably in conjunction with high throughput screening techniques to allow monitoring for expression profile genes after treatment with a candidate agent, see Zlokarnik, *supra*.

Having identified the differentially expressed genes herein, a variety of assays may be executed. In a preferred embodiment, assays may be run on an individual gene or protein level. That is, having identified a particular gene as up regulated in prostate cancer, test compounds can be screened for the ability to modulate gene expression or for binding to the prostate cancer protein. "Modulation" thus includes both an increase and a decrease in gene expression. The preferred amount of modulation will depend on the original change of the gene expression in normal versus tissue undergoing prostate cancer, with changes of at least 10%, preferably 50%, more preferably 100-300%, and in some embodiments 300-1000% or greater. Thus, if a gene exhibits a 4-fold increase in prostate cancer tissue compared to normal tissue, a decrease of about four-fold is often desired; similarly, a 10-fold decrease in prostate cancer tissue compared to normal tissue often provides a target value of a 10-fold increase in expression to be induced by the test compound.

The amount of gene expression may be monitored using nucleic acid probes and the quantification of gene expression levels, or, alternatively, the gene product itself can be monitored, e.g., through the use of antibodies to the prostate cancer protein and standard

immunoassays. Proteomics and separation techniques may also allow quantification of expression.

In a preferred embodiment, gene expression or protein monitoring of a number of entities, i.e., an expression profile, is monitored simultaneously. Such profiles will typically involve a plurality of those entities described herein..

In this embodiment, the prostate cancer nucleic acid probes are attached to biochips as outlined herein for the detection and quantification of prostate cancer sequences in a particular cell. Alternatively, PCR may be used. Thus, a series, e.g., of microtiter plate, may be used with dispensed primers in desired wells. A PCR reaction can then be performed and analyzed for each well.

Expression monitoring can be performed to identify compounds that modify the expression of one or more prostate cancer-associated sequences, e.g., a polynucleotide sequence set out in Tables 1-16. Generally, in a preferred embodiment, a test modulator is added to the cells prior to analysis. Moreover, screens are also provided to identify agents that modulate prostate cancer, modulate prostate cancer proteins, bind to a prostate cancer protein, or interfere with the binding of a prostate cancer protein and an antibody or other binding partner.

The term "test compound" or "drug candidate" or "modulator" or grammatical equivalents as used herein describes any molecule, e.g., protein, oligopeptide, small organic molecule, polysaccharide, polynucleotide, etc., to be tested for the capacity to directly or indirectly alter the prostate cancer phenotype or the expression of a prostate cancer sequence, e.g., a nucleic acid or protein sequence. In preferred embodiments, modulators alter expression profiles, or expression profile nucleic acids or proteins provided herein. In one embodiment, the modulator suppresses a prostate cancer phenotype, e.g. to a normal tissue fingerprint. In another embodiment, a modulator induced a prostate cancer phenotype. Generally, a plurality of assay mixtures are run in parallel with different agent concentrations to obtain a differential response to the various concentrations. Typically, one of these concentrations serves as a negative control, i.e., at zero concentration or below the level of detection.

Drug candidates encompass numerous chemical classes, though typically they are organic molecules, preferably small organic compounds having a molecular weight of

more than 100 and less than about 2,500 daltons. Preferred small molecules are less than 2000, or less than 1500 or less than 1000 or less than 500 D. Candidate agents comprise functional groups necessary for structural interaction with proteins, particularly hydrogen bonding, and typically include at least an amine, carbonyl, hydroxyl or carboxyl group, preferably at least two of the functional chemical groups. The candidate agents often comprise cyclical carbon or heterocyclic structures and/or aromatic or polyaromatic structures substituted with one or more of the above functional groups. Candidate agents are also found among biomolecules including peptides, saccharides, fatty acids, steroids, purines, pyrimidines, derivatives, structural analogs or combinations thereof. Particularly preferred are peptides.

In one aspect, a modulator will neutralize the effect of a prostate cancer protein. By "neutralize" is meant that activity of a protein is inhibited or blocked and the consequent effect on the cell.

In certain embodiments, combinatorial libraries of potential modulators will be screened for an ability to bind to a prostate cancer polypeptide or to modulate activity. Conventionally, new chemical entities with useful properties are generated by identifying a chemical compound (called a "lead compound") with some desirable property or activity, e.g., inhibiting activity, creating variants of the lead compound, and evaluating the property and activity of those variant compounds. Often, high throughput screening (HTS) methods are employed for such an analysis.

In one preferred embodiment, high throughput screening methods involve providing a library containing a large number of potential therapeutic compounds (candidate compounds). Such "combinatorial chemical libraries" are then screened in one or more assays to identify those library members (particular chemical species or subclasses) that display a desired characteristic activity. The compounds thus identified can serve as conventional "lead compounds" or can themselves be used as potential or actual therapeutics.

A combinatorial chemical library is a collection of diverse chemical compounds generated by either chemical synthesis or biological synthesis by combining a number of chemical "building blocks" such as reagents. For example, a linear combinatorial chemical library, such as a polypeptide (e.g., mutein) library, is formed by combining a set of chemical building blocks called amino acids in every possible way for a given compound

length (i.e., the number of amino acids in a polypeptide compound). Millions of chemical compounds can be synthesized through such combinatorial mixing of chemical building blocks (Gallop *et al.*, *J. Med. Chem.* 37(9):1233-1251 (1994)).

Preparation and screening of combinatorial chemical libraries is well known to those of skill in the art. Such combinatorial chemical libraries include, but are not limited to, peptide libraries (*see, e.g.*, U.S. Patent No. 5,010,175, Furka, *Pept. Prot. Res.* 37:487-493 (1991), Houghton *et al.*, *Nature*, 354:84-88 (1991)), peptoids (PCT Publication No WO 91/19735), encoded peptides (PCT Publication WO 93/20242), random bio-oligomers (PCT Publication WO 92/00091), benzodiazepines (U.S. Pat. No. 5,288,514), diversomers such as hydantoins, benzodiazepines and dipeptides (Hobbs *et al.*, *Proc. Nat. Acad. Sci. USA* 90:6909-6913 (1993)), vinylogous polypeptides (Hagihara *et al.*, *J. Amer. Chem. Soc.* 114:6568 (1992)), nonpeptidal peptidomimetics with a Beta-D-Glucose scaffolding (Hirschmann *et al.*, *J. Amer. Chem. Soc.* 114:9217-9218 (1992)), analogous organic syntheses of small compound libraries (Chen *et al.*, *J. Amer. Chem. Soc.* 116:2661 (1994)), oligocarbamates (Cho, *et al.*, *Science* 261:1303 (1993)), and/or peptidyl phosphonates (Campbell *et al.*, *J. Org. Chem.* 59:658 (1994)). *See, generally*, Gordon *et al.*, *J. Med. Chem.* 37:1385 (1994), nucleic acid libraries (*see, e.g.*, Strategene, Corp.), peptide nucleic acid libraries (*see, e.g.*, U.S. Patent 5,539,083), antibody libraries (*see, e.g.*, Vaughn *et al.*, *Nature Biotechnology* 14(3):309-314 (1996), and PCT/US96/10287), carbohydrate libraries (*see, e.g.*, Liang *et al.*, *Science* 274:1520-1522 (1996), and U.S. Patent No. 5,593,853), and small organic molecule libraries (*see, e.g.*, benzodiazepines, Baum, C&EN, Jan 18, page 33 (1993); isoprenoids, U.S. Patent No. 5,569,588; thiazolidinones and metathiazanones, U.S. Patent No. 5,549,974; pyrrolidines, U.S. Patent Nos. 5,525,735 and 5,519,134; morpholino compounds, U.S. Patent No. 5,506,337; benzodiazepines, U.S. Patent No. 5,288,514; and the like).

Devices for the preparation of combinatorial libraries are commercially available (*see, e.g.*, 357 MPS, 390 MPS, Advanced Chem Tech, Louisville KY, Symphony, Rainin, Woburn, MA, 433A Applied Biosystems, Foster City, CA, 9050 Plus, Millipore, Bedford, MA).

A number of well known robotic systems have also been developed for solution phase chemistries. These systems include automated workstations like the automated synthesis apparatus developed by Takeda Chemical Industries, LTD. (Osaka,

Japan) and many robotic systems utilizing robotic arms (Zymate II, Zymark Corporation, Hopkinton, Mass.; Orca, Hewlett-Packard, Palo Alto, Calif.), which mimic the manual synthetic operations performed by a chemist. Any of the above devices are suitable for use with the present invention. The nature and implementation of modifications to these devices (if any) so that they can operate as discussed herein will be apparent to persons skilled in the relevant art. In addition, numerous combinatorial libraries are themselves commercially available (*see, e.g.*, ComGenex, Princeton, N.J., Asinex, Moscow, Ru, Tripos, Inc., St. Louis, MO, ChemStar, Ltd, Moscow, RU, 3D Pharmaceuticals, Exton, PA, Martek Biosciences, Columbia, MD, *etc.*).

The assays to identify modulators are amenable to high throughput screening. Preferred assays thus detect enhancement or inhibition of prostate cancer gene transcription, inhibition or enhancement of polypeptide expression, and inhibition or enhancement of polypeptide activity.

High throughput assays for the presence, absence, quantification, or other properties of particular nucleic acids or protein products are well known to those of skill in the art. Similarly, binding assays and reporter gene assays are similarly well known. Thus, *e.g.*, U.S. Patent No. 5,559,410 discloses high throughput screening methods for proteins, U.S. Patent No. 5,585,639 discloses high throughput screening methods for nucleic acid binding (*i.e.*, in arrays), while U.S. Patent Nos. 5,576,220 and 5,541,061 disclose high throughput methods of screening for ligand/antibody binding.

In addition, high throughput screening systems are commercially available (*see, e.g.*, Zymark Corp., Hopkinton, MA; Air Technical Industries, Mentor, OH; Beckman Instruments, Inc. Fullerton, CA; Precision Systems, Inc., Natick, MA, *etc.*). These systems typically automate entire procedures, including all sample and reagent pipetting, liquid dispensing, timed incubations, and final readings of the microplate in detector(s) appropriate for the assay. These configurable systems provide high throughput and rapid start up as well as a high degree of flexibility and customization. The manufacturers of such systems provide detailed protocols for various high throughput systems. Thus, *e.g.*, Zymark Corp. provides technical bulletins describing screening systems for detecting the modulation of gene transcription, ligand binding, and the like.

In one embodiment, modulators are proteins, often naturally occurring proteins or fragments of naturally occurring proteins. Thus, *e.g.*, cellular extracts containing proteins, or random or directed digests of proteinaceous cellular extracts, may be used. In this way libraries of proteins may be made for screening in the methods of the invention.

- 5 Particularly preferred in this embodiment are libraries of bacterial, fungal, viral, and mammalian proteins, with the latter being preferred, and human proteins being especially preferred. Particularly useful test compound will be directed to the class of proteins to which the target belongs, *e.g.*, substrates for enzymes or ligands and receptors.

- 10 In a preferred embodiment, modulators are peptides of from about 5 to about 30 amino acids, with from about 5 to about 20 amino acids being preferred, and from about 7 to about 15 being particularly preferred. The peptides may be digests of naturally occurring proteins as is outlined above, random peptides, or "biased" random peptides. By "randomized" or grammatical equivalents herein is meant that each nucleic acid and peptide consists of essentially random nucleotides and amino acids, respectively. Since generally
15 these random peptides (or nucleic acids, discussed below) are chemically synthesized, they may incorporate any nucleotide or amino acid at any position. The synthetic process can be designed to generate randomized proteins or nucleic acids, to allow the formation of all or most of the possible combinations over the length of the sequence, thus forming a library of randomized candidate bioactive proteinaceous agents.

- 20 In one embodiment, the library is fully randomized, with no sequence preferences or constants at any position. In a preferred embodiment, the library is biased. That is, some positions within the sequence are either held constant, or are selected from a limited number of possibilities. For example, in a preferred embodiment, the nucleotides or amino acid residues are randomized within a defined class, *e.g.*, of hydrophobic amino acids, hydrophilic residues, sterically biased (either small or large) residues, towards the creation of
25 nucleic acid binding domains, the creation of cysteines, for cross-linking, prolines for SH-3 domains, serines, threonines, tyrosines or histidines for phosphorylation sites, etc., or to purines, etc.

- Modulators of prostate cancer can also be nucleic acids, as defined below. As
30 described above generally for proteins, nucleic acid modulating agents may be naturally occurring nucleic acids, random nucleic acids, or "biased" random nucleic acids. For

example, digests of procaryotic or eucaryotic genomes may be used as is outlined above for proteins.

In certain embodiments, the activity of a prostate cancer-associated protein is down-regulated, or entirely inhibited, by the use of antisense polynucleotide, *i.e.*, a nucleic acid complementary to, and which can preferably hybridize specifically to, a coding mRNA
5 acid complementary to, and which can preferably hybridize specifically to, a coding mRNA nucleic acid sequence, *e.g.*, a prostate cancer protein mRNA, or a subsequence thereof. Binding of the antisense polynucleotide to the mRNA reduces the translation and/or stability of the mRNA.

In the context of this invention, antisense polynucleotides can comprise
10 naturally-occurring nucleotides, or synthetic species formed from naturally-occurring subunits or their close homologs. Antisense polynucleotides may also have altered sugar moieties or inter-sugar linkages. Exemplary among these are the phosphorothioate and other sulfur containing species which are known for use in the art. Analogs are comprehended by this invention so long as they function effectively to hybridize with the prostate cancer
15 protein mRNA. *See, e.g.*, Isis Pharmaceuticals, Carlsbad, CA; Sequitor, Inc., Natick, MA.

Such antisense polynucleotides can readily be synthesized using recombinant means, or can be synthesized *in vitro*. Equipment for such synthesis is sold by several vendors, including Applied Biosystems. The preparation of other oligonucleotides such as phosphorothioates and alkylated derivatives is also well known to those of skill in the art.

20 Antisense molecules as used herein include antisense or sense oligonucleotides. Sense oligonucleotides can, *e.g.*, be employed to block transcription by binding to the anti-sense strand. The antisense and sense oligonucleotide comprise a single-stranded nucleic acid sequence (either RNA or DNA) capable of binding to target mRNA (sense) or DNA (antisense) sequences for prostate cancer molecules. Antisense or sense
25 oligonucleotides, according to the present invention, comprise a fragment generally at least about 14 nucleotides, preferably from about 14 to 30 nucleotides. The ability to derive an antisense or a sense oligonucleotide, based upon a cDNA sequence encoding a given protein is described in, *e.g.*, Stein & Cohen (*Cancer Res.* 48:2659 (1988) and van der Krol *et al.* (*BioTechniques* 6:958 (1988)).

30 In addition to antisense polynucleotides, ribozymes can be used to target and inhibit transcription of prostate cancer-associated nucleotide sequences. A ribozyme is an

RNA molecule that catalytically cleaves other RNA molecules. Different kinds of ribozymes have been described, including group I ribozymes, hammerhead ribozymes, hairpin ribozymes, RNase P, and axhead ribozymes (*see, e.g., Castanotto et al., Adv. in Pharmacology* 25: 289-317 (1994) for a general review of the properties of different ribozymes).

The general features of hairpin ribozymes are described, e.g., in Hampel *et al., Nucl. Acids Res.* 18:299-304 (1990); European Patent Publication No. 0 360 257; U.S. Patent No. 5,254,678. Methods of preparing are well known to those of skill in the art (*see, e.g., WO 94/26877; Ojwang et al., Proc. Natl. Acad. Sci. USA* 90:6340-6344 (1993); Yamada *et al., Human Gene Therapy* 1:39-45 (1994); Leavitt *et al., Proc. Natl. Acad. Sci. USA* 92:699-703 (1995); Leavitt *et al., Human Gene Therapy* 5:1151-120 (1994); and Yamada *et al., Virology* 205: 121-126 (1994)).

Polynucleotide modulators of prostate cancer may be introduced into a cell containing the target nucleotide sequence by formation of a conjugate with a ligand binding molecule, as described in WO 91/04753. Suitable ligand binding molecules include, but are not limited to, cell surface receptors, growth factors, other cytokines, or other ligands that bind to cell surface receptors. Preferably, conjugation of the ligand binding molecule does not substantially interfere with the ability of the ligand binding molecule to bind to its corresponding molecule or receptor, or block entry of the sense or antisense oligonucleotide or its conjugated version into the cell. Alternatively, a polynucleotide modulator of prostate cancer may be introduced into a cell containing the target nucleic acid sequence, e.g., by formation of an polynucleotide-lipid complex, as described in WO 90/10448. It is understood that the use of antisense molecules or knock out and knock in models may also be used in screening assays as discussed above, in addition to methods of treatment.

As noted above, gene expression monitoring is conveniently used to test candidate modulators (*e.g., protein, nucleic acid or small molecule*). After the candidate agent has been added and the cells allowed to incubate for some period of time, the sample containing a target sequence to be analyzed is added to the biochip. If required, the target sequence is prepared using known techniques. For example, the sample may be treated to lyse the cells, using known lysis buffers, electroporation, etc., with purification and/or amplification such as PCR performed as appropriate. For example, an *in vitro* transcription

with labels covalently attached to the nucleotides is performed. Generally, the nucleic acids are labeled with biotin-FITC or PE, or with cy3 or cy5.

In a preferred embodiment, the target sequence is labeled with, e.g., a fluorescent, a chemiluminescent, a chemical, or a radioactive signal, to provide a means of detecting the target sequence's specific binding to a probe. The label also can be an enzyme, such as, alkaline phosphatase or horseradish peroxidase, which when provided with an appropriate substrate produces a product that can be detected. Alternatively, the label can be a labeled compound or small molecule, such as an enzyme inhibitor, that binds but is not catalyzed or altered by the enzyme. The label also can be a moiety or compound, such as, an epitope tag or biotin which specifically binds to streptavidin. For the example of biotin, the streptavidin is labeled as described above, thereby, providing a detectable signal for the bound target sequence. Unbound labeled streptavidin is typically removed prior to analysis.

As will be appreciated by those in the art, these assays can be direct hybridization assays or can comprise "sandwich assays", which include the use of multiple probes, as is generally outlined in U.S. Patent Nos. 5,681,702, 5,597,909, 5,545,730, 5,594,117, 5,591,584, 5,571,670, 5,580,731, 5,571,670, 5,591,584, 5,624,802, 5,635,352, 5,594,118, 5,359,100, 5,124,246 and 5,681,697, all of which are hereby incorporated by reference. In this embodiment, in general, the target nucleic acid is prepared as outlined above, and then added to the biochip comprising a plurality of nucleic acid probes, under conditions that allow the formation of a hybridization complex.

A variety of hybridization conditions may be used in the present invention, including high, moderate and low stringency conditions as outlined above. The assays are generally run under stringency conditions which allows formation of the label probe hybridization complex only in the presence of target. Stringency can be controlled by altering a step parameter that is a thermodynamic variable, including, but not limited to, temperature, formamide concentration, salt concentration, chaotropic salt concentration pH, organic solvent concentration, etc.

These parameters may also be used to control non-specific binding, as is generally outlined in U.S. Patent No. 5,681,697. Thus it may be desirable to perform certain steps at higher stringency conditions to reduce non-specific binding.

The reactions outlined herein may be accomplished in a variety of ways. Components of the reaction may be added simultaneously, or sequentially, in different orders, with preferred embodiments outlined below. In addition, the reaction may include a variety of other reagents. These include salts, buffers, neutral proteins, e.g. albumin, detergents, *etc.*

5 which may be used to facilitate optimal hybridization and detection, and/or reduce non-specific or background interactions. Reagents that otherwise improve the efficiency of the assay, such as protease inhibitors, nuclease inhibitors, anti-microbial agents, *etc.*, may also be used as appropriate, depending on the sample preparation methods and purity of the target.

The assay data are analyzed to determine the expression levels, and changes in
10 expression levels as between states, of individual genes, forming a gene expression profile.

Screens are performed to identify modulators of the prostate cancer phenotype. In one embodiment, screening is performed to identify modulators that can induce or suppress a particular expression profile, thus preferably generating the associated phenotype. In another embodiment, *e.g.*, for diagnostic applications, having identified
15 differentially expressed genes important in a particular state, screens can be performed to identify modulators that alter expression of individual genes. In an another embodiment, screening is performed to identify modulators that alter a biological function of the expression product of a differentially expressed gene. Again, having identified the importance of a gene in a particular state, screens are performed to identify agents that bind
20 and/or modulate the biological activity of the gene product.

In addition screens can be done for genes that are induced in response to a candidate agent. After identifying a modulator based upon its ability to suppress a prostate cancer expression pattern leading to a normal expression pattern, or to modulate a single prostate cancer gene expression profile so as to mimic the expression of the gene from
25 normal tissue, a screen as described above can be performed to identify genes that are specifically modulated in response to the agent. Comparing expression profiles between normal tissue and agent treated prostate cancer tissue reveals genes that are not expressed in normal tissue or prostate cancer tissue, but are expressed in agent treated tissue. These agent-specific sequences can be identified and used by methods described herein for prostate cancer
30 genes or proteins. In particular these sequences and the proteins they encode find use in marking or identifying agent treated cells. In addition, antibodies can be raised against the

agent induced proteins and used to target novel therapeutics to the treated prostate cancer tissue sample.

Thus, in one embodiment, a test compound is administered to a population of prostate cancer cells, that have an associated prostate cancer expression profile. By
5 “administration” or “contacting” herein is meant that the candidate agent is added to the cells in such a manner as to allow the agent to act upon the cell, whether by uptake and intracellular action, or by action at the cell surface. In some embodiments, nucleic acid encoding a proteinaceous candidate agent (i.e., a peptide) may be put into a viral construct such as an adenoviral or retroviral construct, and added to the cell, such that expression of
10 the peptide agent is accomplished, e.g., PCT US97/01019. Regulatable gene therapy systems can also be used.

Once the test compound has been administered to the cells, the cells can be washed if desired and are allowed to incubate under preferably physiological conditions for some period of time. The cells are then harvested and a new gene expression profile is
15 generated, as outlined herein.

Thus, e.g., prostate cancer tissue may be screened for agents that modulate, e.g., induce or suppress the prostate cancer phenotype. A change in at least one gene, preferably many, of the expression profile indicates that the agent has an effect on prostate cancer activity. By defining such a signature for the prostate cancer phenotype, screens for
20 new drugs that alter the phenotype can be devised. With this approach, the drug target need not be known and need not be represented in the original expression screening platform, nor does the level of transcript for the target protein need to change.

In a preferred embodiment, as outlined above, screens may be done on individual genes and gene products (proteins). That is, having identified a particular
25 differentially expressed gene as important in a particular state, screening of modulators of either the expression of the gene or the gene product itself can be done. The gene products of differentially expressed genes are sometimes referred to herein as “prostate cancer proteins” or a “prostate cancer modulatory protein”. The prostate cancer modulatory protein may be a fragment, or alternatively, be the full length protein to the fragment encoded by the nucleic
30 acids of Tables 1-16. Preferably, the prostate cancer modulatory protein is a fragment. In a preferred embodiment, the prostate cancer amino acid sequence which is used to determine

sequence identity or similarity is encoded by a nucleic acid of Tables 1-16. In another embodiment, the sequences are naturally occurring allelic variants of a protein encoded by a nucleic acid of Tables 1-16. In another embodiment, the sequences are sequence variants as further described herein.

5 Preferably, the prostate cancer modulatory protein is a fragment of approximately 14 to 24 amino acids long. More preferably the fragment is a soluble fragment. Preferably, the fragment includes a non-transmembrane region. In a preferred embodiment, the fragment has an N-terminal Cys to aid in solubility. In one embodiment, the C-terminus of the fragment is kept as a free acid and the N-terminus is a free amine to aid in
10 coupling, i.e., to cysteine.

 In one embodiment the prostate cancer proteins are conjugated to an immunogenic agent as discussed herein. In one embodiment the prostate cancer protein is conjugated to BSA.

 Measurements of prostate cancer polypeptide activity, or of prostate cancer or
15 the prostate cancer phenotype can be performed using a variety of assays. For example, the effects of the test compounds upon the function of the prostate cancer polypeptides can be measured by examining parameters described above. A suitable physiological change that affects activity can be used to assess the influence of a test compound on the polypeptides of this invention. When the functional consequences are determined using intact cells or
20 animals, one can also measure a variety of effects such as, in the case of prostate cancer associated with tumors, tumor growth, tumor metastasis, neovascularization, hormone release, transcriptional changes to both known and uncharacterized genetic markers (e.g., northern blots), changes in cell metabolism such as cell growth or pH changes, and changes in intracellular second messengers such as cGMP. In the assays of the invention, mammalian
25 prostate cancer polypeptide is typically used, e.g., mouse, preferably human.

 Assays to identify compounds with modulating activity can be performed *in vitro*. For example, a prostate cancer polypeptide is first contacted with a potential modulator and incubated for a suitable amount of time, e.g., from 0.5 to 48 hours. In one embodiment, the prostate cancer polypeptide levels are determined *in vitro* by measuring the level of
30 protein or mRNA. The level of protein is measured using immunoassays such as western blotting, ELISA and the like with an antibody that selectively binds to the prostate cancer

polypeptide or a fragment thereof. For measurement of mRNA, amplification, e.g., using PCR, LCR, or hybridization assays, e.g., northern hybridization, RNase protection, dot blotting, are preferred. The level of protein or mRNA is detected using directly or indirectly labeled detection agents, e.g., fluorescently or radioactively labeled nucleic acids,
5 radioactively or enzymatically labeled antibodies, and the like, as described herein.

Alternatively, a reporter gene system can be devised using the prostate cancer protein promoter operably linked to a reporter gene such as luciferase, green fluorescent protein, CAT, or β -gal. The reporter construct is typically transfected into a cell. After treatment with a potential modulator, the amount of reporter gene transcription, translation, or
10 activity is measured according to standard techniques known to those of skill in the art.

In a preferred embodiment, as outlined above, screens may be done on individual genes and gene products (proteins). That is, having identified a particular differentially expressed gene as important in a particular state, screening of modulators of the expression of the gene or the gene product itself can be done. The gene products of
15 differentially expressed genes are sometimes referred to herein as "prostate cancer proteins." The prostate cancer protein may be a fragment, or alternatively, be the full length protein to a fragment shown herein.

In one embodiment, screening for modulators of expression of specific genes is performed. Typically, the expression of only one or a few genes are evaluated. In another
20 embodiment, screens are designed to first find compounds that bind to differentially expressed proteins. These compounds are then evaluated for the ability to modulate differentially expressed activity. Moreover, once initial candidate compounds are identified, variants can be further screened to better evaluate structure activity relationships.

In a preferred embodiment, binding assays are done. In general, purified or
25 isolated gene product is used; that is, the gene products of one or more differentially expressed nucleic acids are made. For example, antibodies are generated to the protein gene products, and standard immunoassays are run to determine the amount of protein present. Alternatively, cells comprising the prostate cancer proteins can be used in the assays.

Thus, in a preferred embodiment, the methods comprise combining a prostate
30 cancer protein and a candidate compound, and determining the binding of the compound to the prostate cancer protein. Preferred embodiments utilize the human prostate cancer protein,

although other mammalian proteins may also be used, e.g. for the development of animal models of human disease. In some embodiments, as outlined herein, variant or derivative prostate cancer proteins may be used.

Generally, in a preferred embodiment of the methods herein, the prostate cancer protein or the candidate agent is non-diffusably bound to an insoluble support having isolated sample receiving areas (e.g. a microtiter plate, an array, etc.). The insoluble supports may be made of any composition to which the compositions can be bound, is readily separated from soluble material, and is otherwise compatible with the overall method of screening. The surface of such supports may be solid or porous and of any convenient shape. Examples of suitable insoluble supports include microtiter plates, arrays, membranes and beads. These are typically made of glass, plastic (e.g., polystyrene), polysaccharides, nylon or nitrocellulose, teflon™, etc. Microtiter plates and arrays are especially convenient because a large number of assays can be carried out simultaneously, using small amounts of reagents and samples. The particular manner of binding of the composition is not crucial so long as it is compatible with the reagents and overall methods of the invention, maintains the activity of the composition and is nondiffusable. Preferred methods of binding include the use of antibodies (which do not sterically block either the ligand binding site or activation sequence when the protein is bound to the support), direct binding to "sticky" or ionic supports, chemical crosslinking, the synthesis of the protein or agent on the surface, etc. Following binding of the protein or agent, excess unbound material is removed by washing. The sample receiving areas may then be blocked through incubation with bovine serum albumin (BSA), casein or other innocuous protein or other moiety.

In a preferred embodiment, the prostate cancer protein is bound to the support, and a test compound is added to the assay. Alternatively, the candidate agent is bound to the support and the prostate cancer protein is added. Novel binding agents include specific antibodies, non-natural binding agents identified in screens of chemical libraries, peptide analogs, etc. Of particular interest are screening assays for agents that have a low toxicity for human cells. A wide variety of assays may be used for this purpose, including labeled in vitro protein-protein binding assays, electrophoretic mobility shift assays, immunoassays for protein binding, functional assays (phosphorylation assays, etc.) and the like.

The determination of the binding of the test modulating compound to the prostate cancer protein may be done in a number of ways. In a preferred embodiment, the compound is labeled, and binding determined directly, e.g., by attaching all or a portion of the prostate cancer protein to a solid support, adding a labeled candidate agent (e.g., a
5 fluorescent label), washing off excess reagent, and determining whether the label is present on the solid support. Various blocking and washing steps may be utilized as appropriate.

In some embodiments, only one of the components is labeled, e.g., the proteins (or proteinaceous candidate compounds) can be labeled. Alternatively, more than one component can be labeled with different labels, e.g., ^{125}I for the proteins and a fluorophore
10 for the compound. Proximity reagents, e.g., quenching or energy transfer reagents are also useful.

In one embodiment, the binding of the test compound is determined by competitive binding assay. The competitor is a binding moiety known to bind to the target molecule (i.e., a prostate cancer protein), such as an antibody, peptide, binding partner,
15 ligand, etc. Under certain circumstances, there may be competitive binding between the compound and the binding moiety, with the binding moiety displacing the compound. In one embodiment, the test compound is labeled. Either the compound, or the competitor, or both, is added first to the protein for a time sufficient to allow binding, if present. Incubations may be performed at a temperature which facilitates optimal activity, typically between 4 and
20 40°C. Incubation periods are typically optimized, e.g., to facilitate rapid high throughput screening. Typically between 0.1 and 1 hour will be sufficient. Excess reagent is generally removed or washed away. The second component is then added, and the presence or absence of the labeled component is followed, to indicate binding.

In a preferred embodiment, the competitor is added first, followed by the test
25 compound. Displacement of the competitor is an indication that the test compound is binding to the prostate cancer protein and thus is capable of binding to, and potentially modulating, the activity of the prostate cancer protein. In this embodiment, either component can be labeled. Thus, e.g., if the competitor is labeled, the presence of label in the wash solution indicates displacement by the agent. Alternatively, if the test compound is labeled, the
30 presence of the label on the support indicates displacement.

In an alternative embodiment, the test compound is added first, with incubation and washing, followed by the competitor. The absence of binding by the competitor may indicate that the test compound is bound to the prostate cancer protein with a higher affinity. Thus, if the test compound is labeled, the presence of the label on the support, coupled with a lack of competitor binding, may indicate that the test compound is capable of binding to the prostate cancer protein.

In a preferred embodiment, the methods comprise differential screening to identify agents that are capable of modulating the activity of the prostate cancer proteins. In this embodiment, the methods comprise combining a prostate cancer protein and a competitor in a first sample. A second sample comprises a test compound, a prostate cancer protein, and a competitor. The binding of the competitor is determined for both samples, and a change, or difference in binding between the two samples indicates the presence of an agent capable of binding to the prostate cancer protein and potentially modulating its activity. That is, if the binding of the competitor is different in the second sample relative to the first sample, the agent is capable of binding to the prostate cancer protein.

Alternatively, differential screening is used to identify drug candidates that bind to the native prostate cancer protein, but cannot bind to modified prostate cancer proteins. The structure of the prostate cancer protein may be modeled, and used in rational drug design to synthesize agents that interact with that site. Drug candidates that affect the activity of a prostate cancer protein are also identified by screening drugs for the ability to either enhance or reduce the activity of the protein.

Positive controls and negative controls may be used in the assays. Preferably control and test samples are performed in at least triplicate to obtain statistically significant results. Incubation of all samples is for a time sufficient for the binding of the agent to the protein. Following incubation, samples are washed free of non-specifically bound material and the amount of bound, generally labeled agent determined. For example, where a radiolabel is employed, the samples may be counted in a scintillation counter to determine the amount of bound compound.

A variety of other reagents may be included in the screening assays. These include reagents like salts, neutral proteins, e.g. albumin, detergents, etc. which may be used to facilitate optimal protein-protein binding and/or reduce non-specific or background

interactions. Also reagents that otherwise improve the efficiency of the assay, such as protease inhibitors, nuclease inhibitors, anti-microbial agents, etc., may be used. The mixture of components may be added in an order that provides for the requisite binding.

5 In a preferred embodiment, the invention provides methods for screening for a compound capable of modulating the activity of a prostate cancer protein. The methods comprise adding a test compound, as defined above, to a cell comprising prostate cancer proteins. Preferred cell types include almost any cell. The cells contain a recombinant nucleic acid that encodes a prostate cancer protein. In a preferred embodiment, a library of candidate agents are tested on a plurality of cells.

10 In one aspect, the assays are evaluated in the presence or absence or previous or subsequent exposure of physiological signals, e.g. hormones, antibodies, peptides, antigens, cytokines, growth factors, action potentials, pharmacological agents including chemotherapeutics, radiation, carcinogenics, or other cells (i.e. cell-cell contacts). In another example, the determinations are determined at different stages of the cell cycle process.

15 In this way, compounds that modulate prostate cancer agents are identified. Compounds with pharmacological activity are able to enhance or interfere with the activity of the prostate cancer protein. Once identified, similar structures are evaluated to identify critical structural feature of the compound.

20 In one embodiment, a method of inhibiting prostate cancer cell division is provided. The method comprises administration of a prostate cancer inhibitor. In another embodiment, a method of inhibiting prostate cancer is provided. The method comprises administration of a prostate cancer inhibitor. In a further embodiment, methods of treating cells or individuals with prostate cancer are provided. The method comprises administration of a prostate cancer inhibitor.

25 In one embodiment, a prostate cancer inhibitor is an antibody as discussed above. In another embodiment, the prostate cancer inhibitor is an antisense molecule.

A variety of cell growth, proliferation, and metastasis assays are known to those of skill in the art, as described below.

Soft agar growth or colony formation in suspension

30 Normal cells require a solid substrate to attach and grow. When the cells are transformed, they lose this phenotype and grow detached from the substrate. For example,

transformed cells can grow in stirred suspension culture or suspended in semi-solid media, such as semi-solid or soft agar. The transformed cells, when transfected with tumor suppressor genes, regenerate normal phenotype and require a solid substrate to attach and grow. Soft agar growth or colony formation in suspension assays can be used to identify
5 modulators of prostate cancer sequences, which when expressed in host cells, inhibit abnormal cellular proliferation and transformation. A therapeutic compound would reduce or eliminate the host cells' ability to grow in stirred suspension culture or suspended in semi-solid media, such as semi-solid or soft.

Techniques for soft agar growth or colony formation in suspension assays are
10 described in Freshney, *Culture of Animal Cells a Manual of Basic Technique* (3rd ed., 1994), herein incorporated by reference. See also, the methods section of Garkavtsev *et al.* (1996), *supra*, herein incorporated by reference.

Contact inhibition and density limitation of growth

Normal cells typically grow in a flat and organized pattern in a petri dish until
15 they touch other cells. When the cells touch one another, they are contact inhibited and stop growing. When cells are transformed, however, the cells are not contact inhibited and continue to grow to high densities in disorganized foci. Thus, the transformed cells grow to a higher saturation density than normal cells. This can be detected morphologically by the formation of a disoriented monolayer of cells or rounded cells in foci within the regular
20 pattern of normal surrounding cells. Alternatively, labeling index with (³H)-thymidine at saturation density can be used to measure density limitation of growth. See Freshney (1994), *supra*. The transformed cells, when transfected with tumor suppressor genes, regenerate a normal phenotype and become contact inhibited and would grow to a lower density.

In this assay, labeling index with (³H)-thymidine at saturation density is a
25 preferred method of measuring density limitation of growth. Transformed host cells are transfected with a prostate cancer-associated sequence and are grown for 24 hours at saturation density in non-limiting medium conditions. The percentage of cells labeling with (³H)-thymidine is determined autoradiographically. See, Freshney (1994), *supra*.

Growth factor or serum dependence

Transformed cells have a lower serum dependence than their normal counterparts (*see, e.g.,* Temin, *J. Natl. Cancer Inst.* 37:167-175 (1966); Eagle *et al.*, *J. Exp. Med.* 131:836-879 (1970)); Freshney, *supra*. This is in part due to release of various growth factors by the transformed cells. Growth factor or serum dependence of transformed host cells can be compared with that of control.

Tumor specific markers levels

Tumor cells release an increased amount of certain factors (hereinafter "tumor specific markers") than their normal counterparts. For example, plasminogen activator (PA) is released from human glioma at a higher level than from normal brain cells (*see, e.g.,* Gullino, *Angiogenesis, tumor vascularization, and potential interference with tumor growth*, in *Biological Responses in Cancer*, pp. 178-184 (Mihich (ed.) 1985)). Similarly, Tumor angiogenesis factor (TAF) is released at a higher level in tumor cells than their normal counterparts. *See, e.g.,* Folkman, *Angiogenesis and Cancer*, *Sem Cancer Biol.* (1992)).

Various techniques which measure the release of these factors are described in Freshney (1994), *supra*. Also, *see*, Unkless *et al.*, *J. Biol. Chem.* 249:4295-4305 (1974); Strickland & Beers, *J. Biol. Chem.* 251:5694-5702 (1976); Whur *et al.*, *Br. J. Cancer* 42:305-312 (1980); Gullino, *Angiogenesis, tumor vascularization, and potential interference with tumor growth*, in *Biological Responses in Cancer*, pp. 178-184 (Mihich (ed.) 1985); Freshney *Anticancer Res.* 5:111-130 (1985).

Invasiveness into Matrigel

The degree of invasiveness into Matrigel or some other extracellular matrix constituent can be used as an assay to identify compounds that modulate prostate cancer-associated sequences. Tumor cells exhibit a good correlation between malignancy and invasiveness of cells into Matrigel or some other extracellular matrix constituent. In this assay, tumorigenic cells are typically used as host cells. Expression of a tumor suppressor gene in these host cells would decrease invasiveness of the host cells.

Techniques described in Freshney (1994), *supra*, can be used. Briefly, the level of invasion of host cells can be measured by using filters coated with Matrigel or some

other extracellular matrix constituent. Penetration into the gel, or through to the distal side of the filter, is rated as invasiveness, and rated histologically by number of cells and distance moved, or by prelabeling the cells with ^{125}I and counting the radioactivity on the distal side of the filter or bottom of the dish. See, e.g., Freshney (1984), *supra*.

5

Tumor growth in vivo

Effects of prostate cancer-associated sequences on cell growth can be tested in transgenic or immune-suppressed mice. Knock-out transgenic mice can be made, in which the prostate cancer gene is disrupted or in which a prostate cancer gene is inserted. Knock-out transgenic mice can be made by insertion of a marker gene or other heterologous gene into the endogenous prostate cancer gene site in the mouse genome via homologous recombination. Such mice can also be made by substituting the endogenous prostate cancer gene with a mutated version of the prostate cancer gene, or by mutating the endogenous prostate cancer gene, e.g., by exposure to carcinogens.

15 A DNA construct is introduced into the nuclei of embryonic stem cells. Cells containing the newly engineered genetic lesion are injected into a host mouse embryo, which is re-implanted into a recipient female. Some of these embryos develop into chimeric mice that possess germ cells partially derived from the mutant cell line. Therefore, by breeding the chimeric mice it is possible to obtain a new line of mice containing the introduced genetic lesion (see, e.g., Capecchi *et al.*, *Science* 244:1288 (1989)). Chimeric targeted mice can be derived according to Hogan *et al.*, *Manipulating the Mouse Embryo: A Laboratory Manual*, Cold Spring Harbor Laboratory (1988) and *Teratocarcinomas and Embryonic Stem Cells: A Practical Approach*, Robertson, ed., IRL Press, Washington, D.C., (1987).

25 Alternatively, various immune-suppressed or immune-deficient host animals can be used. For example, genetically athymic "nude" mouse (see, e.g., Giovanella *et al.*, *J. Natl. Cancer Inst.* 52:921 (1974)), a SCID mouse, a thymectomized mouse, or an irradiated mouse (see, e.g., Bradley *et al.*, *Br. J. Cancer* 38:263 (1978); Selby *et al.*, *Br. J. Cancer* 41:52 (1980)) can be used as a host. Transplantable tumor cells (typically about 10^6 cells) injected into isogenic hosts will produce invasive tumors in a high proportions of cases, while
30 normal cells of similar origin will not. In hosts which developed invasive tumors, cells expressing a prostate cancer-associated sequences are injected subcutaneously. After a

suitable length of time, preferably 4-8 weeks, tumor growth is measured (e.g., by volume or by its two largest dimensions) and compared to the control. Tumors that have statistically significant reduction (using, e.g., Student's T test) are said to have inhibited growth.

5 **Methods of identifying variant prostate cancer-associated sequences**

Without being bound by theory, expression of various prostate cancer sequences is correlated with prostate cancer. Accordingly, disorders based on mutant or variant prostate cancer genes may be determined. In one embodiment, the invention provides methods for identifying cells containing variant prostate cancer genes, e.g., determining all or
10 part of the sequence of at least one endogenous prostate cancer genes in a cell. This may be accomplished using any number of sequencing techniques. In a preferred embodiment, the invention provides methods of identifying the prostate cancer genotype of an individual, e.g., determining all or part of the sequence of at least one prostate cancer gene of the individual. This is generally done in at least one tissue of the individual, and may include the evaluation
15 of a number of tissues or different samples of the same tissue. The method may include comparing the sequence of the sequenced prostate cancer gene to a known prostate cancer gene, i.e., a wild-type gene.

The sequence of all or part of the prostate cancer gene can then be compared to the sequence of a known prostate cancer gene to determine if any differences exist. This
20 can be done using any number of known homology programs, such as Bestfit, etc. In a preferred embodiment, the presence of a difference in the sequence between the prostate cancer gene of the patient and the known prostate cancer gene correlates with a disease state or a propensity for a disease state, as outlined herein.

In a preferred embodiment, the prostate cancer genes are used as probes to
25 determine the number of copies of the prostate cancer gene in the genome.

In another preferred embodiment, the prostate cancer genes are used as probes to determine the chromosomal localization of the prostate cancer genes. Information such as chromosomal localization finds use in providing a diagnosis or prognosis in particular when chromosomal abnormalities such as translocations, and the like are identified in the prostate
30 cancer gene locus.

Administration of pharmaceutical and vaccine compositions

In one embodiment, a therapeutically effective dose of a prostate cancer protein or modulator thereof, is administered to a patient. By "therapeutically effective dose" herein is meant a dose that produces effects for which it is administered. The exact dose will depend on the purpose of the treatment, and will be ascertainable by one skilled in the art using known techniques (e.g., Ansel *et al.*, *Pharmaceutical Dosage Forms and Drug Delivery*; Lieberman, *Pharmaceutical Dosage Forms* (vols. 1-3, 1992), Dekker, ISBN 0824770846, 082476918X, 0824712692, 0824716981; Lloyd, *The Art, Science and Technology of Pharmaceutical Compounding* (1999); and Pickar, *Dosage Calculations* (1999)). As is known in the art, adjustments for prostate cancer degradation, systemic versus localized delivery, and rate of new protease synthesis, as well as the age, body weight, general health, sex, diet, time of administration, drug interaction and the severity of the condition may be necessary, and will be ascertainable with routine experimentation by those skilled in the art. U.S. Patent Application N. 09/687,576, further discloses the use of compositions and methods of diagnosis and treatment in prostate cancer is hereby expressly incorporated by reference.

A "patient" for the purposes of the present invention includes both humans and other animals, particularly mammals. Thus the methods are applicable to both human therapy and veterinary applications. In the preferred embodiment the patient is a mammal, preferably a primate, and in the most preferred embodiment the patient is human.

The administration of the prostate cancer proteins and modulators thereof of the present invention can be done in a variety of ways as discussed above, including, but not limited to, orally, subcutaneously, intravenously, intranasally, transdermally, intraperitoneally, intramuscularly, intrapulmonary, vaginally, rectally, or intraocularly. In some instances, e.g., in the treatment of wounds and inflammation, the prostate cancer proteins and modulators may be directly applied as a solution or spray.

The pharmaceutical compositions of the present invention comprise a prostate cancer protein in a form suitable for administration to a patient. In the preferred embodiment, the pharmaceutical compositions are in a water soluble form, such as being present as pharmaceutically acceptable salts, which is meant to include both acid and base addition salts. "Pharmaceutically acceptable acid addition salt" refers to those salts that retain the

biological effectiveness of the free bases and that are not biologically or otherwise undesirable, formed with inorganic acids such as hydrochloric acid, hydrobromic acid, sulfuric acid, nitric acid, phosphoric acid and the like, and organic acids such as acetic acid, propionic acid, glycolic acid, pyruvic acid, oxalic acid, maleic acid, malonic acid, succinic acid, fumaric acid, tartaric acid, citric acid, benzoic acid, cinnamic acid, mandelic acid, methanesulfonic acid, ethanesulfonic acid, p-toluenesulfonic acid, salicylic acid and the like. "Pharmaceutically acceptable base addition salts" include those derived from inorganic bases such as sodium, potassium, lithium, ammonium, calcium, magnesium, iron, zinc, copper, manganese, aluminum salts and the like. Particularly preferred are the ammonium, potassium, sodium, calcium, and magnesium salts. Salts derived from pharmaceutically acceptable organic non-toxic bases include salts of primary, secondary, and tertiary amines, substituted amines including naturally occurring substituted amines, cyclic amines and basic ion exchange resins, such as isopropylamine, trimethylamine, diethylamine, triethylamine, tripropylamine, and ethanolamine.

The pharmaceutical compositions may also include one or more of the following: carrier proteins such as serum albumin; buffers; fillers such as microcrystalline cellulose, lactose, corn and other starches; binding agents; sweeteners and other flavoring agents; coloring agents; and polyethylene glycol.

The pharmaceutical compositions can be administered in a variety of unit dosage forms depending upon the method of administration. For example, unit dosage forms suitable for oral administration include, but are not limited to, powder, tablets, pills, capsules and lozenges. It is recognized that prostate cancer protein modulators (e.g., antibodies, antisense constructs, ribozymes, small organic molecules, *etc.*) when administered orally, should be protected from digestion. This is typically accomplished either by complexing the molecule(s) with a composition to render it resistant to acidic and enzymatic hydrolysis, or by packaging the molecule(s) in an appropriately resistant carrier, such as a liposome or a protection barrier. Means of protecting agents from digestion are well known in the art.

The compositions for administration will commonly comprise a prostate cancer protein modulator dissolved in a pharmaceutically acceptable carrier, preferably an aqueous carrier. A variety of aqueous carriers can be used, e.g., buffered saline and the like. These solutions are sterile and generally free of undesirable matter. These compositions may

be sterilized by conventional, well known sterilization techniques. The compositions may contain pharmaceutically acceptable auxiliary substances as required to approximate physiological conditions such as pH adjusting and buffering agents, toxicity adjusting agents and the like, e.g., sodium acetate, sodium chloride, potassium chloride, calcium chloride, sodium lactate and the like. The concentration of active agent in these formulations can vary widely, and will be selected primarily based on fluid volumes, viscosities, body weight and the like in accordance with the particular mode of administration selected and the patient's needs (e.g., *Remington's Pharmaceutical Science* (15th ed., 1980) and Goodman & Gillman, *The Pharmacological Basis of Therapeutics* (Hardman et al., eds., 1996)).

Thus, a typical pharmaceutical composition for intravenous administration would be about 0.1 to 10 mg per patient per day. Dosages from 0.1 up to about 100 mg per patient per day may be used, particularly when the drug is administered to a secluded site and not into the blood stream, such as into a body cavity or into a lumen of an organ. Substantially higher dosages are possible in topical administration. Actual methods for preparing parenterally administrable compositions will be known or apparent to those skilled in the art, e.g., *Remington's Pharmaceutical Science* and Goodman and Gillman, *The Pharmacological Basis of Therapeutics, supra*.

The compositions containing modulators of prostate cancer proteins can be administered for therapeutic or prophylactic treatments. In therapeutic applications, compositions are administered to a patient suffering from a disease (e.g., a cancer) in an amount sufficient to cure or at least partially arrest the disease and its complications. An amount adequate to accomplish this is defined as a "therapeutically effective dose." Amounts effective for this use will depend upon the severity of the disease and the general state of the patient's health. Single or multiple administrations of the compositions may be administered depending on the dosage and frequency as required and tolerated by the patient. In any event, the composition should provide a sufficient quantity of the agents of this invention to effectively treat the patient. An amount of modulator that is capable of preventing or slowing the development of cancer in a mammal is referred to as a "prophylactically effective dose." The particular dose required for a prophylactic treatment will depend upon the medical condition and history of the mammal, the particular cancer being prevented, as well as other factors such as age, weight, gender, administration route, efficiency, etc. Such prophylactic

treatments may be used, *e.g.*, in a mammal who has previously had cancer to prevent a recurrence of the cancer, or in a mammal who is suspected of having a significant likelihood of developing cancer.

5 It will be appreciated that the present prostate cancer protein-modulating compounds can be administered alone or in combination with additional prostate cancer modulating compounds or with other therapeutic agent, *e.g.*, other anti-cancer agents or treatments.

10 In numerous embodiments, one or more nucleic acids, *e.g.*, polynucleotides comprising nucleic acid sequences set forth in Tables 1-16, such as antisense polynucleotides or ribozymes, will be introduced into cells, *in vitro* or *in vivo*. The present invention provides methods, reagents, vectors, and cells useful for expression of prostate cancer-associated polypeptides and nucleic acids using *in vitro* (cell-free), *ex vivo* or *in vivo* (cell or organism-based) recombinant expression systems.

15 The particular procedure used to introduce the nucleic acids into a host cell for expression of a protein or nucleic acid is application specific. Many procedures for introducing foreign nucleotide sequences into host cells may be used. These include the use of calcium phosphate transfection, spheroplasts, electroporation, liposomes, microinjection, plasma vectors, viral vectors and any of the other well known methods for introducing cloned genomic DNA, cDNA, synthetic DNA or other foreign genetic material into a host cell (*see*,
20 *e.g.*, Berger & Kimmel, *Guide to Molecular Cloning Techniques, Methods in Enzymology* volume 152 (Berger), Ausubel *et al.*, eds., *Current Protocols* (supplemented through 1999), and Sambrook *et al.*, *Molecular Cloning - A Laboratory Manual* (2nd ed., Vol. 1-3, 1989).

25 In a preferred embodiment, prostate cancer proteins and modulators are administered as therapeutic agents, and can be formulated as outlined above. Similarly, prostate cancer genes (including both the full-length sequence, partial sequences, or regulatory sequences of the prostate cancer coding regions) can be administered in a gene therapy application. These prostate cancer genes can include antisense applications, either as gene therapy (*i.e.* for incorporation into the genome) or as antisense compositions, as will be appreciated by those in the art.

30 Prostate cancer polypeptides and polynucleotides can also be administered as vaccine compositions to stimulate HTL, CTL and antibody responses.. Such vaccine

compositions can include, e.g., lipidated peptides (*see, e.g., Vitiello, A. et al., J. Clin. Invest.* 95:341 (1995)), peptide compositions encapsulated in poly(DL-lactide-co-glycolide) ("PLG") microspheres (*see, e.g., Eldridge, et al., Molec. Immunol.* 28:287-294, (1991); Alonso *et al., Vaccine* 12:299-306 (1994); Jones *et al., Vaccine* 13:675-681 (1995)), peptide compositions
5 contained in immune stimulating complexes (ISCOMS) (*see, e.g., Takahashi et al., Nature* 344:873-875 (1990); Hu *et al., Clin Exp Immunol.* 113:235-243 (1998)), multiple antigen peptide systems (MAPs) (*see, e.g., Tam, Proc. Natl. Acad. Sci. U.S.A.* 85:5409-5413 (1988); Tam, *J. Immunol. Methods* 196:17-32 (1996)), peptides formulated as multivalent peptides; peptides for use in ballistic delivery systems, typically crystallized peptides, viral delivery
10 vectors (Perkus, *et al., In: Concepts in vaccine development* (Kaufmann, ed., p. 379, 1996); Chakrabarti, *et al., Nature* 320:535 (1986); Hu *et al., Nature* 320:537 (1986); Kieny, *et al., AIDS Bio/Technology* 4:790 (1986); Top *et al., J. Infect. Dis.* 124:148 (1971); Chanda *et al., Virology* 175:535 (1990)), particles of viral or synthetic origin (*see, e.g., Kofler et al., J. Immunol. Methods.* 192:25 (1996); Eldridge *et al., Sem. Hematol.* 30:16 (1993); Falo *et al.,*
15 *Nature Med.* 7:649 (1995)), adjuvants (Warren *et al., Annu. Rev. Immunol.* 4:369 (1986); Gupta *et al., Vaccine* 11:293 (1993)), liposomes (Reddy *et al., J. Immunol.* 148:1585 (1992); Rock, *Immunol. Today* 17:131 (1996)), or, naked or particle absorbed cDNA (Ulmer, *et al., Science* 259:1745 (1993); Robinson *et al., Vaccine* 11:957 (1993); Shiver *et al., In: Concepts in vaccine development* (Kaufmann, ed., p. 423, 1996); Cease & Berzofsky, *Annu. Rev.*
20 *Immunol.* 12:923 (1994) and Eldridge *et al., Sem. Hematol.* 30:16 (1993)). Toxin-targeted delivery technologies, also known as receptor mediated targeting, such as those of Avant Immunotherapeutics, Inc. (Needham, Massachusetts) may also be used.

Vaccine compositions often include adjuvants. Many adjuvants contain a substance designed to protect the antigen from rapid catabolism, such as aluminum hydroxide
25 or mineral oil, and a stimulator of immune responses, such as lipid A, *Bordetella pertussis* or *Mycobacterium tuberculosis* derived proteins. Certain adjuvants are commercially available as, e.g., Freund's Incomplete Adjuvant and Complete Adjuvant (Difco Laboratories, Detroit, MI); Merck Adjuvant 65 (Merck and Company, Inc., Rahway, NJ); AS-2 (SmithKline Beecham, Philadelphia, PA); aluminum salts such as aluminum hydroxide gel (alum) or
30 aluminum phosphate; salts of calcium, iron or zinc; an insoluble suspension of acylated tyrosine; acylated sugars; cationically or anionically derivatized polysaccharides;

polyphosphazenes; biodegradable microspheres; monophosphoryl lipid A and quil A. Cytokines, such as GM-CSF, interleukin-2, -7, -12, and other like growth factors, may also be used as adjuvants.

Vaccines can be administered as nucleic acid compositions wherein DNA or
5 RNA encoding one or more of the polypeptides, or a fragment thereof, is administered to a patient. This approach is described, for instance, in Wolff *et. al.*, *Science* 247:1465 (1990) as well as U.S. Patent Nos. 5,580,859; 5,589,466; 5,804,566; 5,739,118; 5,736,524; 5,679,647; WO 98/04720; and in more detail below. Examples of DNA-based delivery technologies include "naked DNA", facilitated (bupivacaine, polymers, peptide-mediated) delivery,
10 cationic lipid complexes, and particle-mediated ("gene gun") or pressure-mediated delivery (*see, e.g.*, U.S. Patent No. 5,922,687).

For therapeutic or prophylactic immunization purposes, the peptides of the invention can be expressed by viral or bacterial vectors. Examples of expression vectors include attenuated viral hosts, such as vaccinia or fowlpox. This approach involves the use of
15 vaccinia virus, *e.g.*, as a vector to express nucleotide sequences that encode prostate cancer polypeptides or polypeptide fragments. Upon introduction into a host, the recombinant vaccinia virus expresses the immunogenic peptide, and thereby elicits an immune response. Vaccinia vectors and methods useful in immunization protocols are described in, *e.g.*, U.S. Patent No. 4,722,848. Another vector is BCG (Bacille Calmette Guerin). BCG vectors are
20 described in Stover *et al.*, *Nature* 351:456-460 (1991). A wide variety of other vectors useful for therapeutic administration or immunization *e.g.* adeno and adeno-associated virus vectors, retroviral vectors, *Salmonella typhi* vectors, detoxified anthrax toxin vectors, and the like, will be apparent to those skilled in the art from the description herein (*see, e.g.*, Shata *et al.*, *Mol Med Today* 6:66-71 (2000); Shedlock *et al.*, *J Leukoc Biol* 68:793-806 (2000); Hipp *et al.*, *In Vivo* 14:571-85 (2000)).
25

Methods for the use of genes as DNA vaccines are well known, and include placing a prostate cancer gene or portion of a prostate cancer gene under the control of a regulatable promoter or a tissue-specific promoter for expression in a prostate cancer patient. The prostate cancer gene used for DNA vaccines can encode full-length prostate cancer
30 proteins, but more preferably encodes portions of the prostate cancer proteins including peptides derived from the prostate cancer protein. In one embodiment, a patient is

immunized with a DNA vaccine comprising a plurality of nucleotide sequences derived from a prostate cancer gene. For example, prostate cancer-associated genes or sequence encoding subfragments of a prostate cancer protein are introduced into expression vectors and tested for their immunogenicity in the context of Class I MHC and an ability to generate cytotoxic T cell responses. This procedure provides for production of cytotoxic T cell responses against cells which present antigen, including intracellular epitopes.

In a preferred embodiment, the DNA vaccines include a gene encoding an adjuvant molecule with the DNA vaccine. Such adjuvant molecules include cytokines that increase the immunogenic response to the prostate cancer polypeptide encoded by the DNA vaccine. Additional or alternative adjuvants are available.

In another preferred embodiment prostate cancer genes find use in generating animal models of prostate cancer. When the prostate cancer gene identified is repressed or diminished in cancer tissue, gene therapy technology, e.g., wherein antisense RNA directed to the prostate cancer gene will also diminish or repress expression of the gene. Animal models of prostate cancer find use in screening for modulators of a prostate cancer-associated sequence or modulators of prostate cancer. Similarly, transgenic animal technology including gene knockout technology, e.g. as a result of homologous recombination with an appropriate gene targeting vector, will result in the absence or increased expression of the prostate cancer protein. When desired, tissue-specific expression or knockout of the prostate cancer protein may be necessary.

It is also possible that the prostate cancer protein is overexpressed in prostate cancer. As such, transgenic animals can be generated that overexpress the prostate cancer protein. Depending on the desired expression level, promoters of various strengths can be employed to express the transgene. Also, the number of copies of the integrated transgene can be determined and compared for a determination of the expression level of the transgene. Animals generated by such methods find use as animal models of prostate cancer and are additionally useful in screening for modulators to treat prostate cancer.

Kits for Use in Diagnostic and/or Prognostic Applications

For use in diagnostic, research, and therapeutic applications suggested above, kits are also provided by the invention. In the diagnostic and research applications such kits

may include any or all of the following: assay reagents, buffers, prostate cancer-specific nucleic acids or antibodies, hybridization probes and/or primers, antisense polynucleotides, ribozymes, dominant negative prostate cancer polypeptides or polynucleotides, small molecules inhibitors of prostate cancer-associated sequences *etc.* A therapeutic product may include sterile saline or another pharmaceutically acceptable emulsion and suspension base.

In addition, the kits may include instructional materials containing directions (i.e., protocols) for the practice of the methods of this invention. While the instructional materials typically comprise written or printed materials they are not limited to such. Any medium capable of storing such instructions and communicating them to an end user is contemplated by this invention. Such media include, but are not limited to electronic storage media (e.g., magnetic discs, tapes, cartridges, chips), optical media (e.g., CD ROM), and the like. Such media may include addresses to internet sites that provide such instructional materials.

The present invention also provides for kits for screening for modulators of prostate cancer-associated sequences. Such kits can be prepared from readily available materials and reagents. For example, such kits can comprise one or more of the following materials: a prostate cancer-associated polypeptide or polynucleotide, reaction tubes, and instructions for testing prostate cancer-associated activity. Optionally, the kit contains biologically active prostate cancer protein. A wide variety of kits and components can be prepared according to the present invention, depending upon the intended user of the kit and the particular needs of the user. Diagnosis would typically involve evaluation of a plurality of genes or products. The genes will be selected based on correlations with important parameters in disease which may be identified in historical or outcome data.

EXAMPLES

Example 1: Tissue Preparation, Labeling Chips, and Fingerprints

5 Purifying total RNA from tissue sample using TRIzol Reagent

The sample weight is first estimated. The tissue samples are homogenized in 1 ml of TRIzol per 50 mg of tissue using a homogenizer (e.g., Polytron 3100). The size of the generator/probe used depends upon the sample amount. A generator that is too large for the amount of tissue to be homogenized will cause a loss of sample and lower RNA yield. A
10 larger generator (e.g., 20 mm) is suitable for tissue samples weighing more than 0.6 g. Fill tubes should not be overfilled. If the working volume is greater than 2 ml and no greater than 10 ml, a 15 ml polypropylene tube (Falcon 2059) is suitable for homogenization.

Tissues should be kept frozen until homogenized. The TRIzol is added directly to the frozen tissue before homogenization. Following homogenization, the insoluble
15 material is removed from the homogenate by centrifugation at 7500 x g for 15 min. in a Sorvall superspeed or 12,000 x g for 10 min. in an Eppendorf centrifuge at 4°C. The cleared homogenate is then transferred to a new tube(s). Samples may be frozen and stored at -60 to -70°C for at least one month or else continue with the purification.

The next process is phase separation. The homogenized samples are incubated
20 for 5 minutes at room temperature. Then, 0.2 ml of chloroform per 1ml of TRIzol reagent is added to the homogenization mixture. The tubes are securely capped and shaken vigorously by hand (do not vortex) for 15 seconds. The samples are then incubated at room temp. for 2-3 minutes and next centrifuged at 6500 rpm in a Sorvall superspeed for 30 min. at 4°C.

The next process is RNA Precipitation. The aqueous phase is transferred to a
25 fresh tube. The organic phase can be saved if isolation of DNA or protein is desired. Then 0.5 ml of isopropyl alcohol is added per 1ml of TRIzol reagent used in the original homogenization. Then, the tubes are securely capped and inverted to mix. The samples are then incubated at room temp. for 10 minutes and centrifuged at 6500 rpm in Sorvall for 20 min. at 4°C.

The RNA is then washed. The supernatant is poured off and the pellet washed with cold 75% ethanol. 1 ml of 75% ethanol is used per 1 ml of the TRIzol reagent used in the initial homogenization. The tubes are capped securely and inverted several times to loosen pellet without vortexing. They are next centrifuged at <8000 rpm (<7500 x g) for 5 minutes at 4°C.

The RNA wash is decanted. The pellet is carefully transferred to an Eppendorf tube (sliding down the tube into the new tube by use of a pipet tip to help guide it in if necessary). Tube(s) sizes for precipitating the RNA depending on the working volumes. Larger tubes may take too long to dry. Dry pellet. The RNA is then resuspended in an appropriate volume (e.g., 2 -5 ug/ul) of DEPC H₂O. The absorbance is then measured.

The poly A+ mRNA may next be purified from total RNA by other methods such as Qiagen's RNeasy kit. The poly A + mRNA is purified from total RNA by adding the oligotex suspension which has been heated to 37°C and mixing prior to adding to RNA. The Elution Buffer is incubated at 70°C. If there is precipitate in the buffer, warm up the 2 x Binding Buffer at 65°C. The the total RNA is mixed with DEPC-treated water, 2 x Binding Buffer, and Oligotex according to Table 2 on page 16 of the Oligotex Handbook and next incubated for 3 minutes at 65°C and 10 minutes at room temperature.

The preparation is centrifuged for 2 minutes at 14,000 to 18,000 g; preferably, at a "soft setting," The supernatant is removed without disturbing Oligotex pellet. A little bit of solution can be left behind to reduce the loss of Oligotex. The supernatant is saved until satisfactory binding and elution of poly A+ mRNA has been found.

Then, the preparation is gently resuspended in Wash Buffer OW2 and pipetted onto the spin column and centrifuged at full speed (soft setting if possible) for 1 minute.

Next, the spin column is transferred to a new collection tube and gently resuspended in Wash Buffer OW2 and centrifuged as described herein.

Then, the spin column is transferred to a new tube and eluted with 20 to 100 ul of preheated (70°C) Elution Buffer. The Oligotex resin is gently resuspended by pipetting up and down. The centrifugation is repeated as above and the elution repeated with fresh elution buffer or first eluate to keep the elution volume low.

The absorbance is next read to determine the yield, using diluted Elution Buffer as the blank.

- Before proceeding with cDNA synthesis, the mRNA is precipitated before proceeding with cDNA synthesis, as components leftover or in the Elution Buffer from the
- 5 Oligotex purification procedure will inhibit downstream enzymatic reactions of the mRNA. 0.4 vol. of 7.5 M NH₄OAc + 2.5 vol. of cold 100% ethanol is added and the preparation precipitated at -20°C 1 hour to overnight (or 20-30 min. at -70°C), and centrifuged at 14,000-16,000 x g for 30 minutes at 4°C. Next, the pellet is washed with 0.5 ml of 80% ethanol (-20°C) and then centrifuged at 14,000-16,000 x g for 5 minutes at room temperature.
- 10 The 80% ethanol wash is then repeated. The last bit of ethanol from the pellet is then dried without use of a speed vacuum and the pellet is then resuspended in DEPC H₂O at 1 µg/ul concentration.

Alternatively the RNA may be purified using other methods (e.g., Qiagen's RNeasy kit).

- 15 No more than 100 µg is added to the RNeasy column. The sample volume is adjusted to 100 µl with RNase-free water. 350 µl Buffer RLT and then 250 µl ethanol (100%) are added to the sample. The preparation is then mixed by pipetting and applied to an RNeasy mini spin column for centrifugation (15 sec at >10,000 rpm). If yield is low, reapply the flowthrough to the column and centrifuge again.
- 20 Then, transfer column to a new 2 ml collection tube and add 500 µl Buffer RPE and centrifuge for 15 sec at >10,000 rpm. The flowthrough is discarded. 500 µl Buffer RPE and is then added and the preparation is centrifuged for 15 sec at >10,000 rpm. The flowthrough is discarded. and the column membrane dried by centrifuging for 2 min at maximum speed. The column is transferred to a new 1.5-ml collection tube. 30-50 µl of
- 25 RNase-free water is applied directly onto column membrane. The column is then centrifuged for 1 min at >10,000 rpm and the elution step repeated.

The absorbance is then read to determine yield. If necessary, the material may be ethanol precipitated with ammonium acetate and 2.5X volume 100% ethanol.

- 30 First Strand cDNA Synthesis

The first strand can be made using Gibco's "SuperScript Choice System for cDNA Synthesis" kit. The starting material is 5 ug of total RNA or 1 ug of polyA+ mRNA. For total RNA, 2 ul of SuperScript RT is used; for polyA+ mRNA, 1 ul of SuperScript RT is used. The final volume of first strand synthesis mix is 20 ul. The RNA should be in a volume no greater than 10 ul. The RNA is incubated with 1 ul of 100 pmol T7-T24 oligo for 10 min at 70°C followed by addition on ice of 7 ul of: 4ul 5X 1st Strand Buffer, 2 ul of 0.1M DTT, and 1 ul of 10mM dNTP mix. The preparation is then incubated at 37°C for 2 min before addition of the SuperScript RT followed by incubation at 37°C for 1 hour.

10

Second Strand Synthesis

For the second strand synthesis, place 1st strand reactions on ice and add: 91 ul DEPC H₂O; 30 ul 5X 2nd Strand Buffer; 3 ul 10mM dNTP mix; 1 ul 10 U/ul E.coli DNA Ligase; 4 ul 10 U/ul E.coli DNA Polymerase; and 1 ul 2 U/ul RNase H. Mix and incubate 2 hours at 16°C. Add 2 ul T4 DNA Polymerase. Incubate 5 min at 16°C. Add 10 ul of 0.5M EDTA.

15

Cleaning up cDNA

The cDNA is purified using Phenol:Chloroform:Isoamyl Alcohol (25:24:1) and Phase-Lock gel tubes. The PLG tubes are centrifuged for 30 sec at maximum speed. The cDNA mix is then transferred to PLG tube. An equal volume of phenol:chloroform:isamyl alcohol is then added, the preparation shaken vigorously (no vortexing), and centrifuged for 5 minutes at maximum speed. The top aqueous solution is transferred to a new tube and ethanol precipitated by adding 7.5X 5M NH₄OAc and 2.5X volume of 100% ethanol. Next, it is centrifuged immediately at room temperature for 20 min, maximum speed. The supernatant is removed, and the pellet washed with 2X with cold 80% ethanol. As much ethanol wash as possible should be removed before air drying the pellet; and resuspending it in 3 ul RNase-free water.

20

25

In vitro Transcription (IVT) and labeling with biotin

In vitro Transcription (IVT) and labeling with biotin is performed as follows: Pipet 1.5 ul of cDNA into a thin-wall PCR tube. Make NTP labeling mix by combining 2 ul T7 10xATP (75 mM) (Ambion); 2 ul T7 10xGTP (75 mM) (Ambion); 1.5 ul T7 10xCTP (75 mM) (Ambion); 1.5 ul T7 10xUTP (75 mM) (Ambion); 3.75 ul 10 mM Bio-11-UTP (Boehringer-Mannheim/Roche or Enzo); 3.75 ul 10 mM Bio-16-CTP (Enzo); 2 ul 10x T7 transcription buffer (Ambion); and 2 ul 10x T7 enzyme mix (Ambion). The final volume is 20 ul. Incubate 6 hours at 37°C in a PCR machine. The RNA can be furthered cleaned. Clean-up follows the previous instructions for RNeasy columns or Qiagen's RNeasy protocol handbook. The cRNA often needs to be ethanol precipitated by resuspension in a volume compatible with the fragmentation step.

Fragmentation is performed as follows. 15 ug of labeled RNA is usually fragmented. Try to minimize the fragmentation reaction volume; a 10 ul volume is recommended but 20 ul is all right. Do not go higher than 20 ul because the magnesium in the fragmentation buffer contributes to precipitation in the hybridization buffer. Fragment RNA by incubation at 94 C for 35 minutes in 1 x Fragmentation buffer (5 x Fragmentation buffer is 200 mM Tris-acetate, pH 8.1; 500 mM KOAc; 150 mM MgOAc). The labeled RNA transcript can be analyzed before and after fragmentation. Samples can be heated to 65°C for 15 minutes and electrophoresed on 1% agarose/TBE gels to get an approximate idea of the transcript size range.

For hybridization, 200 ul (10 ug cRNA) of a hybridization mix is put on the chip. If multiple hybridizations are to be done (such as cycling through a 5 chip set), then it is recommended that an initial hybridization mix of 300 ul or more be made. The hybridization mix is: fragment labeled RNA (50 ng/ul final conc.); 50 pM 948-b control oligo; 1.5 pM BioB; 5 pM BioC; 25 pM BioD; 100 pM CRE; 0.1 mg/ml herring sperm DNA; 0.5 mg/ml acetylated BSA; and 300 ul with 1xMES hyb buffer.

The hybridization reaction is conducted with non-biotinylated IVT (purified by RNeasy columns) (see example 1 for steps from tissue to IVT): The following mixture is prepared:

IVT antisense RNA; 4 µg:	µl
Random Hexamers (1 µg/µl):	4 µl
H ₂ O:	<u> µl </u>
	14 µl

- 5 Incubate the above 14 µl mixture at 70°C for 10 min.; then put on ice.

The Reverse transcription procedure uses the following mixture:

0.1 M DTT:	3 µl
50X dNTP mix:	0.6 µl
H ₂ O:	2.4 µl
10 Cy3 or Cy5 dUTP (1mM):	3 µl
SS RT II (BRL):	1 µl
	<u> </u>
	16 µl

The above solution is added to the hybridization reaction and incubated for 30 min., 42°C.

- 15 Then, 1 µl SSII is added and incubated for another hour before being placed on ice.

The 50X dNTP mix contains 25mM of cold dATP, dCTP, and dGTP, 10mM of dTTP and is made by adding 25 µl each of 100mM dATP, dCTP, and dGTP; 10 µl of 100mM dTTP to 15 µl H₂O.]

- RNA degradation is performed as follows. Add 86 µl H₂O, 1.5 µl 1M NaOH/
20 2 mM EDTA and incubate at 65°C, 10 min.. For U-Con 30, 500 µl TE/sample spin at 7000 g for 10 min, save flow through for purification. For Qiagen purification, suspend u-con recovered material in 500 µl buffer PB and proceed using Qiagen protocol. For DNase digestion, add 1 ul of 1/100 dilution of DNase/30 ul Rx and incubate at 37°C for 15 min. Incubate at 5 min 95°C to denature the DNase.

25

Sample preparation

For sample preparation, add Cot-1 DNA, 10 µl; 50X dNTPs, 1 µl; 20X SSC, 2.3 µl; Na pyro phosphate, 7.5 µl; 10 mg/ml Herring sperm DNA; 1 ul of 1/10 dilution to 21.8 final vol. Dry in speed vac. Resuspend in 15 µl H₂O. Add 0.38 µl 10% SDS. Heat

95°C, 2 min and slow cool at room temp. for 20 min. Put on slide and hybridize overnight at 64°C. Washing after the hybridization: 3X SSC/0.03% SDS: 2 min., 37.5 ml 20X SSC+0.75ml 10% SDS in 250ml H₂O; 1X SSC: 5 min., 12.5 ml 20X SSC in 250ml H₂O; 0.2X SSC: 5 min., 2.5 ml 20X SSC in 250ml H₂O. Dry slides and scan at appropriate PMT's and channels.

Example 2: Taxol resistant Xenograft Model of Human Prostate Cancer

Treatment regimens that include paclitaxel (Taxol; Bristol-Myers Squibb Company, Princeton, NJ) have been particularly successful in treating hormone-refractory prostate cancer in the phase II setting (Smith et al., Semin. Oncol. 26(1 Suppl 2):109-11 (1999)). However, many patients develop tumors which are initially, or later become, resistant to taxol. To identify genes that may be involved with resistance to taxol, or are regulated in response to taxol resistance, and therefore may be used to treat, or identify, taxol resistance in patients, the following experiments were carried out.

The androgen-independent human cell line CWR22R was grown as a xenograft in nude mice (Nagabhushan et al., Cancer Res. 56(13):3042-3046 (1996); Agus et al., J. Natl. Cancer Inst. 91(21):1869-1876 (1999); Bubendorf et al., J. Natl. Cancer Inst. 91(20):1758-1764 (1999)). Initially, these xenograft tumors were sensitive to therapeutic doses of taxol. The mice were treated continuously with sub-therapeutic doses, and the tumors were allowed to grow for 3-4 weeks, before surgical removal of the tumors. The tumor from an individual mouse was then minced, and a small portion was then injected into a healthy nude mouse, establishing a second passage of the tumor. This mouse was then treated continuously with the same sub-therapeutic dose of taxol. This process was repeated 14 times, and a portion of each generation of xenograft tumor was collected. There was increasing resistance to therapeutic doses of taxol with each generation. By the end of the process, the tumors were fully resistant to therapeutic doses of taxol. RNA from each generation of tumor was then isolated, and individual mRNA species were quantified using a custom Affymetrix GeneChip® oligonucleotide microarray, with probes to interrogate approximately 35,000

unique mRNA transcripts. Genes were selected that showed a statistically significant up-regulation, or down-regulation, during the subsequent generations of increasingly taxol-resistant tumors. Only one gene was significantly up-regulated, whereas 24 genes were down-regulated; these are presented in Table 10.

The gene sequences identified to be overexpressed in prostate cancer may be used to identify coding regions from the public DNA database. The sequences may be used
5 to either identify genes that encode known proteins, or they may be used to predict the coding regions from genomic DNA using exon prediction algorithms, such as FGENESH (Salamov and Solovyev, 2000, Genome Res. 10:516-522). In addition, one of ordinary skill in the art would understand how to obtain the unigene cluster identification and sequence information according to the exemplar accession numbers provided in Tables 1-16. (see,
10 <http://www.ncbi.nlm.nih.gov/UniGene/>).

15

TABLE1: shows genes, including expression sequence tags, differentially expressed in prostate tumor tissue compared to normal tissue as analyzed using the Affymetrix/Eos Hu01 GeneChip array. Shown are the relative amounts of each gene expressed in prostate tumor samples and various normal tissue samples showing the highest expression of the gene.

10	Pkey:	Unique Eos probeset identifier number		
	ExAccn:	Exemplar Accession number, Genbank accession number		
	UnigeneID:	Unigene number		
	Unigene Title:	Unigene gene title		
	R1:	Ratio of tumor to normal body tissue		
15	Pkey	UnigeneID	ExAccn	Unigene Title
				R1
	131919	Hs.272458	AA121268	ESTs
	120328	Hs.290905	AA196979	ESTs; Weakly similar to (define not ava
20	105201	Hs.31412	AA195626	ESTs
	101486	Hs.1852	M24902	acid phosphatase; prostate
	119073	Hs.279477	R32894	ESTs
	133428	Hs.183752	M34376	microsomal protein; beta-
	128180	Hs.171995	AA595348	kallikrein 3; (prostate specific antigen
25	104080	Hs.57771	AA402971	Homo sapiens mRNA for serine protease (T
	127537	Hs.162859	AA569531	ESTs
	131665	Hs.30343	R22139	ESTs
	101050	Hs.1832	K01911	neuropeptide Y
	130771	Hs.1915	N48058	folate hydrolase (prostate-specific memb
30	108153	Hs.40808	AA054237	ESTs
	107485	Hs.262476	W63793	S-adenosylmethionine decarboxylase 1
	106155	Hs.33287	AA425309	ESTs
	129534	Hs.11260	R73640	ESTs
	100569	Hs.171985	HG2261-HT2351	Antigen, Prostate Specific, Alt. Splice
35	101889	Hs.181350	S39329	kallikrein 2; prostatic
	135389	Hs.99872	U05237	fetal Alzheimer antigen
	101506	Hs.62192	M27436	coagulation factor III (thromboplastin;
	134374	Hs.8236	D62633	ESTs
	133944	Hs.7780	AA045870	ESTs
40	109141	Hs.193380	AA176428	ESTs
	130974	Hs.2178	X57985	H2B histone family; member Q
	114768	Hs.182339	AA149007	ESTs
	104394	Hs.172129	H46617	yp19h1.r1 Soares breast 3NbHBst Homo sap
	125299	Hs.102720	Z39436	ESTs
45	104660	Hs.14846	AA007160	ESTs
	100116	Hs.78045	D00654	actin; gamma 2; smooth muscle; enteric
	131061	Hs.268744	N64328	ESTs; Moderately similar to KIAA0273 [H.
	126645	126645	AI167942	Homo sapiens BAC clone RG041D11 from 7q2
	135153	Hs.95420	N40141	Homo sapiens mRNA for JM27 protein; comp
50	107033	Hs.113314	AA599629	ESTs
	118417		N66048	ESTs; Weakly similar to polymerase [H.s.
	126758	Hs.293960	W37145	ESTs
	115674	Hs.8364	AA406542	ESTs
	134989	Hs.92381	AA236324	ESTs; Weakly similar to [H.] ALU CLASS A
55	107102	Hs.30652	AA609723	ESTs
	116787	Hs.15641	H28581	ESTs
	115719	Hs.59822	AA416997	ESTs
	123209	Hs.203270	AA489711	ESTs
	101664	Hs.121017	M60752	H2A histone family; member A
60	112971	Hs.83883	T17185	ESTs
	102519	Hs.80296	U52969	Purkinje cell protein 4
	117984	Hs.106778	N51919	ESTs
	105840	Hs.22209	AA398533	ESTs
	129523	Hs.274509	M30894	T-cell receptor; gamma cluster
65	132964	Hs.167133	AA031360	ESTs
	121853	Hs.98502	AA425887	ESTs

	115764	Hs.91011	AA421562	anterior gradient 2 (Xenopus laevis; sec	8.9
	119617	Hs.55999	W47380	ESTs	8.9
	100552	Hs.301946	HG2167-HT2237	Protein Kinase H31, Camp-Dependent	8.9
5	105627	Hs.23317	AA281245	ESTs	8.8
	101461	Hs.76422	M22430	phospholipase A2; group IIA (platelets;	8.7
	131725	Hs.31148	AA458264	ESTs; Highly similar to (define not ava	8.5
	124526	Hs.293185	N62096	yz61c5.s1 Soares_multiple_sclerosis_2NbH	8.5
	118528	Hs.49397	N67889	ESTs	8.2
	133845	Hs.76704	T68510	ESTs	8.2
10	133354	Hs.334762	AA055552	ESTs; Weakly similar to KIAA0319 [H.sapi	8.1
	105912	Hs.20415	AA402000	ESTs; Weakly similar to GS3788 [H.sapien	8
	119018	Hs.278695	N95798	ESTs	8
	100394	Hs.66052	D84276	CD38 antigen (p45)	8
15	114132	Hs.24182	Z38688	ESTs	7.9
	116786	Hs.301527	H25836	tumor necrosis factor (ligand) superfam	7.7
	106579	Hs.23023	AA456135	ESTs	7.6
	128790	Hs.105700	AA291725	secreted frizzled-related protein 4	7.5
	114965	Hs.72472	AA250737	ESTs	7.4
	112033	Hs.22627	R43162	ESTs	7.1
20	102398		U42359	Human N33 protein form 1 (N33) gene, exo	7
	101201	Hs.2256	L22524	matrix metalloproteinase 7 (matrilysin;	6.9
	109272	Hs.288462	AA195718	ESTs	6.9
	103145	Hs.169849	X66276	myosin-binding protein C; slow-type	6.9
25	101803	Hs.155691	M86546	pre-B-cell leukemia transcription factor	6.8
	120562	Hs.302267	AA280036	ESTs; Weakly similar to W01A6.c [C.elega	6.8
	109112	Hs.257824	AA169379	ESTs	6.8
	109795	Hs.326416	F10707	ESTs	6.7
	107532	Hs.173684	Z19643	ESTs; Weakly similar to (define not ava	6.7
30	130336	Hs.171895	X07730	kallikrein 3; (prostate specific antigen	6.6
	131425	Hs.26691	AA219134	ESTs	6.6
	120588	Hs.18193	AA281591	Homo sapiens mRNA; cDNA DKFZp586B211 (fr	6.6
	132902	Hs.59838	AA490969	ESTs	6.6
	125674	Hs.323376	W28078	H.sapiens mRNA for transmembrane protein	6.6
35	133724	Hs.75748	U07919	aldehyde dehydrogenase 6	6.5
	130343	Hs.278628	AA490262	ESTs; Moderately similar to APXL gene pr	6.5
	120215	Hs.108787	Z41050	Homo sapiens Mod4p homolog mRNA; complet	6.5
	129215	Hs.126085	AA176867	ESTs	6.5
	131881	Hs.3383	AA010163	upstream regulatory element binding prot	6.5
40	133376	Hs.7232	T23670	ESTs	6.4
	105378	Hs.8768	AA236559	ESTs; Weakly similar to neuronal thread	6.4
	104674	Hs.26289	AA009527	ESTs	6.4
	100727	Hs.334786	X07290	Human HF.12 gene mRNA	6.3
	130150	Hs.15113	AF000573	homogentisate 1,2-dioxygenase (homogent	6.3
45	121770	Hs.278428	AA421714	Homo sapiens mRNA for KIAA0896 protein;	6.3
	123475	Hs.250528	AA599267	ESTs; Weakly similar to ANKYRIN; BRAIN V	6.3
	133061	Hs.286638	AB000584	prostate differentiation factor	6.3
	116429	Hs.279923	AA609710	ESTs; Weakly similar to similar to GTP-b	6.2
	101233	Hs.878	L29008	sorbitol dehydrogenase	6.2
	104691	Hs.37744	AA011176	ESTs	6.2
50	127248		AA325029	EST27953 Cerebellum II Homo sapiens cDNA	6.2
	127775	Hs.178902	H04106	ESTs; Weakly similar to (define not ava	6.2
	105500	Hs.222399	AA256485	ESTs	6.1
	131463	Hs.2714	X74142	forkhead (Drosophila)-like 1	6.1
55	132116	Hs.40289	AA234767	ESTs	6
	130828	Hs.203213	AA053400	ESTs	5.9
	115357	Hs.72988	AA281793	ESTs	5.8
	105496	Hs.301897	AA256323	ESTs	5.7
	116334	Hs.48948	AA491457	ESTs	5.7
	107968	Hs.61539	AA034020	ESTs	5.7
60	120132	Hs.125019	Z38839	ESTs; Weakly similar to HIII ALU SUBFAMI	5.6
	106375	Hs.289072	AA443993	ESTs	5.6
	132550	Hs.170185	AA029597	bone morphogenetic protein 7 (osteogenic	5.6
	124777	Hs.140237	R41933	ESTs; Weakly similar to neuronal thread	5.6
	100311	Hs.337616	D50640	phosphodiesterase 3B; cGMP-inhibited	5.6
65	101791	Hs.82354	M83822	Human beige-like protein (BGL) mRNA; par	5.5
	117698	Hs.45107	N41002	ESTs	5.5
	132387	Hs.281434	R70914	heat shock 70kD protein 1	5.5
	122041	Hs.98732	AA431407	Homo sapiens Chromosome 16 BAC clone CIT	5.5
	133723	Hs.262476	AA088851	S-adenosylmethionine decarboxylase 1	5.5

	113938	W81598	ESTs	5.4
	133015	Hs.246315 AA047036	ESTs	5.4
	125745	Hs.75722 A1283493	ribophorin II	5.4
	107295	Hs.80120 T34527	UDP-N-acetyl-alpha-D-galactosamine; polyp	5.4
5	108186	Hs.7780 AA056482	ESTs	5.3
	100184	Hs.21223 D17408	calponin 1; basic; smooth muscle	5.3
	104466	Hs.326392 N25110	Human guanine nucleotide exchange factor	5.3
	104033	Hs.98944 AA365031	ESTs	5.3
10	110844	Hs.167531 N31952	ESTs; Weakly similar to (define not ava	5.3
	129056	Hs.108338 H70627	ESTs; Weakly similar to III ALU SUBFAM1	5.3
	102805	Hs.25351 U90304	troquols-class homeodomain protein	5.3
	133493	Hs.194369 AA284143	Homo sapiens chromosome 1 atrophin-1 rel	5.3
	129184	Hs.109201 W26769	ESTs; Highly similar to (define not ava	5.2
	134158	Hs.79428 U15174	BCL2/adenovirus E1B 19kD-interacting pro	5.2
15	107240	Hs.159872 D59368	ESTs	5.2
	104787	AA027317	ESTs; Weakly similar to III ALU SUBFAM1	5.2
	123527	Hs.108327 AA608679	damage-specific DNA binding protein 1 (1	5.2
	116646	Hs.194228 F03048	ESTs; Moderately similar to III ALU SUB	5.2
20	101448	Hs.195850 M21589	keratin 5 (epidermolysis bullosa simplex	5.1
	116188	Hs.184598 AA464728	ESTs; Weakly similar to III ALU SUBFAM1	5.1
	126259	Hs.281428 Z21472	ESTs; Moderately similar to III ALU SUB	5.1
	105921	Hs.169119 AA402613	ESTs	5.1
	103375	Hs.54416 X91868	sine oculis homeobox (Drosophila) homolo	5.1
25	128871	Hs.108778 AA400271	ESTs; Highly similar to (define not ava	5.1
	112681	Hs.148932 R87331	ESTs; Moderately similar to semaphorin V	5.1
	105784	Hs.228434 AA350771	ESTs	5.1
	116238	Hs.47144 AA479362	ESTs	5
	102913	Hs.80342 X07696	keratin 15	5
30	103011	Hs.326035 X52541	early growth response 1	5
	126023	H58881	yr36d09.r1 Soares fetal liver spleen 1NF	5
	103709	Hs.13804 AA037318	ESTs	5
	118981	Hs.39288 N83839	ESTs; Weakly similar to III ALU SUBFAM1	5
	134807	Hs.89732 X78932	zinc finger protein 273	5
35	100079	Hs.23311 AB002365	Human mRNA for KIAA0367 gene; partial cd	4.9
	132047	Hs.3786 D83482	EphB6	4.9
	132880	Hs.177537 AA444369	ESTs	4.9
	124049	Hs.74519 F10523	primase; polypeptide 2A (58kD)	4.8
	133330	Hs.71119 U42360	Human N33 mRNA; complete cds	4.8
40	104776	AA026349	ESTs	4.8
	122593	Hs.128749 AA453310	Homo sapiens alpha-methylacyl-CoA racema	4.8
	103912	Hs.143087 AA251078	ESTs	4.8
	113981	Hs.26009 W86307	Homo sapiens mRNA for KIAA0860 protein;	4.8
	105288	Hs.3585 AA233168	ESTs; Weakly similar to coded for by C.	4.8
45	135035	Hs.284186 H89575	ESTs	4.8
	104144	Hs.183390 AA447439	ESTs; Weakly similar to ZINC FINGER PROT	4.8
	129389	Hs.288128 AA621604	ESTs	4.8
	125982	R98091	RAE1 (RNA export 1; S.pombe) homolog	4.8
	125182	Hs.26243 W44682	ESTs	4.8
50	103023	Hs.117850 X53793	multifunctional polypeptide similar to S	4.7
	129735	W80701	ESTs; Weakly similar to HERV-E envelope	4.7
	104479	Hs.106390 N36040	ESTs	4.7
	103731	AA070545	zm7c3.r1 Stratagene neuroepithelium (#93	4.7
	126575	Hs.127602 W72416	ESTs	4.7
55	124578	Hs.231500 N68321	Human glucose transporter-like protein-1	4.7
	130617	Hs.1674 M90516	glutamine-fructose-6-phosphate transamin	4.7
	116752	Hs.91622 H06373	Homo sapiens clone 24456 mRNA sequence	4.7
	100279	Hs.82007 D42084	Human mRNA for KIAA0094 gene; partial cd	4.7
	126288	Hs.89576 A1479264	ESTs	4.7
60	131836	Hs.32990 AA610086	ESTs	4.7
	106717	Hs.239489 AA465093	TIA1 cytotoxic granule-associated RNA-bi	4.7
	114542	Hs.91011 AA055768	ESTs	4.6
	103806	AA130614	zo1f2.r1 Stratagene neuroepithelium NT2R	4.6
	130529	AA173238	small inducible cytokine A5 (RANTES)	4.6
65	115675	Hs.82065 AA406548	ESTs	4.6
	111388	Hs.293798 N95326	ESTs	4.6
	106503	Hs.29879 AA452411	ESTs	4.6
	119943	Hs.14158 W86835	copine III	4.6
	104459	Hs.100070 M91493	EST	4.6
	100774	Hs.89603 HG371-HT1063	Mucin 1, Epithelial, Alt. Splice 6	4.6

	100652	Hs.142653	HQ2825-HT2949	Ret Transforming Gene	4.6
	132015	Hs.3731	D11900	ESTs	4.6
	126086		H70975	yr73g01.r1 Soares fetal liver spleen 1NF	4.6
	130888	Hs.173094	F03819	ESTs	4.6
5	106390	Hs.20166	AAA46964	Prostate stem cell antigen	4.6
	126959		AA199853	ESTs; Moderately similar to IIII ALU SUB	4.5
	131584	Hs.29117	X91648	H.sapiens mRNA for pur alpha extended 3'	4.5
	104838	Hs.20953	AA039481	ESTs	4.5
	125661		R50319	ESTs	4.5
10	103171	Hs.234726	X68733	alpha-1-antichymotrypsin	4.5
	103928	Hs.189160	AA280085	ESTs	4.5
	102899	Hs.75730	X06272	signal recognition particle receptor (d	4.5
	100892	Hs.180789	HQ4557-HT4962	Small Nuclear Ribonucleoprotein U1, 1snr	4.5
	106167	Hs.7958	AA425906	ESTs	4.5
15	129404	Hs.317584	AA172056	ESTs	4.5
	106990	Hs.24758	AA521354	ESTs	4.5
	132316	Hs.44566	U28831	Human protein immuno-reactive with anti-	4.4
	132056	Hs.38176	T89386	Homo sapiens mRNA for KIAA0606 protein;	4.4
	133718	Hs.188760	X15306	neurofilament; heavy polypeptide (200kD)	4.4
20	101470	Hs.1846	M22898	tumor protein p53 (Li-Fraumeni syndrome)	4.4
	131904	Hs.284296	AA143019	ESTs; Highly similar to surface 4 integr	4.4
	105804	Hs.22514	AA383142	ESTs	4.4
	122861	Hs.119394	AA464428	ESTs	4.4
	111336	Hs.28894	N79565	ESTs	4.4
25	121944	Hs.98518	AA429278	ESTs	4.4
	134401	Hs.211577	AA243746	ESTs; Highly similar to CG1 protein [H.s	4.4
	126458	Hs.288969	AA815252	ESTs; Weakly similar to IIII ALU SUBFAM	4.4
	133435	Hs.323966	T23983	ESTs; Moderately similar to IIII ALU SUB	4.4
	105178	Hs.21941	AA187490	ESTs	4.3
30	127315		AA640834	nr27b08.r1 NCL_CGAP_Pr3 Homo sapiens cDN	4.3
	132645	Hs.54424	X87870	H.sapiens mRNA for hepatocyte nuclear fa	4.3
	116162	Hs.282990	AA461487	ESTs; Weakly similar to F52C12.2 [C.eleg	4.3
	118040	Hs.47557	N52876	EST	4.3
	130008	Hs.278427	M31423	cerebellar degeneration-related protein	4.3
35	126607	Hs.114688	W87424	ESTs	4.3
	123061	Hs.105130	AA482030	EST	4.3
	109391	Hs.184245	AA219699	ESTs	4.3
	109175		AA180496	ESTs	4.3
40	127003	Hs.173540	AA550806	ESTs; Weakly similar to (define not ava	4.3
	102547	Hs.46638	U57911	chromosome 11 open reading frame 8	4.3
	134208	Hs.79993	U88871	peroxisomal biogenesis factor 7	4.3
	104258	Hs.5462	AF007216	solute carrier family 4; sodium bicarbon	4.3
	130759	Hs.18946	AA094720	ESTs; Weakly similar to (define not ava	4.3
	132160	Hs.295923	AA281770	seven in absentia (Drosophila) homolog 1	4.3
45	135062	Hs.93872	AA174183	ESTs	4.3
	126510	Hs.334762	R49702	ESTs; Weakly similar to KIAA0319 [H.sapi	4.2
	122055	Hs.98747	AA431732	EST	4.2
	133138	Hs.6574	AF007165	suppressin (nuclear deformed epidermal a	4.2
	109890	Hs.20843	H04649	ESTs	4.2
50	133294	Hs.69997	R79723	H.sapiens mRNA for translin associated z	4.2
	134436	Hs.83190	S80437	fatty acid synthase (3' region) (human,	4.2
	107375	Hs.251064	U88573	NBR2	4.2
	122223	Hs.27413	AA436158	ESTs	4.2
	103044	Hs.248210	X55777	H.sapiens Mahlavu hepatocellular carcino	4.2
55	120125	Hs.59815	W99362	EST	4.2
	128969	Hs.283978	T65327	ESTs; Highly similar to (define not ava	4.2
	129637	Hs.1179	D90359	TATA box binding protein (TBP)-associate	4.2
	106568		AA455921	ESTs; Weakly similar to IIII ALU SUBFAM	4.2
	112605	Hs.29852	R79220	ESTs	4.2
60	103364	Hs.279929	X90872	H.sapiens mRNA for gp25L2 protein	4.2
	132811	Hs.57419	U25435	transcriptional repressor	4.2
	126570	Hs.326292	T79274	ESTs	4.2
	116288	Hs.94109	AA489046	ESTs	4.2
	103024	Hs.105938	X53961	lactotransferrin	4.1
65	129133	Hs.108850	R56728	yg95c6.r1 Soares infant brain 1N1B Homo	4.1
	133167	Hs.6641	N98707	kinesin family member 5C	4.1
	126871	Hs.14051	AA351779	ESTs	4.1
	132333	Hs.45032	AA182157	ESTs	4.1
	107376	Hs.327179	U90545	solute carrier family 17 (sodium phospho	4.1

	128517	Hs.100861	AA280617	ESTs; Weakly similar to p60 katanin [H.s	4.1
	130555	Hs.116774	AA450324	ESTs	4.1
	105765	Hs.24183	AA343514	ESTs	4.1
	126529	Hs.26369	AA133237	ESTs	4.1
5	125928	Hs.181889	H29730	ESTs	4.1
	117280	Hs.172129	N22107	ESTs; Moderately similar to IIII ALU SUB	4.1
	100234	Hs.3085	D29677	KIAA0054 gene product	4.1
	100959	Hs.118127	J00073	actin; alpha; cardiac muscle	4.1
10	107130	Hs.12913	AA620582	ESTs; Weakly similar to (define not ava	4.1
	105035	Hs.8859	AA128486	ESTs	4.1
	126735	Hs.226785	AA808949	glutathione S-transferase pI	4.1
	113056	Hs.8036	T26471	ESTs; Moderately similar to IIII ALU SUB	4
	102460	Hs.211582	U48959	Homo sapiens myosin light chain kinase (4
	106968	Hs.26813	AA504631	ESTs; Weakly similar to (define not ava	4
15	123107	Hs.104207	AA486071	ESTs	4
	127256	Hs.267967	AA327550	ESTs; Weakly similar to IIII ALU SUBFAM1	4
	105329	Hs.22862	AA234561	ESTs	4
	115504	Hs.42736	AA291946	ESTs	4
20	120726	Hs.97293	AA293656	ESTs	4
	103576	Hs.94560	Z26317	desmoglein 2	4
	127889	Hs.144941	AI147408	ESTs	4
	106394	Hs.25320	AA447223	ESTs	4
	128046		AA873285	ESTs	4
25	103391	Hs.114368	X94453	pyrroline-5-carboxylate synthetase (glut	4
	106448	Hs.27004	AA449455	ESTs	4
	126513	Hs.86276	W27801	ESTs; Moderately similar to (define not	4
	129593	Hs.98314	AA487015	ESTs; Weakly similar to IIII ALU SUBFAM1	3.9
	110151	Hs.31608	H18836	ESTs	3.9
	106344	Hs.8645	AA235303	ESTs	3.9
30	104791	Hs.301871	AA029046	ESTs	3.9
	123442	Hs.111498	AA598803	ESTs	3.9
	127800	Hs.79428	AA521047	BCL2/adenovirus E1B 19kD-interacting pro	3.9
	114555	Hs.167904	AA058594	ESTs	3.9
	122138	Hs.163960	AA435549	ESTs	3.9
35	129565	Hs.198726	X77777	vasoactive intestinal peptide receptor 1	3.9
	103471	Hs.75216	Y00815	protein tyrosine phosphatase; receptor t	3.9
	133908	Hs.325474	M83218	caldesmon 1	3.9
	106635	Hs.301985	AA281508	ESTs	3.9
40	134285	Hs.81086	AA480012	solute carrier family 22 (organic cation	3.9
	134125	Hs.50421	R38102	KIAA0203 gene product	3.9
	125828	Hs.241493	AA418069	natural killer-tumor recognition sequenc	3.9
	103695	Hs.188600	AA018758	ESTs	3.9
	100642	Hs.182183	HG2743-HT3926	Caldesmon 1, Alt. Splice 6, Non-Muscle	3.9
45	104334	Hs.78771	D82614	ESTs	3.9
	110242	Hs.18978	H26417	ESTs	3.9
	125298	Hs.289008	Z39255	ESTs	3.9
	104060	Hs.303193	AA397968	zif87a9.r1 Soares_testis_NHT Homo sapiens	3.9
	105823	Hs.293960	AA398197	ESTs	3.9
50	126489	Hs.110445	AA315671	ESTs; Moderately similar to unknown [M.m	3.9
	130752	Hs.18895	D50827	KIAA0137 gene product	3.8
	123494	Hs.112110	AA599786	ESTs	3.8
	104846	Hs.32478	AA040154	ESTs	3.8
	108921	Hs.71721	AA142913	ESTs	3.8
55	115506	Hs.45207	AA282537	ESTs	3.8
	100452	Hs.241552	D87742	Human mRNA for KIAA0268 gene; partial cd	3.8
	104454	Hs.129228	M84443	galactokinase 2	3.8
	108730	Hs.102859	AA126254	ESTs	3.8
	131223	Hs.24427	AA247788	ESTs; Highly similar to (define not ava	3.8
60	104784	Hs.269228	AA027055	ESTs	3.8
	104948	Hs.73848	AA069549	ESTs	3.8
	106932	Hs.9394	AA485926	ESTs	3.8
	101724	Hs.620	M69225	bullous pemphigoid antigen 1 (230/240kD)	3.8
	106140	Hs.14912	AA24524	Homo sapiens mRNA for KIAA0286 gene; par	3.8
65	128135	Hs.269721	AA913491	ESTs	3.8
	120030	Hs.58694	W92051	ESTs	3.8
	128457	Hs.50382	AA007489	zh88g04.r1 Soares_fetal_liver_spleen_1NF	3.8
	123917	Hs.112869	AA621311	EST	3.7
	110714	Hs.17752	H95978	Homo sapiens phosphatidylserine-specific	3.7
	130577	Hs.162	M35410	insulin-like growth factor binding prote	3.7

	117667	Hs.44708	N39214	ser-Thr protein kinase related to the my	3.7
	126104	Hs.39712	N77278	ESTs; Weakly similar to BONE/CARTILAGE P	3.7
	100379	Hs.278721	D82060	Homo sapiens mRNA for membrane protein w	3.7
	115846	Hs.305971	AA404352	ESTs	3.7
5	125792	Hs.193700	AI005398	ESTs; Moderately similar to IIII ALU SUB	3.7
	102162	Hs.1592	U18291	CDC16 (cell division cycle 16; S. cerevi	3.7
	128530	Hs.183475	AA504343	ESTs; Moderately similar to IIII ALU SUB	3.7
	119940	Hs.272531	W86779	EST	3.7
	110769	Hs.23837	N22222	yw34b06.s1 Morton Fetal Cochlea Homo sap	3.7
10	132914	Hs.60293	AA496037	ESTs	3.7
	113594	Hs.15683	T92030	ESTs	3.7
	103702	Hs.279952	AA027793	ESTs; Highly similar to (define not ava	3.7
	130780	Hs.19347	AA248408	ESTs	3.7
	123288	Hs.291025	AA495838	EST	3.7
15	120691	Hs.22380	AA291173	ESTs	3.7
	103153	Hs.75295	X66534	guanylate cyclase 1; soluble; alpha 3	3.7
	129201	Hs.109390	H19969	ESTs	3.7
	114798	Hs.54900	AA159181	ESTs	3.7
	126801	Hs.7337	AA512902	ESTs	3.7
20	105503	Hs.31707	AA256616	ESTs	3.7
	104260	Hs.194283	AF008192	Homo sapiens putative GR6 protein (GR6)	3.7
	125980	Hs.35699	R97219	ESTs	3.7
	123255	Hs.105273	AA490890	ESTs	3.6
	103862	Hs.6363	AA206625	ESTs	3.6
25	100698	Hs.121688	HG3162-HT3339	Transcription Factor lia	3.6
	134917	Hs.166994	X87241	FAT tumor suppressor (Drosophila) homolo	3.6
	103520		Y10511	H.sapiens mRNA for CD176 protein	3.6
	113778	Hs.302738	W15263	ESTs	3.6
	101838	Hs.75511	M92934	connective tissue growth factor	3.6
30	113702		T97307	ESTs; Moderately similar to IIII ALU SUB	3.6
	118201	Hs.48428	N59800	EST	3.6
	116519	Hs.88554	C20780	EST	3.6
	105888	Hs.22983	AA400517	ESTs; Moderately similar to UDP-GLUCOSE:	3.6
	106709	Hs.170291	AA464696	ESTs	3.6
35	127858	Hs.27973	AA806365	oc26h07.s1 NCI_CGAP_GCB1 Homo sapiens cD	3.6
	101984		S81578	dioxin-responsive gene (putative polyade	3.6
	105508	Hs.326416	AA256680	ESTs	3.6
	116844	Hs.337434	H64938	ESTs	3.6
	105372	Hs.142296	AA238481	ESTs	3.6
40	100745	Hs.144630	HG3510-HT3704	V-Erba Related Ear-3 Protein	3.6
	127521	Hs.164018	AA809982	ESTs	3.6
	110758	Hs.274265	N21385	talin	3.6
	107307	Hs.44155	T52099	creatine kinase; mitochondrial 2 (sarcom	3.6
	133200	Hs.183639	AA432248	ESTs	3.6
45	114774	Hs.184325	AA150043	ESTs	3.6
	120265	Hs.270696	AA173759	ESTs; Moderately similar to IIII ALU SUB	3.6
	134359	Hs.199067	M34309	v-erb-b2 avian erythroblastic leukemia v	3.6
	118250	Hs.44829	AA480975	ESTs; Moderately similar to IIII ALU SUB	3.6
	106313	Hs.35841	AA436459	nuclear factor I/X (CCAAT-binding transc	3.6
50	131898	Hs.279780	N52232	ESTs	3.6
	133444	Hs.73783	M27281	vascular endothelial growth factor	3.6
	128232	Hs.334641	H06296	ESTs	3.6
	135357	Hs.78572	AA235803	ESTs	3.5
	457951		AI369384	arylsulfatase D	3.5
55	108407		AA075519	zm87h9.s1 Stratagene ovarian cancer (#93	3.5
	126659		T16245	a disintegrin and metalloproteinase doma	3.5
	104189	Hs.301804	AA485805	ESTs	3.5
	125956	Hs.129014	N53276	ESTs	3.5
	103028	Hs.78386	X54162	Human mRNA for a 64 Kd autoantigen expre	3.5
60	133011	Hs.171921	AA042990	sema domain; immunoglobulin domain (lg);	3.5
	131379	Hs.26176	R49035	ESTs	3.5
	126742	Hs.169359	H64106	yr57e06.r1 Soares fetal liver spleen 1NF	3.5
	105560	Hs.306915	AA262783	ESTs	3.5
	118472	Hs.42179	N68818	ESTs	3.5
65	105623	Hs.30127	AA280895	ESTs; Highly similar to IIII ALU SUBFAM1	3.5
	120262	Hs.145807	AA172076	ESTs; Moderately similar to IIII ALU SUB	3.5
	105027	Hs.26771	AA126472	ESTs	3.5
	130760	Hs.18953	AA128997	phosphodiesterase 9A	3.5
	117473	Hs.155560	N30157	ESTs	3.5

	102663	Hs.168075	U70322	karyopherin (importin) beta 2	3.5
	126349	Hs.13531	AA442868	ESTs; Weakly similar to (define not ava	3.5
	132154	Hs.41119	N57179	ESTs	3.5
5	131689	Hs.30698	AA599653	transcription factor-like 5 (basic helix	3.5
	127862	Hs.163191	AA765305	EST	3.5
	126965	Hs.189810	W26950	Human DNA sequence from PAC 388M5 on chr	3.5
	119071		R31180	ESTs	3.5
	103941	Hs.96593	AA282978	ESTs	3.5
10	110721	Hs.31319	H97678	ESTs	3.5
	126588	Hs.43088	AA011247	ESTs	3.5
	103108	Hs.1857	X62025	phosphodiesterase 6G; cGMP-specific; rod	3.5
	118357	Hs.90797	AA504806	Homo sapiens clone 23620 mRNA sequence	3.5
	105309	Hs.4104	AA233790	ESTs	3.5
	130798	Hs.18525	R39390	ESTs	3.5
15	109101	Hs.52184	AA167708	ESTs	3.5
	103134	Hs.2839	X65724	Norrie disease (pseudoglioma)	3.5
	131788	Hs.301449	X86098	adenovirus 5 E1A binding protein	3.5
	118535	Hs.49418	N67868	ESTs	3.5
20	102582	Hs.11223	U82389	Human putative cytosolic NADP-dependent	3.4
	125905	Hs.6456	T69868	chaperonin containing TCP1; subunit 2 (b	3.4
	109160	Hs.301997	AA179387	ESTs	3.4
	105327	Hs.211593	AA234440	ESTs	3.4
	106588	Hs.57787	AA456598	ESTs	3.4
	122635		AA454085	EST	3.4
25	132413	Hs.260116	AA132969	metalloprotease 1 (pitrilysin family)	3.4
	131938	Hs.34956	AA283620	ESTs	3.4
	133871	Hs.182783	AA454597	ESTs	3.4
	107175	Hs.282503	AA621751	ESTs; Weakly similar to KIAA0601 protein	3.4
30	101188	Hs.184298	L20320	cyclin-dependent kinase 7 (homolog of Xe	3.4
	126422	Hs.237658	H48518	ESTs; Highly similar to apolipoprotein A	3.4
	118475		N66845	ESTs; Weakly similar to IIII ALU CLASS B	3.4
	104558	Hs.88959	R56678	ESTs; Weakly similar to IIII ALU SUBFAM	3.4
	128307	Hs.132005	AI453794	ESTs	3.4
	112254	Hs.25829	R51831	ESTs	3.4
35	125408	Hs.89578	N72353	yv37e12.r1 Soares fetal liver spleen 1NF	3.4
	109834	Hs.175955	H00604	ESTs	3.4
	130844	Hs.20191	D12122	seven in absentia (Drosophila) homolog 2	3.4
	127143	Hs.20843	AA533553	n 88h04.s1 NCL_CGAP_Pr10 Homo sapiens cD	3.4
40	135309	Hs.42500	D25984	ESTs	3.4
	125724	Hs.295978	AA083407	stimulated trans-acting factor (50 kDa)	3.4
	127692	Hs.187883	AI021912	ESTs	3.4
	116674	Hs.92127	F04816	ESTs	3.4
	134700	Hs.8868	AA481414	golgi SNAP receptor complex member 1	3.4
45	114848	Hs.166198	AA234929	ESTs	3.4
	103849	Hs.155983	Z70219	H.sapiens mRNA for 5'UTR for unknown pro	3.4
	134835	Hs.89925	L04569	calcium channel; voltage-dependent; L ty	3.4
	130568	Hs.16085	AA232535	ESTs; Highly similar to (define not ava	3.4
	111331	Hs.15978	N78773	ESTs	3.4
50	106036	Hs.10653	AA412505	ESTs	3.4
	130987	Hs.21893	R45698	ESTs	3.4
	112814	Hs.35828	R98182	ESTs	3.4
	127815	Hs.255015	AA876009	ob93c10.s1 NCL_CGAP_GCB1 Homo sapiens cD	3.4
	100144	Hs.75616	D13643	KIAA0018 gene product	3.4
55	101129	Hs.247992	L10405	Homo sapiens DNA binding protein for sur	3.4
	130874	Hs.20621	T08287	ESTs	3.4
	106882	Hs.26994	AA489009	ESTs	3.4
	103855	Hs.302287	AA195179	ESTs	3.4
	125857		H45213	yo03b08.r1 Soares adult brain N2b5HB55Y	3.3
60	114048	Hs.146085	W94613	ESTs	3.3
	109826	Hs.75354	F13702	ESTs	3.3
	125355	Hs.170098	R45630	ESTs; Highly similar to KIAA0372 [H.sapi	3.3
	104182	Hs.143792	AA479990	ESTs; Weakly similar to glioma amplified	3.3
	100294	Hs.75454	D49396	Human mRNA for Apo1_Human (MER5(Aop1-Mou	3.3
65	131688	Hs.30692	U24153	p21 (CDKN1A)-activated kinase 2	3.3
	118258	Hs.88201	AA481256	ESTs; Weakly similar to (define not ava	3.3
	102034	Hs.230	U05291	fibromodulin	3.3
	130072	Hs.14658	R98606	Human chromosome 5q13.1 clone 5G8 mRNA	3.3
	114615	Hs.159456	AA083812	ESTs; Highly similar to (define not ava	3.3
	128707	Hs.104105	AA136474	Mels (mouse) homolog 2	3.3

	115048	Hs.190057	AA252668	ESTs	3.3
	125862	Hs.31110	H12084	ESTs	3.3
	135142	Hs.24192	R31679	ESTs	3.3
5	103119	Hs.2877	X63629	cadherin 3; P-cadherin (placental)	3.3
	104480	Hs.62604	M91504	ESTs	3.3
	100365	Hs.78284	D78611	mesoderm specific transcript (mouse) hom	3.3
	131524	Hs.301804	N39152	ESTs	3.3
	102165	Hs.159627	U18321	Death associated protein 3	3.3
10	126986	Hs.182575	R39438	solute carrier family 15 (H+/peptide tra	3.3
	124839	Hs.140942	R55784	ESTs	3.3
	100709	Hs.100469	HG3264-HT3441	Al-6 (Gb:U02478)	3.3
	132967	Hs.61635	AA032221	Homo sapiens BAC clone RG041D11 from 7q2	3.3
	102927	Hs.65114	X12876	keratin 18	3.3
15	132616	Hs.283558	AA386264	ESTs	3.3
	125132	Hs.129781	W15495	ESTs	3.3
	111225	Hs.31652	N68989	ESTs	3.3
	114956	Hs.87113	AA243681	ESTs	3.3
	122235	Hs.112227	AA438475	ESTs	3.3
20	112325	Hs.12315	R56055	ESTs	3.3
	123360	Hs.178604	AA504784	ESTs	3.3
	105150	Hs.155995	AA169640	Homo sapiens mRNA for KIAA0643 protein;	3.3
	107391	Hs.284294	W02877	ESTs	3.3
	113058	Hs.7569	T26893	EST	3.3
25	134371	Hs.82318	S69790	Brush-1	3.3
	125669	Hs.333256	R51308	ESTs; Moderately similar to III ALU SUB	3.3
	111506	Hs.294105	R07726	ESTs	3.3
	122974	Hs.194215	AA478825	ESTs	3.3
	102369	Hs.299857	U39840	hepatocyte nuclear factor 3; alpha	3.3
30	120408	Hs.180151	AA235045	ESTs	3.3
	117993	Hs.47402	N52039	ESTs; Weakly similar to III ALU SUBFAMI	3.3
	129588	Hs.11500	AA437118	ESTs	3.3
	128138	Hs.126494	AI200825	ESTs	3.3
	127265		AA332751	EST37214 Embryo, 8 week I Homo sapiens c	3.3
35	107674	Hs.41143	AA011027	Homo sapiens mRNA for KIAA0581 protein;	3.2
	104866	Hs.293691	AA045342	ESTs	3.2
	103427	Hs.250655	X97303	H.sapiens mRNA for Pig-12 protein	3.2
	132980	Hs.334334	AA458761	ESTs	3.2
	127017	Hs.251946	AA740146	ESTs	3.2
40	132313	Hs.44481	U13220	forkhead (Drosophila)-like 6	3.2
	106880	Hs.32425	AA488889	ESTs	3.2
	107039	Hs.169780	AA599751	homologous to yeast nitrogen permease (c	3.2
	120870	Hs.282581	AA357172	ESTs	3.2
	107920	Hs.284207	AA027951	ESTs	3.2
45	104165	Hs.105118	AA459160	EST	3.2
	107012	Hs.63908	AA598745	ESTs	3.2
	103605	Hs.194857	Z35402	H.sapiens gene encoding E-cadherin, exon	3.2
	124008	Hs.270018	D60302	ESTs	3.2
	101300	Hs.74137	L40391	Homo sapiens (clone s153) mRNA fragment	3.2
50	101183	Hs.795	L19779	H2A histone family; member O	3.2
	125596		R25698	yg44h11.12 Soares infant brain 1N1B Homo	3.2
	127261		AA661567	nu86b02.s1 NCL CGAP_Alv1 Homo sapiens cD	3.2
	120090	Hs.59554	W94591	ESTs	3.2
	129393	Hs.166982	D13435	phosphatidylinositol glycan; class F	3.2
55	120923	Hs.97129	AA382283	ESTs	3.2
	118907	Hs.274258	N91003	ESTs	3.2
	111552	Hs.191185	R09411	ESTs	3.2
	104431	Hs.99913	J03019	adrenergic; beta-1-; receptor	3.2
	133551	Hs.278634	D83480	Human mRNA for KIAA0146 gene; partial cd	3.2
60	131615	Hs.182803	D14533	xeroderma pigmentosum; complementation g	3.2
	126547	Hs.84072	U47732	transmembrane 4 superfamily member 3	3.2
	103172	Hs.116774	X68742	Integrin; alpha 1	3.2
	113867	Hs.24095	W68845	ESTs	3.2
	133323	Hs.70937	Z83735	H3 histone family; member K	3.2
65	111597	Hs.189716	R11499	ESTs	3.2
	121515	Hs.104698	AA412133	ESTs	3.2
	107445	Hs.6639	W28406	ESTs	3.2
	106887	Hs.334335	AA489091	ESTs	3.2
	123052	Hs.185768	AA481808	ESTs	3.2
	107072	Hs.130760	AA609113	Homo sapiens mRNA; cDNA DKFZp586N0318 (f	3.2

	102214	Hs.32964	U23752	SRY (sex-determining region Y)-box 11	3.2
	123147		AA487961	ab11h6.s1 Stratagene lung (#93721) Homo	3.2
	125435	Hs.272138	R00940	ye87g03.r1 Soares fetal liver spleen 1NF	3.2
5	116246	Hs.250646	AA479961	ESTs; Highly similar to ubiquitin-conjug	3.2
	105169	Hs.180789	AA180321	Homo sapiens (clone S164) mRNA; 3' end o	3.2
	134001	Hs.78344	AF001548	myosin; heavy polypeptide 11; smooth mus	3.2
	124866	Hs.304389	R68571	ESTs	3.2
	133205	Hs.67619	AA089559	Homo sapiens mRNA; chromosome 1 specific	3.2
10	102988	Hs.182378	X17648	colony stimulating factor 1 (macrophage)	3.2
	101232	Hs.242894	L28997	ADP-ribosylation factor-like 1	3.1
	132906	Hs.234898	AA142857	ESTs; Highly similar to geminin [H.sapie	3.1
	104281	Hs.5669	C14290	ESTs	3.1
	123926	Hs.227833	AA621348	ESTs; Highly similar to (define not ava	3.1
15	134464	Hs.239720	N79354	ESTs; Weakly similar to Rga [D.melanogas	3.1
	105322	Hs.16348	AA234100	ESTs	3.1
	100631	Hs.48332	HG2709-HT2805	Serine/Threonine Kinase (Gb.225431)	3.1
	130791	Hs.199263	AA259102	ESTs; Highly similar to (define not ava	3.1
	131220	Hs.300855	R77200	ESTs	3.1
20	113237	Hs.123642	T62857	ESTs	3.1
	125562	Hs.98968	AI494372	ESTs	3.1
	134110	Hs.79136	U41060	Human breast cancer; estrogen regulated	3.1
	132393	Hs.47334	W85888	ESTs; Moderately similar to !!! ALU SUB	3.1
	107439	Hs.296842	W27995	ESTs; Moderately similar to non-muscle m	3.1
25	125863	Hs.40719	AA299096	Homo sapiens mRNA; cDNA DKFZp564M0916 (f	3.1
	105811	Hs.288192	AA394121	ESTs	3.1
	129284	Hs.296141	AA104023	ESTs	3.1
	125321	Hs.178294	T86652	ESTs	3.1
	107332	Hs.183297	T87750	ESTs	3.1
30	123570	Hs.109653	AA608955	ESTs	3.1
	100384	Hs.90800	D83648	matrix metalloproteinase 16 (membrane-in	3.1
	109063	Hs.38972	AA161043	tetraspan 1	3.1
	133284	Hs.182828	U09367	zinc finger protein 136 (clone pHZ-20)	3.1
	131839	Hs.33010	H80622	Homo sapiens mRNA for KIAA0633 protein;	3.1
	117606	Hs.44698	N35115	ESTs	3.1
35	418998	Hs.287849	F13215	ESTs	3.1
	125180	Hs.103120	W58344	ESTs	3.1
	100789		HG3893-HT4163	Phosphoglucomutase 1, Alt. Splice	3.1
	126017	Hs.159440	H60487	ESTs	3.1
40	132452	Hs.247324	AA005262	Homo sapiens DNA sequence from PAC 262D1	3.1
	129077	Hs.108479	H78888	ESTs	3.1
	126563	Hs.181368	W26247	U5 snRNP-specific protein (220 kD); orth	3.1
	129650	Hs.118258	N52554	ESTs	3.1
	123465		AA599033	ESTs	3.1
45	126486	Hs.152316	AA345339	EST51345 Gall bladder II Homo sapiens cD	3.1
	126460	Hs.187031	W01616	za36d05.r1 Soares fetal liver spleen 1NF	3.1
	118697	Hs.43234	N72094	ESTs	3.1
	103860	Hs.38057	AA203742	ESTs	3.1
	127968	Hs.124347	AA971439	ESTs	3.1
50	124984	Hs.223241	T47566	yb15c11.s1 Stratagene placenta (#937225)	3.1
	103903	Hs.15220	AA249334	j312.seq.F Human fetal heart, Lambda ZAP	3.1
	106697	Hs.22242	AA463737	ESTs	3.1
	130892	Hs.20993	AA442604	ESTs; Weakly similar to Ydr374cp [S.cere	3
	114032	Hs.35014	W82779	ESTs	3
55	128835	Hs.106390	W15528	ESTs	3
	103667	Hs.247815	Z80788	H.sapiens H4I gene	3
	126264	Hs.250614	N42897	yy13h06.r1 Soares melanocyte 2NbHM Homo	3
	132628	Hs.21275	D25755	ESTs	3
	131107	Hs.75354	N87590	ESTs	3
60	126780	Hs.5811	R12421	ESTs	3
	127363	Hs.22116	AA307744	Homo sapiens Cdc14B1 phosphatase mRNA; c	3
	103690	Hs.84063	AA016188	ESTs	3
	102589	Hs.8867	U62015	Homo sapiens Cyr61 mRNA, complete cds	3
	125144	Hs.24336	W37999	ESTs	3
65	132977	Hs.301404	U28686	RNA binding motif protein 3	3
	120714	Hs.148170	AA292689	ESTs	3
	101038	Hs.79411	J05249	replication protein A2 (32kD)	3
	102856	Hs.248177	X00090	Human histone H3 gene	3
	105516	Hs.30738	AA257871	ESTs	3
	131137	Hs.33287	U85193	nuclear factor I/B	3

	127221	Hs.241551	AI354332	ESTs	3
	411888	Hs.24104	R26708	ESTs	3
	131684	Hs.3066	U26174	granzyme K (serine protease; granzyme 3;	3
	100629	Hs.21291	HG2706-HT2802	Serine/Threonine Kinase (Gb:Z25428)	3
5	119944	Hs.58915	W86838	EST	3
	113801	Hs.118281	W38418	zinc finger protein 266	3
	133780	Hs.76152	M14219	decorin	3
	104690	Hs.14449	AA010889	ESTs	3
	126371	Hs.304139	N57645	EST	3
10	127635	Hs.116346	AA766903	ESTs	3
	128434	Hs.143880	AI190914	ESTs	3
	435781	Hs.187555	AA701941	ESTs	3
	125025	Hs.50748	T71561	ESTs	3
	124940	Hs.103804	R99599	heterogeneous nuclear ribonucleoprotein	3
15	128742	Hs.251531	D00763	proteasome (prosome; macropain) subunit;	3
	130972	Hs.21739	AA370302	Homo sapiens chromosome 2; 10 repeat reg	3
	112068	Hs.22545	R43910	ESTs	3
	105346	Hs.263727	AA235465	ESTs; Moderately similar to III ALU SUB	3
	130972	Hs.21739	AA370302	Homo sapiens mRNA; cDNA DKFZp58611518 (f	3
20	131230	Hs.274407	AA149987	thymus specific serine peptidase	3
	133743	Hs.76847	N79435	ESTs	3
	127402	Hs.227849	AA358869	ESTs; Highly similar to SEC13-RELATED PR	3
	117483	Hs.44189	N30428	ESTs	3
	123659	Hs.112699	AA609368	ESTs	3
25	103963	Hs.63290	AA298588	EST114219 HSC172 cells II Homo sapiens c	3
	103795	Hs.7367	AA112222	ESTs; Moderately similar to (define not	3
	115092	Hs.80975	AA255903	CD39-like 4	2.9
	134831	Hs.89890	S72370	pyruvate carboxylase	2.9
	128579	Hs.101810	AA093378	ESTs; Weakly similar to III ALU SUBFAMI	2.9
30	134183	Hs.7980	F09570	ESTs	2.9
	123522	Hs.112575	AA608577	ESTs	2.9
	107109	Hs.32783	AA609943	ESTs	2.9
	134694	Hs.88556	D50405	histone deacetylase 1	2.9
	134399	Hs.82689	H99801	tumor rejection antigen (gp96) 1	2.9
35	134632	Hs.174139	AA398710	H. sapiens RNA for CLCN3	2.9
	106683	Hs.14512	AA481495	ESTs	2.9
	108555		AA084983	zn13e12.s1 Stratagene hNT neuron (#93723	2.9
	100953	Hs.2110	HG945-HT945	Nucleic Acid-Binding Protein (Gb:1.12693)	2.9
	130597	Hs.16492	AA173998	ESTs; Weakly similar to weakly similar t	2.9
40	101813	Hs.139226	M87338	replication factor C (activator 1) 2 (40	2.9
	106636	Hs.288	AA459950	ESTs	2.9
	129109	Hs.108708	AA491295	calcium/calmodulin-dependent protein kin	2.9
	125819	Hs.251871	AA044840	stromal cell-derived factor 1	2.9
45	106282	Hs.9857	AA433946	ESTs; Weakly similar to (define not ava	2.9
	100386	Hs.301836	D83703	peroxisomal biogenesis factor 6	2.9
	114546	Hs.88074	AA056263	ESTs; Moderately similar to III ALU SUB	2.9
	105914	Hs.9701	AA402224	Homo sapiens growth arrest and DNA-damag	2.9
	108552		AA084912	zn11c7.s1 Stratagene hNT neuron (#93723	2.9
50	126505	Hs.190057	W26894	16a11 Human retina cDNA randomly primed	2.9
	134098	Hs.79066	X06323	Human MRL3 mRNA for ribosomal protein L3	2.9
	129721	Hs.211539	L19161	eukaryotic translation initiation factor	2.9
	100076	Hs.277422	AB000897	Homo sapiens mRNA for cadherin FIB3, par	2.9
	117466	Hs.44104	N29862	ESTs	2.9
55	106335	Hs.36688	AA437258	ESTs; Moderately similar to WAP four-dis	2.9
	134510	Hs.250870	U25265	protein kinase; mitogen-activated; kinas	2.9
	105835	Hs.32995	AA398412	ESTs	2.9
	106611	Hs.26267	AA458904	ESTs; Weakly similar to torsinA [H.sapie	2.9
	134087	Hs.173824	U51166	thymine-DNA glycosylase	2.9
60	100641	Hs.182183	HG2743-HT2848	Caldesmon 1, Alt. Splice 4, Non-Muscle	2.9
	104602		R86920	ESTs	2.9
	117203	Hs.42738	H99799	ESTs	2.9
	131889	Hs.34073	AA401912	BH-protocadherin (brain-heart)	2.9
	101707	Hs.155212	M65131	methylmalonyl Coenzyme A mutase	2.9
	115271	Hs.5724	AA278422	ESTs	2.9
65	125812	Hs.287912	H73420	lectin; mannose-binding; 1	2.9
	110740	Hs.18762	H99575	ESTs	2.9
	103406	Hs.285728	X95677	H.sapiens mRNA for ArgBPIB protein	2.9
	104577	Hs.132390	R71539	ESTs	2.9
	102772	Hs.161002	U83115	absent in melanoma 1	2.9

	131710	Hs.30985	AA233225	ESTs; Highly similar to (define not ava	2.9
	125231	Hs.268903	W84714	ESTs	2.9
	127380	Hs.15535	AI417137	Homo sapiens clone 24582 mRNA sequence	2.9
5	104229	Hs.61289	AB002346	inositol phosphate 5'-phosphatase 2 (syn	2.9
	126600	Hs.191385	AA699949	ESTs	2.9
	125175	Hs.303030	W52355	EST	2.9
	103849	Hs.34578	AA187045	ESTs; Weakly similar to IIII ALU SUBFAM1	2.9
	102126	Hs.78961	U14575	protein phosphatase 1; regulatory (inhb	2.9
10	124906	Hs.107815	R87647	ESTs	2.9
	131148	Hs.303125	C00038	ESTs	2.9
	123159	Hs.218329	AA488658	heat shock 70kD protein 1	2.9
	133667	Hs.75462	U72649	Human BTG2 (BTG2) mRNA; complete cds	2.9
	105182	Hs.18271	AA191014	ESTs; Weakly similar to Ydr372cp [S.cere	2.9
15	133968	Hs.232068	D15050	Human mRNA for transcription factor AREB	2.9
	117425	Hs.338901	N27154	ESTs	2.9
	111087	Hs.37837	N59645	ESTs	2.9
	129641	Hs.11805	N66068	ESTs	2.9
	128639	Hs.102897	N91248	ESTs	2.9
20	133209	Hs.79265	AA114183	ESTs; Moderately similar to glutamate py	2.9
	135154	Hs.267812	AA128433	sorting nexin 4	2.9
	126838	Hs.279609	AA858097	pigment epithelium-derived factor	2.9
	103803	Hs.108149	AA127898	ESTs	2.9
	102139	Hs.2128	U15932	dual specificity phosphatase 5	2.9
25	128104		AA971000	op67g11.s1 Soares_NFL_T_GBC_S1 Homo sapi	2.8
	127834	Hs.337631	AA761415	nz22d08.s1 NCL_CGAP_GC81 Homo sapiens cD	2.8
	133101	Hs.180952	AA488230	ESTs	2.8
	127250	Hs.217918	AI023717	ESTs	2.8
	135063	Hs.93883	D10537	myelin protein zero (Charcot-Marie-Tooth	2.8
30	126323	Hs.68644	N45014	yy80g08.r1 Soares_multiple_sclerosis_2Nb	2.8
	121873	Hs.145896	AA426270	ESTs	2.8
	122090	Hs.98684	AA432141	ESTs	2.8
	118728	Hs.322645	N73705	ESTs	2.8
	135400	Hs.99915	M23263	androgen receptor (dihydrotestosterone r	2.8
35	125278	Hs.129998	W93523	ESTs	2.8
	124387	Hs.109019	N27637	ESTs	2.8
	124803	Hs.12186	R45480	cyclin K	2.8
	H45968	Hs.32149	H45968	ESTs	2.8
	104261	Hs.5409	AF008442	RNA polymerase I subunit	2.8
40	105366	Hs.282093	AA236356	ESTs	2.8
	106070	Hs.5957	AA417781	Homo sapiens clone 24416 mRNA sequence	2.8
	131356	Hs.25960	M13241	v-myc avian myelocytomatosis viral relat	2.8
	112009	Hs.26255	R42714	EST	2.8
	133199	Hs.250175	AA609773	Homo sapiens clone 23904 mRNA sequence	2.8
45	110379	Hs.33130	H44825	ESTs	2.8
	103890	Hs.72085	AA236843	ESTs; Weakly similar to unknown [S.cerev	2.8
	128152		R20353	yg20f10.r1 Soares Infant brain 1NB Homo	2.8
	107008	Hs.23740	AA598710	ESTs	2.8
	135243	Hs.97101	AA215333	ESTs	2.8
50	103058	Hs.184510	X57348	stratiffin	2.8
	132020	Hs.293845	AA428990	ESTs	2.8
	116354	Hs.292568	AA504282	ESTs	2.8
	125867	Hs.12372	H98141	ESTs	2.8
	120603	Hs.98541	AA282787	ESTs; Highly similar to (define not ava	2.8
55	115119	Hs.46847	AA256524	Human DNA sequence from clone 30M3 on ch	2.8
	133865	Hs.170290	F09315	discs; large (Drosophila) homolog 5	2.8
	109415	Hs.110826	AA227219	Homo sapiens CAGF9 mRNA; partial cds	2.8
	128687	Hs.23767	Z38910	ESTs	2.8
	109984	Hs.10299	H09594	ESTs; Moderately similar to IIII ALU SUB	2.8
60	133179	Hs.66731	U81599	homeo box B13	2.8
	115998	Hs.336629	AA448488	ESTs; Weakly similar to zinc finger prot	2.8
	112180	Hs.25067	R49116	EST	2.8
	120428	Hs.173694	AA236822	ESTs; Moderately similar to (define not	2.8
	108241	Hs.6019	AA430108	ESTs	2.8
65	131060	Hs.22564	AA160890	myosin VI	2.8
	111383	Hs.40919	N94527	ESTs	2.8
	102123	Hs.1594	U14518	centromere protein A (17kD)	2.8
	102722	Hs.79981	U79242	Human clone 23560 mRNA sequence	2.8
	129887	Hs.274324	W92041	PCAF associated factor 65 alpha	2.8
	126683	Hs.181297	AA714635	ESTs	2.8

	104367	Hs.134342	H17438	ESTs; Weakly similar to seven transmembrane	2.8
	107316	Hs.193700	T63174	ESTs; Moderately similar to III ALU SUB	2.8
	128059	Hs.145098	AA972446	ESTs	2.8
	124447		N48000	ESTs	2.8
5	111398	Hs.125585	R00088	deafness; X-linked 1; progressive	2.8
	134085	Hs.79018	U20979	chromatin assembly factor I (150 kDa)	2.8
	124788	Hs.100912	R43543	ESTs	2.8
	112248	Hs.326416	R51361	ESTs	2.8
	121309	Hs.87312	AA402482	ESTs	2.8
10	103076	Hs.75319	X59818	ribonucleotide reductase M2 polypeptide	2.8
	107071	Hs.35188	AA608053	ESTs	2.8
	104425	Hs.35380	H88498	ESTs	2.8
	132991	Hs.62245	AA446906	solute carrier family 25 (mitochondrial)	2.8
	104958	Hs.29669	AA084602	ESTs	2.8
15	121153	Hs.97694	AA399640	ESTs	2.8
	131216	Hs.243901	D31058	ESTs	2.8
	109682	Hs.22869	F09289	ESTs	2.8
	131990	Hs.168818	H77734	ESTs; Moderately similar to roundabout 1	2.8
	132027	Hs.181444	N78844	ESTs; Weakly similar to R12C12.6 [C.eleg]	2.8
20	127383	Hs.180478	AA447990	ESTs	2.8
	132598	Hs.530	M81379	collagen; type IV; alpha 3 (Goodpasture)	2.8
	101121	Hs.1313	L09753	tumor necrosis factor (ligand) superfamily	2.8
	123000	Hs.105640	AA479347	ESTs	2.8
	121329	Hs.1755	AA404324	ESTs	2.8
25	100481	Hs.121489	HG1098-HT1098	Cystatin D	2.7
	113803	Hs.283683	W42789	ESTs	2.7
	110934	Hs.169001	N48708	ESTs; Weakly similar to cytochrome P-450	2.7
	432888		T88823	ESTs	2.7
	121802	Hs.188898	AA424328	ESTs	2.7
30	130396	Hs.155313	AB002331	Human mRNA for KIAA0333 gene; partial cd	2.7
	121103	Hs.97897	AA398936	ESTs; Weakly similar to (define not ava	2.7
	131129	Hs.23240	R27298	ESTs	2.7
	130943	Hs.272429	D50855	calcium-sensing receptor (hypocalcemic)	2.7
	134678	Hs.87819	W28051	ESTs; Weakly similar to keratin 9; cytos	2.7
35	111900	Hs.25318	R39044	ESTs	2.7
	106025	Hs.173334	AA412083	ESTs	2.7
	126144	Hs.40639	N39696	yx2a07.r1 Soares melanocyte 2NbHM Homo	2.7
	103248	Hs.75282	X77383	cathepsin O	2.7
	127230	Hs.274170	H30501	Homo sapiens Opa-interacting protein OIP	2.7
40	101584	Hs.84072	M35252	transmembrane 4 superfamily member 3	2.7
	124131	Hs.187489	H19980	ESTs	2.7
	129689	Hs.77873	AA130158	ESTs	2.7
	132892	Hs.9973	W92787	ESTs	2.7
	120827	Hs.132857	AA347717	ESTs	2.7
45	134579	Hs.85983	N23222	ESTs; Moderately similar to III ALU SUB	2.7
	106149	Hs.258301	AA424881	ESTs	2.7
	132037	Hs.332541	AA203849	ESTs; Weakly similar to HEM45 [H.sapiens]	2.7
	130542	Hs.179825	U84675	Human sperm membrane protein BS-63 mRNA,	2.7
	122851	Hs.99593	AA463627	ESTs	2.7
50	134983	Hs.186384	D28235	prostaglandin-endoperoxide synthase 2 (p	2.7
	120537	Hs.160422	AA262790	ESTs	2.7
	131038	Hs.174140	X64330	ATP citrate lyase	2.7
	133889	Hs.211582	AA099391	ESTs	2.7
55	128847	Hs.106529	AA424189	zv81e01.r1 Soares_total_fetus_Nb2HF8_8w	2.7
	112755	Hs.306044	R93802	ESTs	2.7
	423239		AA323591	EST26392 Cerebellum II Homo sapiens cDNA	2.7
	105031	Hs.12321	AA127240	ESTs	2.7
	126021	Hs.187518	AA775894	ESTs	2.7
	102118		U13706	Human ELAV-like neuronal protein 1 isofo	2.7
60	133394	Hs.237225	R16759	ESTs; Weakly similar to (define not ava	2.7
	104267	Hs.278439	C00358	ESTs	2.7
	107614	Hs.40241	AA004878	ESTs; Highly similar to (define not ava	2.7
	129809	Hs.1259	X55283	astaloglycoprotein receptor 2	2.7
	112109	Hs.283309	R45221	ESTs; Weakly similar to III ALU SUBFAM1	2.7
65	128422		T85681	yd60c06.r1 Soares fetal liver spleen 1NF	2.7
	109494	Hs.43899	AA233702	ESTs	2.7
	118698	Hs.282284	N72088	Homo sapiens RNA polymerase III largest	2.7
	106053	Hs.36727	AA416963	ESTs; Highly similar to histone H2A [H.s	2.7
	104440	Hs.284380	L20492	gamma-glutamyltransferase 1	2.7

	129426	Hs.111323	AA412087	EST; Highly similar to (define not ava	2.7
	123798		AA620411	small inducible cytokine A5 (RANTES)	2.7
	106716	Hs.238928	AA484962	ESTs	2.7
5	103663		Z78291	Z78291 Homo sapiens brain fetus Homo sap	2.7
	114162	Hs.22265	Z38909	ESTs	2.7
	113063	Hs.5027	T32438	ESTs	2.7
	127697		AA773857	af80c09.r1 Soares_NhHMPu_S1 Homo sapiens	2.7
	130621	Hs.16803	AA621718	ESTs; Weakly similar to (define not ava	2.7
10	116245	Hs.42796	AA479958	ESTs; Highly similar to (define not ava	2.7
	125499		R11878	y49d11.r1 Soares infant brain 1NIB Homo	2.7
	133960	Hs.77899	M18267	tropomyosin 1 (alpha)	2.7
	104470	Hs.246358	N28943	ESTs; Weakly similar to Similar to colla	2.7
	134982	Hs.92308	N48086	ESTs	2.7
15	106803	Hs.284295	AA479114	ESTs	2.7
	104899	Hs.285574	AA054726	ESTs	2.7
	125401	Hs.337585	AI204637	ESTs; Moderately similar to KIAA0350 [H.	2.7
	111253	Hs.15768	N70042	ESTs; Moderately similar to !!! ALU SUB	2.7
	118449	Hs.164478	N68413	ESTs; Weakly similar to (define not ava	2.7
20	134507	Hs.84318	M63488	replication protein A1 (70kD)	2.7
	121609	Hs.98185	AA416887	EST	2.7
	113835	Hs.27475	W56590	ESTs	2.7
	113962	Hs.285290	W86375	ESTs; Highly similar to (define not ava	2.7
	121913	Hs.98558	AA428062	ESTs	2.7
25	108194	Hs.218717	AA057250	ESTs	2.7
	130799	Hs.12696	AA464273	ESTs	2.7
	123184	Hs.18166	AA489072	Homo sapiens mRNA for KIAA0870 protein;	2.7
	103420	Hs.173497	X97065	SEC23-like protein B	2.7
	106186	Hs.6315	AA427398	acetylserotonin N-methyltransferase-like	2.7
30	101349		L77559	Homo sapiens DGS-B partial mRNA	2.7
	112854	Hs.6855	T16559	ESTs	2.7
	133054	Hs.291079	R07876	ESTs; Weakly similar to unknown [S.cerev	2.7
	128131	Hs.25640	AI283162	claudin 3	2.6
	101864	Hs.75777	M95787	transgelin	2.6
35	111948	Hs.26303	R40752	ESTs	2.6
	130145	Hs.151051	U07820	protein kinase mitogen-activated 10 (MAP	2.6
	126507	Hs.23984	AI362218	ESTs	2.6
	117903	Hs.47111	N50740	ESTs	2.6
	116345	Hs.199067	AA496991	ESTs	2.6
40	132227	Hs.4248	AA412620	ESTs	2.6
	125746	Hs.274256	H03574	y42b06.r1 Soares placenta Nb2HP Homo sa	2.6
	105073	Hs.89463	AA137034	ESTs	2.6
	102764		U82310	Homo sapiens unknown protein mRNA, parti	2.6
	131367	Hs.173933	AA458687	ESTs	2.6
45	130792	Hs.19500	AA307896	nuclear localization signal deleted in v	2.6
	107427	Hs.46736	W26975	ESTs	2.6
	117477	Hs.44175	N30328	ESTs	2.6
	106290	Hs.16364	AA435542	ESTs	2.6
	126829	Hs.7910	R11547	ESTs	2.6
50	118836	Hs.173001	N79820	ESTs	2.6
	100147	Hs.136348	D13666	osteoblast specific factor 2 (fascilin	2.6
	104278	Hs.109253	C02582	ESTs; Highly similar to (define not ava	2.6
	135051	Hs.83484	C15324	ESTs	2.6
	126081	Hs.227835	AI348024	collagen; type I; alpha 1	2.6
55	123579		AA608983	af5d4.s1 Soares_testis_NHT Homo sapiens	2.6
	130115	Hs.149923	M31627	X-box binding protein 1	2.6
	101434	Hs.1430	M20218	coagulation factor XI (plasma thrombopla	2.6
	122962	Hs.104720	AA478429	ESTs; Moderately similar to !!! ALU SUB	2.6
	126151	Hs.40808	AA324743	ESTs	2.6
60	128925	Hs.21851	D61676	Homo sapiens mRNA; cDNA DKFZp586J2118 (f	2.6
	128919	Hs.103391	L27559	Insulin-like growth factor binding prote	2.6
	130296	Hs.154103	R09288	LIM protein (similar to rat protein kina	2.6
	128402	Hs.191637	AA457244	ESTs	2.6
	129273	Hs.109968	W63783	ESTs	2.6
65	125483	Hs.7788	F07759	ESTs	2.6
	132953	Hs.321284	AA029927	ESTs	2.6
	130963	Hs.21639	U57099	nuclear protein; marker for differentiat	2.6
	120614	Hs.194154	AA284281	ESTs; Weakly similar to !!! ALU SUBFAM1	2.6
	123251	Hs.103267	AA490858	ESTs; Moderately similar to Rabin3 [R.no	2.6
	121710	Hs.96744	AA418011	ESTs	2.6

	125428	Hs.851	W74608	ESTs; Highly similar to (define not ava	2.6
	115908	Hs.82302	AA436616	ESTs	2.6
	108432		AA076626	Homo sapiens clone 23851 mRNA sequence	2.6
5	126191	Hs.191911	H97728	ESTs	2.6
	106164	Hs.281434	AA425773	ESTs	2.6
	111519	Hs.268615	R08165	ESTs	2.6
	134590	Hs.173840	W58612	ESTs	2.6
	102565		U59748	Human desert hedgehog (hDHH) mRNA, parti	2.6
10	129879	Hs.13109	AA194973	ESTs	2.6
	114264	Hs.334609	Z40074	ESTs	2.6
	106236	Hs.21104	AA429951	ESTs	2.6
	135182	Hs.321709	AF000234	purinergic receptor P2X; ligand-gated lo	2.6
	109833	Hs.29889	H00580	ESTs	2.6
15	105756	Hs.8535	AA303088	ESTs; Weakly similar to transformation-r	2.6
	121422	Hs.97967	AA406210	ESTs	2.6
	130417	Hs.155485	U58522	Human huntingtin interacting protein (Hl	2.6
	124312	Hs.102329	H94647	ESTs	2.6
	108998	Hs.97189	AA156058	ESTs	2.6
20	127081	Hs.180591	R88362	ESTs; Weakly similar to weak similarity	2.6
	129574	Hs.11463	AA458603	ESTs; Weakly similar to (define not ava	2.6
	112410	Hs.26904	R61680	ESTs	2.6
	123929	Hs.112981	AA621364	ESTs	2.6
	122905	Hs.104835	AA470070	ESTs	2.6
25	116399	Hs.110637	AA599729	Homo sapiens homeobox protein A10 (HOXA1	2.6
	130279	Hs.153934	AA424044	core-binding factor; runt domain; alpha	2.6
	130021	Hs.1435	M24470	guanosine monophosphate reductase	2.6
	100585	Hs.199160	HG2387-HT2463	Trithorax Homolog Hrx	2.6
	104965	Hs.30177	AA084104	ESTs	2.6
30	117711	Hs.46485	N45201	EST	2.6
	124782	Hs.48712	R44357	ESTs	2.6
	111289	Hs.74313	N73808	ESTs	2.6
	103616	Hs.32971	Z46973	phosphoinositide-3-kinase; class 3	2.6
	133629	Hs.195614	D13642	KIAA0017 gene product	2.6
35	126484	Hs.169977	AI086782	ESTs	2.6
	100858		HG4245-HT4515	Forkhead Family Afx1	2.6
	133547	Hs.301927	X02883	T-cell receptor; alpha (V;D;J;C)	2.6
	126680	Hs.133865	F07097	ESTs	2.6
	125739	Hs.92137	AA428557	v-myc avian myelocytomatosis viral oncog	2.6
40	102276	Hs.10247	U30999	Human (mamc) mRNA, 3'UTR	2.6
	105586	Hs.191538	AA279137	ESTs	2.6
	103978	Hs.34136	AA307443	ESTs	2.6
	125054	Hs.268601	T80622	ESTs; Weakly similar to (define not ava	2.6
	114212	Hs.21201	Z39338	ESTs; Highly similar to (define not ava	2.6
45	116959	Hs.40022	H79310	EST	2.6
	109228	Hs.306995	AA193366	ESTs	2.6
	133989	Hs.78202	U29175	SWI/SNF related; matrix associated; acti	2.6
	100640	Hs.182183	HG2743-HT2845	Caldesmon 1, Alt. Splice 3, Non-Muscle	2.6
	133093	Hs.285996	AA598749	ESTs	2.6
50	114308	Hs.6540	Z40861	ESTs	2.6
	106060	Hs.171391	AA417287	C-terminal binding protein 2	2.5
	107748	Hs.60772	AA017258	EST	2.5
	100134	Hs.49	D13264	macrophage scavenger receptor 1	2.5
	133969	Hs.78	U13044	GA-binding protein transcription factor;	2.5
55	130992	Hs.74316	AA455001	ESTs	2.5
	127493	Hs.291701	AA808081	oc39a08.s1 NCI_CGAP_GCB1 Homo sapiens cD	2.5
	132889	Hs.203961	N26855	ESTs	2.5
	117570	Hs.44583	N34415	EST	2.5
	124644	Hs.109654	N91279	ESTs	2.5
60	103558	Hs.2785	Z19574	keratin 17	2.5
	132883	Hs.5897	AA047151	ESTs	2.5
	102009	Hs.62643	U02680	protein tyrosine kinase 9	2.5
	116058	Hs.20159	AA454156	ESTs	2.5
	121989	Hs.193784	AA430044	ESTs	2.5
65	131257	Hs.24908	AA256042	ESTs	2.5
	100320	Hs.75275	D50916	homolog of yeast (S. cerevisiae) ufd2	2.5
	102959	Hs.121524	X15722	glutathione reductase	2.5
	132969	Hs.6166	AA047616	ESTs	2.5
	130869	Hs.2057	AA128100	uridine monophosphate synthetase (orotat	2.5
	129645	Hs.118131	L38928	5,10-methylenetetrahydrofolate synthetase	2.5

	126399	Hs.83883	AA128075	z16d08.r1 Soares_pregnant_uterus_NbHPU	2.5
	134069	Hs.78935	U29607	Homo sapiens eIF-2-associated p67 homolo	2.5
	109816	Hs.61960	F11013	ESTs; Weakly similar to KIAA0176 [H.sapl	2.5
	134801	Hs.89695	X02160	Insulin receptor	2.5
5	104232	Hs.10587	AB002351	Human mRNA for KIAA0353 gene; partial cd	2.5
	107381	Hs.159486	U72513	Human RPL13-2 pseudogene mRNA; complete	2.5
	106057	Hs.289074	AA417067	ESTs	2.5
	134252	Hs.80720	AA031782	Homo sapiens mRNA; cDNA DKFZp586B1722 (f	2.5
	128062	Hs.105547	AA379500	ESTs	2.5
10	110009	Hs.6614	H10933	ESTs	2.5
	111375	Hs.20432	N93698	ESTs	2.5
	122642	Hs.99361	AA454186	ESTs	2.5
	127989	Hs.69851	AA837495	ESTs; Weakly similar to Wiskott-Aldrich	2.5
	105029	Hs.13268	AA126855	ESTs	2.5
15	105082	Hs.26765	AA143763	ESTs; Weakly similar to Similarity to S.	2.5

TABLE 1A show the accession numbers for those primekeys lacking unigeneID's for Table 1. For each probeset we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

	Pkey: CAT number: Accession:	Unique Eos probeset identifier number Gene cluster number Genbank accession numbers	
	Pkey	CAT number	Accessions
	108552	111555_1	AA071210 AA069899 AA071438 AA084912 AA084803 AA079371 AA079370
	126023	1596080_1	H57661 H58881
	126086	1606216_1	H75681 H70975
	102565	32479_1	AB010994 U59748 AA064680
	101964	48158_-7	S81578
	125499	1562851_1	H10543 R11878
	125596	1708455_1	R25698 R56582 R56018
	118417	37188_1	AF080229 AF080231 AF080230 AF080232 AF080233 AF080234 BE550633 AI636743 AW614951 BE467547 AI680833 AI633818 N29986 U87592 U87593 U87590 U87591 S46404 U87587 AA463992 AW206802 AI970376 AI583718 AI672574 N25695 AW665466 AI818326 AA126128 AI480345 AW013827 AA248638 AI214968 AA204735 AA207155 AA206262 AA204833 AW003247 AW496808 AI080480 AI631703 AI651023 AI867418 AW818140 AA502500 AI206199 AI671282 AI352545 BE501030 AI652535 BE465762 AA206331 AW451866 AA471088 AA206342 AA204834 AA206100 AW021661 AA332922 N66048 AA703396 H82278 AW139734 H82683 U87589 U87595 H69001 U87594 BE468420 AI624817 BE466611 AI206344 AA574397 AA348354 AI493182
	125661	327827_1	AA491830 R50173 R55192 R50320 AI732306 AI732305 AI820727 AI820728 R55191 R50319 R50227
	125957	1583542_1	H41694 H45213
	125982	1766315_1	R88091 W82898
	127248	227560_1	AA364185 AA325029 AW862050
	103731	112052_1	AA070545 AA131490 AA131373
	127261	231687_1	AA330501 AA661567
	127265	232391_1	AA331503 AA332751 AW982542
	126659	1541209_1	T16245 R19694 F13545 H10299 T66048 T65279 H18006
	127315	37938_1	AF116622 AI114507 AA640834 AA377899
	103806	112618_1	AA130614 AA071410
	128104	502608_1	AA906093 AA971000
	104602	624482_2	H47610 R86920
	128152	297868_1	F07973 R20353 AA442660
	128422	1811283_1	T77784 T85681
	127897	446527_1	AA773681 AA773857
	106566	120358_1	BE298210 AI672315 AW086489 BE298417 AA455921 AA902537 BE327124 R14963 AA085210 AW274273 AI333584 AI369742 AI039658 AI885095 AI476470 AI287650 AI885299 AI985381 AW592624 AW340136 AI266556 AA456390 AI310815 AA484951
	129735	44573_2	AI950087 N70208 R97040 N36809 AI308119 AW967677 N35320 AI251473 H59397 AW971573 R97278 W01059 AW967671 AA908598 AA251875 AI820501 AI820532 W87891 T85904 U71456 T82391 BE328571 T75102 R34725 AA884922 BE328517 AI219788 AA884444 N92578 F13493 AA927794 AI560251 AW874068 AL134043 AW235363 AA663345 AW008282 AA488864 AA283144 AI890387 AI950344 AI741346 AI689062 AA282915 AW102698 AI872193 AI763273 AW173586 AW150329 AI653832 AI762688 AA988777 AA488892 AI356394 AW103813 AI539642 AA642789 AA856975 AW505512 AI961530 AW629970 BE612681 AW276997 AW513601 AW512843 AA044209 AW856538 AA180009 AA337499 AW961101 AA251669 AA251874 AI818225 AW205862 AI683338 AI858509 AW276905 AI633006 AA972584 AA908741 AW072629 AW513996 AA283273 AA969759 N75628 N22388 H84729 H60052 T92487 AI022058 AA780419 AA551005 W80701 AW613456 AI373032 AI564269 F00531 H83488 W37181 W78802 R66056 AI002839 R67840 AA300207 AW959581 T63226 F04005
	123147	219802_-2	AA487961
	130529	158447_1	AA178953 AA182740
	123579	genbank_AA608983	AA608983
	109175	genbank_AA180496	AA180496
	100789	tgr_HT4163	S67998
	100858	tgr_HT4515	U10072

	123788	579959_1	AA620411 AA287491
	102118	entrez_U13706	U13706
	102398	entrez_U42359	U42359
	102764	entrez_U82310	U82310
5	118475	genbank_N66845	N66845
	104776	genbank_AA026349	AA026349
	104787	genbank_AA027317	AA027317
	113702	genbank_T97307	T97307
	113938	genbank_W81598	W81598
10	122635	genbank_AA454085	AA454085
	108407	genbank_AA075519	AA075519
	108432	genbank_AA076626	AA076626
	108555	genbank_AA084963	AA084963
	101349	entrez_L77559	L77559
15	124447	genbank_N48000	N48000
	119071	genbank_R31180	R31180
	103520	entrez_Y10511	Y10511
	103663	genbank_Z78291	Z78291
	128046	877605_1	AA873285 AI025782
20	126859	548044_1	AA189853 AA206355
	123465	genbank_AA599033	AA599033

MISSING AT THE TIME OF PUBLICATION

TABLE 2: shows a preferred subset of the Accession numbers for genes found in Table 1 which are differentially expressed in prostate tumor tissue compared to normal prostate tissue.

5

10 Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigeneID: Unigene number
 Unigene Title: Unigene gene title
 R1: Ratio of tumor to normal body tissue (Relaxed ratio (87/70))

15	Pkey	ExAccn	UnigeneID	Unigene Title	R1
	131918	AA121266	Hs.272458	ESTs	37.2
	120328	AA186979	Hs.290905	ESTs; Weakly similar to (define not ava	32.6
	101488	M24902	Hs.1852	acid phosphatase; prostate	25.2
	118073	R32894	Hs.279477	ESTs	24.8
20	133428	M34376	Hs.183752	microseminoprotein; beta-	23.8
	128180	AA595348	Hs.171995	kallikrein 3; (prostate specific antigen	21.4
	104080	AA402971	Hs.57771	Homo sapiens mRNA for serine protease (T	18.9
	127537	AA569531	Hs.162859	ESTs	18.8
	131665	R22139	Hs.30343	ESTs	17.4
25	101050	K01911	Hs.1832	neuropeptide Y	17.3
	130771	N48056	Hs.1915	folate hydrolase (prostate-specific memb	17
	107485	W63793	Hs.262476	S-adenosylmethionine decarboxylase 1	16.7
	106155	AA425309	Hs.33287	ESTs	16.5
	129534	R73640	Hs.11260	ESTs	16.4
30	100569	HQ2281+HT2351		Antigen, Prostate Specific, Alt. Splice	16
	101889	S39329	Hs.181350	kallikrein 2; prostatic	15.4
	135389	U05237	Hs.99872	fetal Alzheimer antigen	15
	133944	AA045870	Hs.7780	ESTs	12.5
	130974	X57985	Hs.2178	H2B histone family; member Q	11.8
35	114768	AA149007	Hs.182339	ESTs	11.8
	104660	AA007160	Hs.14846	ESTs	11.4
	131061	N64328	Hs.268744	ESTs; Moderately similar to KIAA0273 [H.	10.9
	128645	AI167942	Hs.61635	Homo sapiens BAC clone RG041D11 from 7q2	10.7
	135153	N40141	Hs.95420	Homo sapiens mRNA for JM27-protein; comp	10.6
40	107033	AA599629	Hs.113314	ESTs	10.6
	118417	N66048		ESTs; Weakly similar to polymerase [H.sa	10.5
	126758	W37145	Hs.293960	ESTs	10.2
	107102	AA609723	Hs.30652	ESTs	10.1
	116787	H28581	Hs.15641	ESTs	10.1
45	115719	AA416997	Hs.59622	ESTs	10
	123209	AA489711	Hs.203270	ESTs	9.9
	101664	M60752	Hs.121017	H2A histone family; member A	9.8
	112971	T17185	Hs.83883	ESTs	9.7
	117984	N51919	Hs.106778	ESTs	9.7
50	128523	M30894	Hs.274509	T-cell receptor; gamma cluster	9.4
	132984	AA031360	Hs.167133	ESTs	9.2
	121853	AA425887	Hs.98502	ESTs	9
	119617	W47380	Hs.55999	ESTs	8.9
	105627	AA281245	Hs.23317	ESTs	8.8
55	101461	M22430	Hs.76422	phospholipase A2; group IIA (platelets;	8.7
	124526	N62096	Hs.293185	yz61c5.s1 Soares_multiple_sclerosis_2NbH	8.5
	133845	T68510	Hs.76704	ESTs	8.2
	133354	AA055552	Hs.334762	ESTs; Weakly similar to KIAA0319 [H.sapi	8.1
	119018	N95796	Hs.278695	ESTs	8
60	100394	D84276	Hs.86052	CD38 antigen (p45)	8
	106579	AA456135	Hs.23023	ESTs	7.6
	114965	AA250737	Hs.72472	ESTs	7.4
	112033	R43162	Hs.22627	ESTs	7.1
	102398	U42359		Human N33 protein form 1 (N33) gene, exo	7
65	101201	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin;	6.9
	101803	M86546	Hs.155691	pre-B-cell leukemia transcription factor	6.8
	120552	AA280036	Hs.302267	ESTs; Weakly similar to W01A6.c [C.elega	6.8

	109112	AA169379	Hs.257924	ESTs	6.8
	109785	F10707	Hs.326416	ESTs	6.7
	130336	X07730	Hs.171995	kallikrein 3; (prostate specific antigen	6.6
	131425	AA219134	Hs.28691	ESTs	6.6
5	132802	AA490969	Hs.59838	ESTs	6.6
	133724	U07819	Hs.75746	aldehyde dehydrogenase 6	6.5
	120215	Z41050	Hs.108787	Homo sapiens Mcd4p homolog mRNA; complet	6.5
	131881	AA010183	Hs.3383	upstream regulatory element binding prot	6.5
	100727	X07290	Hs.334786	Human HF.12 gene mRNA	6.3
10	121770	AA421714	Hs.278428	Homo sapiens mRNA for KIAA0896 protein;	6.3
	123475	AA599267	Hs.250528	ESTs; Weakly similar to ANKYRIN; BRAIN V	6.3
	133061	AB000584	Hs.296638	prostate differentiation factor	6.3
	116429	AA609710	Hs.279923	ESTs; Weakly similar to similar to GTP-b	6.2
	101233	L29008	Hs.878	sorbitol dehydrogenase	6.2
15	104891	AA011176	Hs.37744	ESTs	6.2
	127248	AA325029	EST27953	Cerebellum II Homo sapiens cDNA	6.2
	105500	AA256485	Hs.222399	ESTs	6.1
	130828	AA053400	Hs.203213	ESTs	5.9
	115357	AA281793	Hs.72988	ESTs	5.8
20	116334	AA491457	Hs.48948	ESTs	5.7
	120132	Z38839	Hs.125019	ESTs; Weakly similar to IIII ALU SUBFAM I	5.6
	106375	AA443993	Hs.289072	ESTs	5.6
	124777	R41933	Hs.140237	ESTs; Weakly similar to neuronal thread	5.6
	101791	M83822	Hs.62354	Human beige-like protein (BGL) mRNA; par	5.5
25	117898	N41002	Hs.45107	ESTs	5.5
	122041	AA431407	Hs.88732	Homo sapiens Chromosome 16 BAC clone CIT	5.5
	133723	AA088851	Hs.262476	S-adenosylmethionine decarboxylase 1	5.5
	113938	W81598		ESTs	5.4
	133015	AA047038	Hs.248315	ESTs	5.4
30	108188	AA056482	Hs.7780	ESTs	5.3
	104468	N25110	Hs.326392	Human guanine nucleotide exchange factor	5.3
	104033	AA365031	Hs.98944	ESTs	5.3
	110844	N31952	Hs.167531	ESTs; Weakly similar to (define not ava	5.3
	129056	H70627	Hs.108336	ESTs; Weakly similar to IIII ALU SUBFAM I	5.3
35	133493	AA284143	Hs.194369	Homo sapiens chromosome 1 atrophin-1 rel	5.3
	129184	W28769	Hs.109201	ESTs; Highly similar to (define not ava	5.2
	101448	M21389	Hs.195850	keratin 5 (epidermolysis bullosa simplex	5.1
	116188	AA484728	Hs.184598	ESTs; Weakly similar to IIII ALU SUBFAM I	5.1
	105921	AA402613	Hs.169119	ESTs	5.1
40	103375	X91868	Hs.54416	sine oculis homeobox (Drosophila) homolo	5.1
	128871	AA400271	Hs.106778	ESTs; Highly similar to (define not ava	5.1
	116238	AA479362	Hs.47144	ESTs	5
	102913	X07686	Hs.80342	keratin 15	5
	103011	X52541	Hs.326035	early growth response 1	5
45	118981	N93839	Hs.39288	ESTs; Weakly similar to IIII ALU SUBFAM I	5

TABLE 2A shows the accession numbers for those primekeys lacking unigeneID's for Table 2. For each probeset we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

10	Pkey: CAT number: Accession:	Unique Eos probeset Identifier number Gene cluster number Genbank accession numbers
15	Pkey CAT number Accession	
20	118417 37186_1	AF080229 AF080231 AF080230 AF080232 AF080233 AF080234 BE550633 AI636743 AW614951 BE467547 AI680833 AI633818 N29986 U87592 U87593 U87590 U87591 S48404 U87587 AA463992 AW206802 AI970376 AI583718 AI672574 N25695 AW665468 AI818326 AA126128 AI480345 AW013827 AA248638 AI214968 AA204735 AA207155 AA208262 AA204833 AW003247 AW496808 AI080480 AI631703 AI651023 AI867418 AW818140 AA502500 AI206199 AI671282 AI352545 BE501030 AI652535 BE465782 AA206331 AW451868 AA471088 AA206342 AA204834 AA206100 AW021661 AA332922 N66048 AA703396 H92278 AW139734 H92683 U87589 U87595 H69001 U87594 BE466420 AI624817 BE466611 AI206344 AA574397 AA348354 AI493192
25	127248 227560_1	AA364195 AA325029 AW962050
	107033 235652_1	AI141999 AA730178 R44544 R41778 AW300793 AW966157 AA918501 AA599629 AI082195 AI198537 AW006520 AW236663 AW151420 AI826987 AI810832 AI669102 AI201981 N27331 AA335566 T84622 BE085347 BE085269
	102398 entrez_U42359	U42359
	113938 genbank_W81598	W81598

TABLE 3: shows genes, including expression sequence tags, differentially expressed in prostate tumor tissue compared to normal tissue as analyzed using the Affymetrix/Eos Hu02 GeneChip array. Shown are the relative amounts of each gene expressed in prostate tumor samples and various normal tissue samples showing the highest expression of the gene.

10	Pkey:	Unique Eos probeset identifier number			
	ExAccn:	Exemplar Accession number, Genbank accession number			
	UnigeneID:	Unigene number			
	Unigene Title:	Unigene gene title			
15	R1:	Ratio of tumor to normal body tissue			
	Pkey	ExAccn	UnigeneID	Unigene Title	R1
20	100131	D12485	Hs.11951	phosphodiesterase 1/nucleotide pyrophosph	6.3
	100235	D29954	Hs.13421	KIAA0056 protein	5.1
	100570	HG2261-HT2352	Hs.171995	Antigen, Prostate Specific, Alt. Splice	9
	100819	HG4020-HT4290	Hs.2387	Transglutaminase	10.5
	101063	L00354	Hs.80247	cholecystokinin	8.5
	101247	L33801	Hs.78802	glycogen synthase kinase 3 beta	4.7
25	101418	M17254	Hs.279477	v-ets avian erythroblastosis virus E26 o	4.7
	101447	M21305		Human alpha satellite and satellite 3 ju	11
	101485	M24736	Hs.89546	selectin E (endothelial adhesion molecu	9.8
	101514	M28214	Hs.123072	RAB3B; member RAS oncogene family	6.2
	101626	M57399	Hs.44	pleiotrophin (heparin binding growth fac	8.4
30	101863	M60750	Hs.2178	H2B histone family; member A	4.9
	101758	M77838	Hs.79217	pyrroline-5-carboxylate reductase 1	5.4
	101768	M81118	Hs.78989		7.5
	101817	M88163	Hs.152282	SW/SNF related; matrix associated; acti	5.5
	101888	M99701	Hs.95243	transcription elongation factor A (SII)-	5.7
35	102031	U04898	Hs.2156	RAR-related orphan receptor A	13.2
	102052	U07559	Hs.505	ISL1 transcription factor; LIM/homeodoma	8.9
	102221	U24576	Hs.3844	LIM domain only 4	5.8
	102233	U26173	Hs.79334	nuclear factor; interleukin 3 regulated	7.4
40	102302	U33052	Hs.69171	protein kinase C-like 2	8.2
	102348	U37519	Hs.87539	aldehyde dehydrogenase 8	5.9
	102457	U48807	Hs.2359	dual specificity phosphatase 4	5.1
	102473	U49857	Hs.180398	LIM domain-containing preferred transloc	5.7
	102669	U71207	Hs.29279	eyes absent (Drosophila) homolog 2	9
	102698	U75272	Hs.1867	progastricsin (pepsinogen C)	10.6
45	102751	U80034	Hs.68583	mitochondrial intermediate peptidase	15.6
	102823	U90914	Hs.5057	carboxypeptidase D	4.9
	102869	X02544	Hs.572	orosomucoid 1	22.6
	103031	X54667	Hs.123114	cystatin S	4.7
	103043	X55733	Hs.93379	eukaryotic translation initiation factor	4.9
50	103093	X60708	Hs.44926	dipeptidylpeptidase IV (CD26; adenosine	5.8
	103376	X92098	Hs.323378	coated vesicle membrane protein	5.2
	103401	X95240	Hs.54431	specific granule protein (28 kDa); cyste	7.4
	103613	Z46829	Hs.2316	SRY (sex-determining region Y)-box 9 (ca	5.2
	103677	Z83806		H.sapiens mRNA for axonemal dynein heavy	4.9
55	103962	AA298180	Hs.83243	ESTs	6
	104084	AA410529	Hs.30732	ESTs	6.4
	104257	AF006265	Hs.9222	estrogen receptor-binding fragment-assoc	6.8
	104301	D45332	Hs.6783	ESTs	10.5
	104769	AA025887	Hs.293943	ESTs; Weakly similar to IIII ALU SUBFAMI	6.3
60	104851	AA040882	Hs.10290	U5 snRNP-specific 40 kDa protein (hPrp8-	4.9
	104896	AA054228	Hs.23165	ESTs	5.8
	104956	AA074880	Hs.20509	ESTs; Weakly similar to hypothetical pro	6.4
	104957	AA074919	Hs.10028	ESTs; Weakly similar to ORF YJL063c [S.c	4.8
	104967	AA084506	Hs.291000	ESTs	6.5
65	105099	AA150776	Hs.23729	Homo sapiens clone 24405 mRNA sequence	7
	105298	AA233459	Hs.26369	ESTs	5.1

	105304	AA233553	Hs.190325	ESTs	4.7
	105370	AA236476	Hs.22791	ESTs; Weakly similar to transmembrane pr	10.3
	105427	AA251330	Hs.28248	ESTs	5
	105542	AA261858	Hs.286957	ESTs; Weakly similar to heat shock prota	8.8
5	105628	AA281251	Hs.79828	ESTs; Weakly similar to putative zinc fi	5.5
	105640	AA281623	Hs.6685	ESTs; Weakly similar to KIAA0742 protein	8
	105845	AA282138	Hs.11325	ESTs	14
	105691	AA287097	Hs.289068	transcription factor 4	6.3
	105730	AA292701	Hs.5364	DKFZP5641052 protein	4.9
10	105808	AA393808	Hs.286131	KIAA0438 gene product	7
	105826	AA398243	Hs.194477	ESTs; Moderately similar to similar to N	5
	105903	AA401433	Hs.200018	ESTs; Weakly similar to diphosphoinosito	9.9
	105906	AA401633	Hs.22380	ESTs	11.5
	106065	AA417558	Hs.25206	ESTs	5.1
15	106094	AA419481	Hs.23317	ESTs	10.9
	106157	AA425367	Hs.34892	ESTs	6.6
	106184	AA426643	Hs.10762	ESTs	8.5
	106211	AA428240	Hs.126083	ESTs	8.4
	106213	AA428258	Hs.8769	Homo sapiens mRNA; cDNA DKFZp564E153 (fr	5.7
20	106272	AA432074	Hs.323099	ESTs	5.8
	106369	AA443828	Hs.288855	ESTs	6.3
	106400	AA447621	Hs.94109	ESTs	5.4
	106474	AA450212	Hs.42484	Homo sapiens mRNA; cDNA DKFZp564C053 (fr	9.2
	106507	AA452584	Hs.267819	protein phosphatase 1; regulatory (inhib	5.6
25	106523	AA453441	Hs.31511	ESTs	4.7
	106532	AA453628	Hs.37443	ESTs	4.7
	106557	AA455087	Hs.22247	ESTs	5.7
	106576	AA456039	Hs.105421	ESTs	7.2
	106618	AA459249	Hs.8715	ESTs; Weakly similar to Similarity with	5.6
30	106820	AA481037	Hs.12592	ESTs	5.4
	106846	AA485223	Hs.34892	ESTs	5.3
	106973	AA505141	Hs.11923	Human DNA sequence from clone 167A19 on	7.5
	107110	AA609952	Hs.12784	KIAA0293 protein	6.1
	107127	AA620504	Hs.179898	ESTs	7.1
35	107159	AA621340	Hs.10600	ESTs; Weakly similar to ORF YKR081c [S.c	5.2
	107217	D51095	Hs.35861	DKFZP566E1621 protein	15.1
	107365	U78294	Hs.111256	arachidonate 15-lipoxygenase; second typ	4.7
	107630	AA007218	Hs.60178	ESTs	5.3
	107734	AA016225	Hs.7517	ESTs	4.8
40	107760	AA018042	Hs.252085	EST	7.8
	107997	AA037388	Hs.82223	Human DNA sequence from clone 141H5 on c	10.5
	108012	AA039616	Hs.173334	ESTs	6.5
	108520	AA084138	Hs.46788	ESTs	7.9
	108583	AA088278	Hs.68826	ESTs	5.6
45	108613	AA100957	Hs.69165	ESTs	6
	108664	AA113349	Hs.69588	EST	6.3
	108677	AA115629	Hs.118531	ESTs	5.9
	108807	AA129968	Hs.48378	ESTs; Weakly similar to PROTEIN PHOSPHAT	5.8
	108910	AA136590		ESTs	5
50	108933	AA147224	Hs.337232	ESTs	12.7
	108948	AA149579	Hs.118258	ESTs	6.8
	109014	AA156780	Hs.262038	ESTs	15.3
	109124	AA171529	Hs.183887	ESTs	6.1
	109142	AA178438	Hs.41295	ESTs	5.1
55	109277	AA186332	Hs.86043	ESTs	5.5
	109342	AA213620		Homo sapiens mRNA; cDNA DKFZp566M1418 (fr	
	109562	F01811	Hs.187931	ESTs; Moderately similar to voltage-gate	10.8
	109565	F01930	Hs.23648	ESTs	7
	109648	F04600	Hs.7154	ESTs	9.9
60	109799	F10770	Hs.180378	Homo sapiens clone 669 unknown mRNA; com	6.4
	109859	H02308	Hs.20792	ESTs	5.3
	110181	H20276	Hs.31742	ESTs	16.8
	110854	N32919	Hs.27931	ESTs	10
	110924	N47938	Hs.12940	yy04a09.s1 Scores_multiple_sclerosis_2Nb	5.6
65	111048	N55514	Hs.318584	ESTs	6.9
	111091	N59858	Hs.33032	Homo sapiens mRNA; cDNA DKFZp434N185 (fr	5.2
	111157	N66613	Hs.99364	ESTs	5
	111184	N66857	Hs.122489	ESTs; Weakly similar to III ALU CLASS C	5.8
	111221	N68869	Hs.15119	ESTs	6.2

	111348	N90041	Hs.9585	ESTs	5.4
	111353	N90430	Hs.6618	ESTs	5.3
	111495	R07210	Hs.9683	ESTs	5.8
	111540	R08850	Hs.9786	ESTs	6
5	111579	R10657	Hs.167115	KIAA0830 protein	12.6
	111581	R10684	Hs.5794	ESTs	7.1
	111734	R25375	Hs.128749	ESTs	6.2
	111861	R37460	Hs.25231	ESTs	9.4
	111870	R37778	Hs.18685	ESTs; Weakly similar to hypothetical pro	6.5
10	111937	R40431	Hs.14846	Homo sapiens mRNA; cDNA DKFZp564D016 (fr	4.8
	111987	R42036	Hs.6763	KIAA0942 protein	6.4
	112184	R49173	Hs.330242	ESTs	5.6
	112288	R53765	Hs.158135	KIAA0981 protein	9.3
	112380	R59740	Hs.5740	ESTs	4.7
15	112452	R63841	Hs.157461	ESTs	6
	112601	R79111	Hs.78225	annexin A1	5.4
	112753	R93696	Hs.169882	ESTs	5.8
	112902	T09262	Hs.129190	ESTs	5.1
	112984	T23457	Hs.289014	ESTs	4.9
20	113021	T23855	Hs.129836	KIAA1028 protein	10.8
	113083	T40530	Hs.266957	ESTs; Weakly similar to heat shock prote	5.7
	113200	T57773	Hs.10263	ESTs	7.3
	113494	T88878	Hs.86538	ESTs	8.7
	113849	W60439	Hs.8858	ESTs; Moderately similar to cbp146 [M.mu	4.9
25	113883	W72382	Hs.11958	oxidative 3 alpha hydroxysteroid dehydro	4.7
	113950	W85765	Hs.30504	Homo sapiens mRNA; cDNA DKFZp434E082 (fr	6.7
	113986	W87482	Hs.21894	ESTs	5.9
	113989	W87544	Hs.268828	ESTs	4.7
	114124	Z38595	Hs.125019	ESTs; Highly similar to KIAA0886 protein	21.3
30	114340	Z41395	Hs.143611	ESTs	9.6
	114346	Z41450	Hs.130489	ESTs	5.2
	114435	AA018218	Hs.164975	Bicaudal D (Drosophila) homolog 1	7.4
	114463	AA025370	Hs.40109	KIAA0872 protein	8.2
	114652	AA101416	Hs.107149	ESTs; Weakly similar to PTB-ASSOCIATED S	5.4
35	114721	AA131450	Hs.103822	ESTs	4.8
	114730	AA133527	Hs.331328	ESTs; Weakly similar to The KIAA0138 gen	5.1
	114833	AA234362	Hs.87159	ESTs; Moderately similar to CGI-66 prote	5.5
	114860	AA235112	Hs.42179	ESTs; Moderately similar to similar to m	6.3
	114884	AA235811	Hs.283672	ESTs	5.2
40	114895	AA236177	Hs.76591	KIAA0887 protein	4.7
	114908	AA238545	Hs.54973	ESTs	5.2
	114932	AA242751	Hs.16218	KIAA0903 protein	5.7
	115084	AA255568	Hs.42484	Homo sapiens mRNA; cDNA DKFZp564C053 (fr	5.2
	115140	AA258030	Hs.279938	ESTs; Weakly similar to supported by GEN	5.9
45	115468	AA287061	Hs.48499	ESTs; Highly similar to Bdelight protein	4.7
	115583	AA398913	Hs.45231	LDLC1 protein	7.8
	115709	AA412519	Hs.58279	ESTs	4.8
	115772	AA423872	Hs.131740	ESTs	5
	115774	AA424029	Hs.288390	ESTs; Moderately similar to dynamin; int	5.4
50	115776	AA424038	Hs.81897	ESTs	5
	115821	AA427528	Hs.130965	ESTs; Weakly similar to ZINC FINGER PROT	13.7
	115955	AA448121	Hs.44198	Homo sapiens BAC clone RG054D04 from 7q3	10.6
	116024	AA451748	Hs.83883	Human DNA sequence from clone 718J7 on c	6.8
	116108	AA457566	Hs.28777	ESTs	6
55	116117	AA459117	Hs.31575	SEC63; endoplasmic reticulum translocon	7.3
	116146	AA460701	Hs.15423	ESTs	5.5
	116298	AA489033	Hs.62601	Homo sapiens mRNA; cDNA DKFZp586K1318 (fr	5.7
	116379	AA521472	Hs.71252	ESTs	5.9
	116393	AA539463	Hs.306051	protein phosphatase 2 (formerly 2A); reg	5.9
60	116401	AA539963	Hs.59698	ESTs	7.9
	116416	AA609219	Hs.39982	ESTs	9.2
	116587	D59325	Hs.121429	ESTs	5.2
	116601	D80055	Hs.45140	ESTs	4.9
	116684	F09156	Hs.66095	ESTs	7.2
65	116722	F13654		HSFH32 Stratagene cat#937212 (1992) Hom	5.5
	116766	H13260	Hs.95097	ESTs	5.9
	117453	N29568	Hs.108319	thyroid hormone receptor-associated prot	6.9
	117557	N33920	Hs.44532	diubiquitin	4.8
	117708	N45114	Hs.126280	ESTs	6.3

	118001	N52151	Hs.47447	ESTs	11.4
	118229	N62339	Hs.166254	heat shock 90kD protein 1; alpha	6.2
	118599	N69207	Hs.203697	ESTs	5.8
5	118645	N70358	Hs.125180	growth hormone receptor	7.1
	118873	N89881	Hs.44577	ESTs	6
	118985	N94303	Hs.55028	ESTs	9.3
	119107	R42424	Hs.63841	ESTs	6
	119128	R45175	Hs.117183	ESTs	17.9
	119271	T16387	Hs.65328	ESTs	8
10	119367	T78324	Hs.250895	ESTs	5
	119721	W69440	Hs.48376	ESTs	15.4
	119741	W70205	Hs.43670	kinesin family member 3A	10.1
	119780	W72967	Hs.191381	ESTs; Weakly similar to hypothetical pro	5.3
	120217	Z41078	Hs.66035	ESTs	4.8
15	120266	AA173939	Hs.205442	ESTs; Weakly similar to inner centromere	8.8
	120294	AA190888	Hs.153881	ESTs; Highly similar to NY-REN-62 antigen	4.9
	120418	AA236010	Hs.26613	Homo sapiens mRNA; cDNA DKFZp586F1323 (4.7
	120486	AA253400	Hs.137569	tumor protein 63 kDa with strong homolog	5.8
	120524	AA261852	Hs.192905	ESTs	4.9
20	120571	AA280738	Hs.34892	ESTs	8.8
	120596	AA282074	Hs.237323	ESTs	6.2
	120713	AA292655	Hs.96557	ESTs	9.9
	120992	AA398248	Hs.97694	ESTs	16.4
	121429	AA406293	Hs.41167	ESTs	6.9
25	121503	AA412049	Hs.290347	ESTs	7.6
	121512	AA412105	Hs.193736	ESTs	5.8
	121816	AA424814	Hs.48827	ESTs	4.6
	122027	AA431302	Hs.98721	EST; Weakly similar to N-copine [H.sapi	5.6
	122294	AA437311	Hs.98927	ESTs	5.7
30	122411	AA446859	Hs.99083	ESTs	6.5
	122791	AA460158	Hs.129838	KIAA1028 protein	12.4
	122792	AA460225	Hs.99519	ESTs	5.1
	122869	AA478539	Hs.104338	ESTs	4.9
	123035	AA485724	Hs.27413	ESTs	5.4
35	123100	AA485957	Hs.306219	Homo sapiens clone 25032 mRNA sequence	5
	123295	AA495981	Hs.250830	ESTs	4.7
	123311	AA498252	Hs.105069	ESTs	7.4
	123593	AA609006	Hs.111240	ESTs	9.1
	123619	AA609200		ESTs	4.7
40	123645	AA609310	Hs.188691	ESTs	4.8
	123709	AA609651	Hs.112742	ESTs	7
	123968	C14333	Hs.108327	damage-specific DNA binding protein 1 (1	5
	124178	H45998	Hs.97101	putative G protein-coupled receptor	6.8
	124352	N21626	Hs.102406	ESTs	10.2
45	124357	N22401		yw37g07.s1 Morton Fetal Cochlea Homo sap	10.8
	124515	N58172	Hs.109370	ESTs	14.2
	124911	R88992	Hs.174195	ESTs	4.8
	125154	W38419		ESTs	4.7
	125992	W01626		za36e07.r1 Soares fetal liver spleen 1NF	5.1
50	126802	AA947601	Hs.97056	ESTs	6.1
	126812	Z36290	Hs.173933	ESTs; Weakly similar to NUCLEAR FACTOR 1	4.6
	127080	AA662913	Hs.190173	ESTs	5
	127308	AA507628	Hs.334390	ESTs	4.8
	127370	AI024352	Hs.70337	immunoglobulin superfamily; member 4	4.7
55	127386	AI457411	Hs.108728	ESTs	4.8
	127865	AA828760	Hs.282059	ESTs	4.8
	128172	AI400862	Hs.265130	ESTs	5
	128305	AI039722	Hs.279009	ESTs	5.8
	128420	AI088155	Hs.41296	ESTs; Weakly similar to unknown [H.sapi	17
60	128467	AA176446	Hs.180428	ESTs; Weakly similar to hypothetical 43.	4.8
	128610	L38608	Hs.10247	activated leucocyte cell adhesion molecu	7.9
	128625	AA242816	Hs.102652	ESTs; Weakly similar to KIAA0437 [H.sapi	8.1
	128651	AA446990	Hs.103135	ESTs	6.5
	129088	AA215971	Hs.194431	KIAA0992 protein	5.2
65	129138	N26391	Hs.250723	ESTs	5.1
	129171	AA234048	Hs.7753	calumenin	5.8
	129229	AA211941	Hs.109643	polyadenylate binding protein-Interactin	5.8
	129386	N27624	Hs.260024	Cdc42 effector protein 3	5.2
	129467	AA410311	Hs.44208	ESTs	5.1

	129584	H22136	Hs.75295	guanylate cyclase 1; soluble; alpha 3	16.3
	129699	AA458578	Hs.12017	KIAA0439 protein; homolog of yeast ubiqu	9.2
	129821	F11019	Hs.12696	cortactin SH3 domain-binding protein	8.8
5	129823	X00948	Hs.105314	relaxin 2 (H2)	9.1
	129847	W46767	Hs.296178	ESTs; Weakly similar to RNA POLYMERASE I	5.4
	129912	AA047344	Hs.107213	ESTs; Highly similar to NY-REN-6 antigen	6.5
	129958	L20591	Hs.1378	annexin A3	5.1
	129977	J04078	Hs.1395	early growth response 2 (Krox-20) (Drosop	8.6
10	130061	U82256	Hs.172851	arginase; type II	7.4
	130241	U78313	Hs.153203	MyoD family inhibitor	4.9
	130486	N21679	Hs.180059	ESTs	5.8
	130541	X05608	Hs.211584	neurofilament; light polypeptide (68kD)	6.7
	130619	AA477739	Hs.12532	ESTs	6.4
	130925	N71935	Hs.169378	multiple PDZ domain protein	7.9
15	130938	AA013250	Hs.21398	ESTs; Moderately similar to PUTATIVE GLU	6.2
	130971	H20332	Hs.301444	signal sequence receptor; gamma (translo	6.4
	131066	F09006	Hs.22558	ESTs	5
	131126	F09012	Hs.181326	myotubularin related protein 2	6.4
20	131310	J02980	Hs.2551	adrenergic; beta-2; receptor; surface	7.9
	131487	AA253220	Hs.27373	Homo sapiens mRNA; cDNA DKFZp56401763 (f5.9	15.9
	131581	X58841	Hs.294101	pre-B-cell leukemia transcription factor	7.6
	131562	U90551	Hs.28777	H2A histone family; member L	5.1
	131579	N62922	Hs.29088	ESTs	11
25	131629	AA442119	Hs.238809	ESTs	4.9
	131682	AA428368	Hs.30654	ESTs	4.8
	131699	R68657	Hs.90421	ESTs; Moderately similar to IIII ALU SUB	6.5
	131785	N32724	Hs.32317	Sox-like transcriptional factor	5.6
	132053	H93381	Hs.38085	ESTs; Weakly similar to putative glycine	7.2
	132122	U65082	Hs.40403	Cbp/p300-interacting transactivator; wil	5.6
30	132191	AA449431	Hs.288361	KIAA0741 gene product	8
	132256	AA608858	Hs.431	murine leukemia viral (bmi-1) oncogene h	5.5
	132482	AA429478	Hs.238126	ESTs; Highly similar to CGI-49 protein [6.6
	132533	AA021608	Hs.172510	ESTs	5.8
35	132572	AA448297	Hs.237825	signal recognition particle 72kD	6.2
	132581	R42266	Hs.52256	ESTs; Weakly similar to beta-TrCP protei	16
	132700	N47109	Hs.5521	ESTs	6.8
	132701	AA279359	Hs.55220	BCL2-associated athanogene 2	5.3
	132725	L41887	Hs.184167	splicing factor; arginine/serine-rich 7	7.8
40	132763	N74897	Hs.278894	DEAD/H (Asp-Glu-Ala-Asp/His) box polypep	5.9
	132790	X75535	Hs.168670	peroxisomal farnesylated protein	8
	132839	U76189	Hs.61152	exostoses (multiple)-like 2	5.2
	133142	F03321	Hs.65874	ESTs	5.2
	133342	U29589	Hs.7138	cholinergic receptor; muscarinic 3	10.3
45	133434	AA278852	Hs.30212	ESTs	5.8
	133453	M68941	Hs.73826	protein tyrosine phosphatase; non-recept	4.9
	133520	X74331	Hs.74519	primase; polypeptide 2A (58kD)	13.1
	133544	T33873	Hs.74624	protein tyrosine phosphatase; receptor t	4.6
	133608	D13315	Hs.75207	glyoxalase I	4.8
50	133628	H75939	Hs.75277	Homo sapiens mRNA; cDNA DKFZp586M141 (fr 5	5
	133633	D21262	Hs.75337	nucleolar phosphoprotein p130	6.3
	133797	S66431	Hs.76272	retinoblastoma-binding protein 2	6
	133928	N34096	Hs.7766	ubiquitin-conjugating enzyme E2E 1 (homo	5.4
	134095	U47414	Hs.79069	cyclin G2	5.2
55	134249	N89827	Hs.80667	RALBP1 associated Eps domain containing	6.5
	134321	AA418230	Hs.8172	ESTs	7
	134453	X70683	Hs.83484	SRY (sex determining region Y)-box 4	4.7
	134542	X57025	Hs.85112	insulin-like growth factor 1 (somatomedi	7.7
	134570	U66615	Hs.172280	SWI/SNF related; matrix associated; acti	6.4
60	134592	U82613	Hs.289104	Alu-binding protein with zinc finger dom	5.4
	134654	W23625	Hs.8739	ESTs; Weakly similar to ORF YGR200c [S.c	5
	134666	AA482319	Hs.8752	putative type II membrane protein	6.4
	134806	Z49099	Hs.89718	spermine synthase	6.7
	134951	AA431480	Hs.169358	ESTs	9.8
65	135066	X04602	Hs.93913	Interleukin 6 (interferon; beta 2)	5.7
	135155	AA358268	Hs.166556	ESTs; Moderately similar to transcriptio	4.9
	135411	L10333	Hs.99947	reticulon 1	5.3
	300023	M10093		AFFX control: 18S ribosomal RNA	4.6
	300254	AW079607	Hs.55610	ESTs; Weakly similar to ZnT-3 [H.sapiens	7.8
	300273	AW013907	Hs.167531	ESTs; Moderately similar to predicted us	11.5

	300319	AW157648	Hs.153506	ESTs; Weakly similar to microtubule-act	8.5
	300566	H86709	Hs.326392	son of sevenless (Drosophila) homolog 1	5.8
	300578	AI989417	Hs.134289	ESTs	4.4
	300671	AI239708	Hs.93810	ESTs	7.9
5	300675	AA039352	Hs.125034	ESTs; Weakly similar to ORF YDL040c [S.c	4.5
	300680	AW468068	Hs.24817	ESTs; Weakly similar to KIAA0986 protein	5.2
	300782	AI497778	Hs.20509	ESTs	6.4
	300810	AI076890	Hs.146847	ESTs	5.8
10	300813	AA406411	Hs.208341	ESTs; Weakly similar to KIAA0989 protein	10.6
	300823	AI863068	Hs.106823	ESTs; Weakly similar to putative zinc fi	5.6
	300834	AF109300	Hs.147924	ESTs	6.7
	300923	AW138372	Hs.1852	ESTs	7.6
	300962	AA593373	Hs.293744	ESTs	5.5
15	301015	AA947682	Hs.20252	ESTs; Weakly similar to Chain A; Cdc42hs	7
	301042	AI559131	Hs.197733	ESTs	24.9
	301242	AW161535	Hs.23782	ESTs	11.8
	301254	AI049624	Hs.283390	EST cluster (not in UniGene) with exon h	4.3
	301262	H29500	Hs.7130	ESTs; Moderately similar to N-coptine [H.	4.3
20	301388	AA156879	Hs.262038	ESTs; Weakly similar to ZINC FINGER PROT	6.6
	301563	AI802948	Hs.44208	ESTs; Weakly similar to match to ESTs AA	5.7
	301658	AW008475	Hs.151258	EST cluster (not in UniGene) with exon h	6.8
	301689	Z44810	Hs.301789	ESTs; Weakly similar to similar to C.ele	6.3
	301783	AI046347	Hs.83937	Homo sapiens PAC clone DJ1159004 from 7p	6.2
25	301805	AI800004	Hs.142846	ESTs; Weakly similar to MesP1 [M.musculu	8.5
	301848	R20002	Hs.6823	ESTs; Weakly similar to Intrinsic factor	4.6
	301891	AF131855	Hs.278591	Homo sapiens clone 25056 mRNA sequence	6.3
	302005	AI869868	Hs.123119	ESTs	36.8
	302056	AI457532	Hs.30488	ESTs; Moderately similar to ROSA26AS [M.	9.5
30	302067	H05698	Hs.222399	ESTs; Weakly similar to protein-tyrosine	5.8
	302099	AL021397	Hs.137576	ribosomal protein L34 pseudogene 1	8.8
	302147	AB022680	Hs.151717	KIAA0437 protein	5.9
	302214	AJ001454	Hs.159425	Homo sapiens mRNA for testican-3	4.3
	302236	AI128606	Hs.6557	zinc finger protein 161	4.3
35	302358	DB1150	Hs.322848	EST cluster (not in UniGene) with exon h	5.5
	302410	NM_004917	Hs.218366	EST cluster (not in UniGene) with exon h	26.8
	302486	AC003682	Hs.183512	multiple UniGene matches	8.2
	302582	NM_000522	Hs.249185	EST cluster (not in UniGene) with exon h	6.4
	302785	AA425562	Hs.11065	EST cluster (not in UniGene) with exon h	5
40	302782	AA343696	Hs.46821	ESTs; Weakly similar to putative [H.sapi	4.8
	302881	AA508363	Hs.105314	relaxin 1 (H1)	78.8
	302892	N58545	Hs.42346	histone deacetylase 3	8.5
	302970	AW118352	Hs.312679	EST cluster (not in UniGene) with exon h	7.4
	302977	AW263124	Hs.315111	EST cluster (not in UniGene) with exon h	5.5
45	303029	AF199613		EST cluster (not in UniGene) with exon h	4.6
	303125	AF161352	Hs.111782	EST cluster (not in UniGene) with exon h	5.8
	303280	AI571580	Hs.170307	ESTs	4.3
	303306	AA215297	Hs.61441	EST cluster (not in UniGene) with exon h	6.4
	303309	AL134164	Hs.145418	ESTs	6.6
50	303344	AA255977	Hs.250646	ESTs; Highly similar to ubiquitin-conjug	19.5
	303380	AA298471	Hs.326567	EST cluster (not in UniGene) with exon h	6.6
	303401	AA758552	Hs.309497	ESTs	6.8
	303525	AW516519	Hs.273284	ESTs	4.8
	303528	AA348111	Hs.96900	ESTs	12.1
55	303540	AA355607	Hs.309490	ESTs; Weakly similar to MMSET type I [H.	8.2
	303572	AW338520	Hs.242540	ESTs	8.4
	303685	AW500108	Hs.23643	EST cluster (not in UniGene) with exon h	4.9
	303699	D30691	Hs.19525	EST cluster (not in UniGene) with exon h	15.7
	303702	AW500748	Hs.224861	ESTs; Weakly similar to 73 kDA subunit o	6.3
60	303718	AI741397	Hs.114658	ESTs	4.8
	303722	AA521510	Hs.145010	ESTs	12.5
	303732	AW502405	Hs.125759	ESTs; Weakly similar to tumor suppressor	4.3
	303735	AA707750	Hs.169055	ESTs; Weakly similar to cis-Golgi matr	5.4
	303752	AI017288	Hs.5957	EST cluster (not in UniGene) with exon h	5.3
65	303753	AW503733	Hs.9414	ESTs	13
	303813	AI275850	Hs.114658	EST cluster (not in UniGene) with exon h	7.8
	304053	R00493	Hs.125565	translocase of inner mitochondrial membr	4.8
	304218	N66373	Hs.27973	ESTs; Weakly similar to ZK354.7 [C.elega	6
	305200	AA668128	Hs.45207	EST singleton (not in UniGene) with exon	5.7
	306718	AI024916	Hs.251354	ESTs	5.7

	307848	AI364188	EST singleton (not in UniGene) with exon	7.3
	307871	AI368665	Hs.31476 EST singleton (not in UniGene) with exon	5.4
	308050	AJ460004	Hs.31608 EST singleton (not in UniGene) with exon	8.1
5	308362	AI813519	Hs.105749 EST singleton (not in UniGene) with exon	5.5
	308923	AI863051	Hs.279815 ESTs	4.4
	309116	AI927149	Hs.29787 ribosomal protein L10	4.5
	309375	AW075342	Hs.9271 EST singleton (not in UniGene) with exon	7.4
	309674	AW205604	Hs.266009 ESTs; Weakly similar to IIII ALU SUBFAM1	5
10	310095	AI921750	Hs.144871 ESTs	5
	310098	AI685841	Hs.161354 ESTs	11.6
	310250	AJ478629	Hs.158465 ESTs	5.8
	310365	AI262148	Hs.145569 ESTs	9.7
	310382	AI734009	Hs.127699 EST cluster (not in UniGene)	10.4
15	310409	AI612775	Hs.145710 ESTs	4.6
	310431	AJ420227	Hs.149358 ESTs	72.9
	310573	AW292180	Hs.156142 ESTs	7.6
	310598	AI338013	Hs.140546 ESTs	9.2
	310639	AW269082	Hs.175162 ESTs	4.5
20	310787	AW262580	Hs.147874 ESTs	4.9
	310816	AI973051	Hs.224965 ESTs	7.6
	311251	AI855662	Hs.197698 ESTs	41.3
	311280	AI767957	Hs.198248 ESTs; Weakly similar to Y38A8.1 gene pro	4.5
	311330	AI679524	Hs.201629 ESTs; Moderately similar to IIII ALU SUB	4.8
25	311515	AW136713	Hs.23862 ESTs	5.9
	311574	AI824863	Hs.211420 ESTs	4.8
	311587	AI828254	Hs.271019 ESTs	5.8
	311596	AI682088	Hs.79375 ESTs	26.4
	311631	AI809519	Hs.27133 ESTs	6.4
30	311688	AW025661	Hs.240090 ESTs	7.4
	311783	AI682478	Hs.13528 EST	4.8
	311826	AA765470	Hs.85092 ESTs	6.7
	311853	AW014013	Hs.107056 ESTs	5.3
	311901	R16890	Hs.137135 ESTs	5.6
35	311932	AW451854	Hs.257482 ESTs	4.3
	312153	AA759250	Hs.118625 cytochrome b-561	11
	312182	AA834800	Hs.326263 EST cluster (not in UniGene)	16.9
	312242	AI380207	Hs.125276 ESTs	4.7
	312296	C01367	Hs.127128 ESTs	5.3
40	312407	R46180	Hs.153485 ESTs	6.2
	312424	AA847398	Hs.291997 ESTs	4.8
	312425	R49353	Hs.283892 ESTs	5.2
	312480	R68651	Hs.144997 ESTs	9.5
	312518	C17785	Hs.182738 ESTs	6.3
45	312521	AA033609	Hs.239884 ESTs	11.2
	312527	AI695522	Hs.191271 ESTs	4.7
	312539	AI004377	Hs.200360 ESTs	7
	312548	AI623511	Hs.118567 ESTs	5.1
	312563	AA976064	Hs.180842 ESTs	6.5
50	312623	AA694607	Hs.176956 EST cluster (not in UniGene)	10.8
	312857	AA772279	Hs.126914 ESTs	5
	312890	AI813654	Hs.5657 ESTs	5.8
	312903	AA939266	Hs.278626 ESTs	7.7
	312905	H92571	Hs.234478 ESTs	6.5
55	312976	AA838271	Hs.125830 ESTs	4.8
	312983	AI079278	Hs.269899 ESTs	5.1
	312996	AA249018	Hs.154331 EST cluster (not in UniGene)	7
	313035	N36417	Hs.144928 ESTs	6.3
	313168	AI801098	Hs.151500 ESTs	4.3
60	313188	AI039702	Hs.179573 collagen; type I; alpha 2	4.8
	313218	AA827805	Hs.124298 ESTs	5
	313226	AI200281	Hs.123910 ESTs	5.9
	313325	AI420611	Hs.127832 ESTs	4.6
	313326	AI088120	Hs.122329 ESTs	7.4
65	313425	AA745689	Hs.188838 ESTs; Weakly similar to similar to zinc	6.3
	313499	AI261390	Hs.146085 ESTs	5.6
	313540	AI797301	Hs.5740 ESTs	5.9
	313568	AW467376	Hs.129640 ESTs	4.3
	313569	AI273418	Hs.135146 ESTs; Weakly similar to ZK1058.5 [C.eleg	4.6
	313603	AW468119	Hs.287631 EST cluster (not in UniGene)	6.8

	313615	AW285194	Hs.301697	DKFZP434N126 protein	5.2
	313625	AW468402	Hs.254020	ESTs	7.8
	313634	AA688282	Hs.337786	ESTs	4.4
5	313635	AA507227	Hs.6390	ESTs	8.1
	313638	AI753075	Hs.104627	ESTs	6.7
	313670	C16690	Hs.23767	EST cluster (not in UniGene)	4.4
	313671	W49823	Hs.104613	ESTs	4.4
	313676	AA861697	Hs.120591	EST cluster (not in UniGene)	13.4
10	313703	AI161293	Hs.280380	ESTs; Weakly similar to KIAA0525 protein	10
	313712	AA768553	Hs.74170	ESTs	5.2
	313800	AW288132	Hs.55098	ESTs	5.4
	313879	AI535895	Hs.221024	ESTs	4.3
	314121	AI732100	Hs.187619	ESTs	13.6
15	314123	AW245993	Hs.223394	ESTs	6.4
	314171	AI821895	Hs.193481	ESTs	28.4
	314188	AL138431	Hs.164243	ESTs	4.8
	314219	AL036001	Hs.48376	ESTs	5.7
	314236	AA743396	Hs.189023	ESTs	4.9
20	314237	AA732359	Hs.96264	ESTs	4.4
	314284	AA731431	Hs.293484	EST cluster (not in UniGene)	6.4
	314305	AI280112	Hs.125232	ESTs	5.3
	314343	AI754701	Hs.328476	ESTs; Weakly similar to alternatively sp	6.2
	314530	AI052358	Hs.193726	ESTs	4.5
25	314691	AW207206	Hs.136319	ESTs	17
	314695	AW502698	Hs.118152	ESTs	8.9
	314785	AI538226	Hs.32976	ESTs	9.4
	314801	AA481027	Hs.109045	ESTs; Weakly similar to ORF YGR245c [S.c	8
	314864	AA483811	Hs.294068	ESTs	8
30	314807	AI672225	Hs.222888	ESTs	19.3
	314916	AA548908	Hs.122244	ESTs	4.5
	314954	AA521381	Hs.187726	ESTs	5.3
	314981	AA524953	Hs.293334	ESTs	4.6
	315021	AA533447	Hs.312889	EST cluster (not in UniGene)	5.1
35	315051	AW282425	Hs.163484	EST	15.5
	315052	AA876910	Hs.134427	ESTs	20
	315073	AW452948	Hs.257631	ESTs	5.3
	315084	AI821085		ESTs	8.2
	315214	AI915927	Hs.34771	ESTs	5.4
40	315220	AI420753	Hs.66731	ESTs	5.1
	315278	AI885544	Hs.12450	ESTs	5.8
	315282	AI222165	Hs.144923	ESTs	4.5
	315368	AW281663	Hs.104696	ESTs	8
	315369	AA764918	Hs.256531	ESTs	4.8
45	315378	AI263393	Hs.145008	ESTs	8.2
	315379	AI378329	Hs.126629	ESTs	5.4
	315402	AW283424	Hs.75354	ESTs	5.1
	315442	AA977835	Hs.127274	ESTs	6.6
	315443	AW003416	Hs.160604	ESTs	5.5
50	315528	R37257	Hs.184780	ESTs	8.1
	315593	AW198103	Hs.158154	ESTs	9.9
	315634	AA837085	Hs.220585	ESTs	7.8
	315705	AW448285	Hs.313636	ESTs	8.8
	315707	AI418055	Hs.181160	ESTs	5.1
55	315714	AA744015	Hs.298138	EST cluster (not in UniGene)	8.1
	315740	T05558	Hs.156880	EST cluster (not in UniGene)	6.8
	315762	AI391470	Hs.158618	ESTs	5.3
	315769	AA744875	Hs.189413	ESTs	5
	315843	AA679430	Hs.191697	ESTs	5.7
60	315890	AI600041	Hs.190555	ESTs	9.2
	316012	AA764950	Hs.119898	ESTs	4.3
	316038	AA708016	Hs.190389	ESTs	5.9
	316055	AA693880	Hs.6947	EST cluster (not in UniGene)	6.7
	316074	AW517542	Hs.293273	ESTs	5.5
65	316100	AW203986	Hs.213003	ESTs	5.1
	316169	AI127483	Hs.120451	ESTs	8.2
	316442	AA760894	Hs.153023	ESTs	17.1
	316491	AA768025	Hs.186854	EST	4.8
	316504	AW135854	Hs.132458	ESTs	4.3
	316687	AW015940	Hs.232234	ESTs	7.6

	316854	AA831215	Hs.159068	ESTs; Weakly similar to predicted using	5.1
	316905	AW138241	Hs.210846	ESTs	6.4
	317008	AW051597	Hs.143707	ESTs	4.4
5	317019	AA854968	Hs.127699	ESTs	11
	317194	AW445167	Hs.126036	ESTs	13.5
	317224	D56780	Hs.93029	ESTs	8.7
	317404	AI806887	Hs.128594	ESTs	8.7
	317501	AA931245	Hs.137097	ESTs	11.1
	317548	AI654187	Hs.195704	ESTs	14.2
10	317651	AW282779	Hs.169799	ESTs	5.8
	317758	AI733277	Hs.128321	ESTs	5.4
	317850	N29974	Hs.152882	EST cluster (not in UniGene)	11.4
	317869	AW295184	Hs.129142	ESTs; Weakly similar to DEOXYRIBONUCLEASE	13.8
	317902	AI828602	Hs.211265	ESTs	5.3
15	317916	AI565071	Hs.159883	ESTs	7.7
	318239	AI085198	Hs.164228	ESTs	13.1
	318268	AI817736	Hs.182490	ESTs	6.2
	318327	AW294013	Hs.200942	ESTs	4.8
20	318363	R45530	Hs.1440	gamma-aminobutyric acid (GABA) A recepto	8
	318428	AI949409	Hs.194591	ESTs	12.3
	318464	AI151010	Hs.157774	ESTs	4.3
	318524	AW291511	Hs.159068	ESTs	25.9
	318540	T30280	Hs.274803	EST cluster (not in UniGene)	7
25	318591	AW206808	Hs.115325	ESTs	4.8
	318615	AI133817	Hs.10177	ESTs	5.5
	318648	AW175665	Hs.278695	ESTs	5.7
	318667	AI493742	Hs.165210	ESTs	11
	318668	W26276	Hs.138075	ESTs	5.9
30	318753	AA578285	Hs.7130	copine IV	5.5
	319080	Z45131	Hs.23023	ESTs	16.9
	319181	F06504	Hs.27384	EST cluster (not in UniGene)	4.8
	319191	AF071538	Hs.79414	prostate epithelium-specific Ets transcr	6.6
	319233	R21054	Hs.180532	ESTs	4.9
35	319586	D78808	Hs.283683	ESTs	8.2
	319750	AA621808	Hs.117956	ESTs	9.3
	319763	AA460775	Hs.6295	ESTs	14.3
	319824	AA424268	Hs.123642	EST cluster (not in UniGene)	12.8
	319838	AA337642	Hs.85262	nuclear factor related to kappa B bindin	5.1
40	319913	AA179304	Hs.271588	ESTs; Moderately similar to IIII ALU SUB	4.3
	319964	T80579	Hs.290270	ESTs	5.8
	320076	AI653733	Hs.271593	ESTs	8.5
	320102	AW298219	Hs.115325	RAB7; member RAS oncogene family-like 1	9.8
	320187	T89949	Hs.303428	EST cluster (not in UniGene)	9.8
45	320211	AL039402	Hs.125783	DEME-6 protein	7.9
	320324	AF071202	Hs.139338	ATP-binding cassette; sub-family C (CFTR	56.2
	320455	R49889	Hs.24144	EST cluster (not in UniGene)	8.3
	320464	AI089817	Hs.237148	ESTs	5.4
	320561	NM_006953	Hs.159330	EST cluster (not in UniGene)	7
50	320574	AL049443	Hs.161283	Homo sapiens mRNA; cDNA DKFZp586N2020 (f4.4	74.4
	320576	AL049977	Hs.162209	Homo sapiens mRNA; cDNA DKFZp564C122 (fr	6.7
	320654	AW263088	Hs.118112	ESTs	6
	320796	AF038968	Hs.31218	secretory carrier membrane protein 1	13.5
	320800	AI681006	Hs.71721	ESTs	6.2
55	320813	AW360847	Hs.16578	ESTs	9.3
	320853	AI473796	Hs.135904	ESTs	8.1
	320856	D59945	Hs.65368	EST cluster (not in UniGene)	6
	320899	AA633772	Hs.116798	ESTs	9.2
	320918	AW195012	Hs.293970	ESTs	5
60	320973	H19732	Hs.247917	ESTs	5.9
	321099	AA018386	Hs.64341	ESTs	4.8
	321180	H52462	Hs.163872	EST cluster (not in UniGene)	5.8
	321318	AB033041	Hs.137507	EST cluster (not in UniGene)	8.4
	321382	AW372449	Hs.175982	EST cluster (not in UniGene)	7.3
65	321441	AW297633	Hs.118498	ESTs	14.7
	321538	H80483	Hs.46903	EST cluster (not in UniGene)	9.2
	321609	H86021	Hs.182538	ESTs; Weakly similar to hMmTRA1b (H.sapi	4.8
	321638	AI791838	Hs.183465	ESTs	5.5
	321638	AI356352	Hs.108932	ESTs	4.8
	321644	AI204177	Hs.237396	ESTs	6.6

	321681	AA233821	Hs.190173	EST cluster (not in UniGene)	4.6
	321726	X91221	Hs.144485	EST cluster (not in UniGene)	5
	321758	U29112	Hs.196151	EST cluster (not in UniGene)	6.2
	321877	AL109784	Hs.189222	EST cluster (not in UniGene)	4.6
5	321899	N55158	Hs.29468	ESTs	4.6
	321902	AA746374	Hs.145010	ESTs	8.2
	322007	AW410646	Hs.164649	ESTs	5.1
	322055	AL137646	Hs.146001	EST cluster (not in UniGene)	4.3
	322092	AF085833	Hs.135624	EST cluster (not in UniGene)	4.3
10	322221	AI890619	Hs.179662	nucleosome assembly protein 1-like 1	4.4
	322278	AF086283		EST cluster (not in UniGene)	5.8
	322303	W07459	Hs.157601	EST cluster (not in UniGene)	22
	322437	AW393804	Hs.170253	ESTs; Weakly similar to rabaptin-4 [H.sa	4.4
	322493	AF143235	Hs.279819	EST cluster (not in UniGene)	7.2
15	322782	AA056060	Hs.202577	EST cluster (not in UniGene)	18.4
	322811	AA782292	Hs.105872	ESTs	6.9
	322818	AW043782	Hs.283618	ESTs	10.7
	322826	AI807883	Hs.180059	ESTs	5
20	322887	AI986306	Hs.86149	ESTs; Weakly similar to KIAA0969 protein	11.9
	322889	AA081924	Hs.124918	ESTs	7.1
	322924	AA669253	Hs.136075	ESTs	4.5
	322982	AI351191	Hs.128430	ESTs	6.8
	322994	AA422116	Hs.191461	ESTs	4.7
25	323040	AA336609	Hs.10862	ESTs	6.9
	323041	AL118747	Hs.26891	EST cluster (not in UniGene)	8.3
	323045	AA148950	Hs.188836	ESTs	4.6
	323048	AL118923	Hs.175110	EST cluster (not in UniGene)	7.5
	323070	AA157728	Hs.264330	ESTs	7.5
30	323071	AA157867	Hs.5722	ESTs	4.7
	323097	Z44354	Hs.296261	guanine nucleotide binding protein (G pr	4.9
	323131	AA176982	Hs.270124	EST cluster (not in UniGene)	6.1
	323136	AL120351	Hs.30177	EST cluster (not in UniGene)	4.3
	323175	AI827137	Hs.336454	ESTs	6.2
35	323218	AF131846	Hs.13396	Homo sapiens clone 25028 mRNA sequence	6.3
	323226	AF055019	Hs.21906	Homo sapiens clone 24670 mRNA sequence	12.6
	323236	AA363148	Hs.293960	ESTs	10.9
	323262	AI829770	Hs.190642	ESTs	7.6
	323276	AA836452	Hs.323822	ESTs	7.8
40	323287	AA639902	Hs.104215	ESTs	24.7
	323335	AI655499	Hs.161712	ESTs	14.1
	323341	AL134875	Hs.108646	ESTs	5.3
	323362	AL135067	Hs.117182	ESTs	6.1
	323486	C05276	Hs.299221	ESTs; Moderately similar to [PYRUVATE DE	8.5
45	323496	AI826801	Hs.300700	ESTs	4.5
	323507	H71721	Hs.128387	ESTs	4.4
	323545	AI814405	Hs.224569	ESTs	5.8
	323623	AA314280	Hs.146589	EST cluster (not in UniGene)	5
	323663	AW263526	Hs.243023	ESTs	7.7
50	323691	AA317561	Hs.145599	EST cluster (not in UniGene)	5.9
	323810	AA740405	Hs.108806	ESTs	6.2
	323846	AA337621	Hs.137635	ESTs	6
	323929	AA354940	Hs.145958	ESTs	10.7
	323959	AI836775	Hs.6831	ESTs	5.4
55	323996	AA367032	Hs.217882	ESTs	5.8
	323997	AA844907	Hs.274454	EST cluster (not in UniGene)	4.4
	324019	AW177009		EST cluster (not in UniGene)	4.6
	324130	AL046575	Hs.130198	ESTs	11
	324295	AI146686	Hs.143691	ESTs	13.7
60	324296	AI524039	Hs.192524	ESTs	6.8
	324307	AA627642	Hs.4994	transducer of ERBB2; 2 (TOB2)	4.9
	324330	AA884766		EST cluster (not in UniGene)	4.3
	324385	F28212	Hs.284247	EST cluster (not in UniGene)	4.7
	324430	AA464018	Hs.184598	EST cluster (not in UniGene)	13.6
65	324452	AW014022	Hs.170853	ESTs	7.6
	324547	AW501974	Hs.74170	ESTs	5.8
	324603	AW016378	Hs.292934	ESTs	24.2
	324617	AA508552	Hs.195839	ESTs	54
	324618	AI346282	Hs.87159	ESTs	4.8
	324620	AA448021	Hs.84109	EST cluster (not in UniGene)	5.7

	324626	AI685484	ESTs	9	
	324658	AI694767	Hs.129179 ESTs	22	
	324676	AW503943	Hs.112451 ESTs	4.9	
5	324691	AI217983	Hs.293341 ESTs; Weakly similar to Pro-a2(XI) [H.sa	10.6	
	324698	AA641092	Hs.257339 ESTs	10.2	
	324713	AW340249	Hs.163440 ESTs	5.5	
	324715	AI739168	Hs.131798 EST cluster (not in UniGene)	7.2	
	324718	AI557019	Hs.116467 ESTs	34.4	
10	324720	AA578904	Hs.292437 ESTs	4.8	
	324752	AI278919	Hs.272072 ESTs; Moderately similar to III ALU SUB	7.9	
	324753	AA612626	Hs.144871 EST cluster (not in UniGene)	5.2	
	324790	AI334367	Hs.159337 ESTs	7.6	
	324801	AI819924	Hs.14553 ESTs	12.8	
15	324804	AI692552	ESTs	6.5	
	324845	AA361016	Hs.337533 ESTs	4.5	
	324888	AI564134	Hs.136102 KIAA0853 protein	4.4	
	324929	AI741633	Hs.125350 ESTs	6.5	
	324951	AA613792	EST cluster (not in UniGene)	5.1	
20	325108	AA401863	Hs.22380 ESTs	7.1	
	326816		CH.20_hs gi 6552458	9.6	
	326897		CH.21_hs gi 5867660	4.8	
	327098		CH.21_hs gi 6682516	4.3	
	328492		CH.07_hs gi 5868455	5.8	
25	329362		CH.X_hs gi 5868837	4.3	
	329929		CH.16_p2 gi 6165201	5.5	
	329960		CH.16_p2 gi 5091594	7.6	
	330020		CH.16_p2 gi 6671887	6	
	330211		CH.05_p2 gi 6013592	12.6	
30	330384	M23263	androgen receptor (dihydrotestosterone r	9	
	330430	HG2261-HT2352	Hs.321110	Antigen, Prostate Specific, Alt. Splice	13.8
	330546	U31382	Hs.299857 guanine nucleotide binding protein 4	6	
	330551	U39840	hepatocyte nuclear factor 3; alpha	4.9	
	330658	AA319514	Hs.30732 ESTs	6	
35	330700	AA037415	Hs.20999 ESTs	5.5	
	330704	AA056557	Hs.6759 ESTs	5.1	
	330705	AA102571	Hs.157078 ESTs	11.7	
	330706	AA121140	Hs.177578 ESTs; Moderately similar to kynurenine a	14.5	
	330712	AA167269	Hs.52620 ESTs	5	
40	330725	AA252033	Hs.24052 ESTs; Weakly similar to III ALU SUBFAM1	7.2	
	330732	AA281092	Hs.35254 ESTs	4.9	
	330762	AA449677	Hs.15251 Human DNA sequence from clone 437M21 on	18.5	
	330763	AA450200	Hs.143187 FK506-binding protein 3 (25kD)	4.3	
	330772	AA479114	Hs.11356 ESTs	5.8	
45	330786	D60374	EST	4.6	
	330892	AA149579	Hs.91202 ESTs	15.3	
	330949	H01458	Hs.142896 ESTs	10.3	
	330977	H20828	Hs.315181 ESTs	4.4	
	331017	N24619	Hs.108920 ESTs	11.8	
50	331099	R36671	Hs.14846 ESTs	11.6	
	331128	R51361	Hs.268714 ESTs	4.8	
	331151	R82331	Hs.268838 ESTs	13	
	331185	T64447	Hs.168439 ESTs	4.9	
	331320	AA262999	Hs.300141 ESTs	4.8	
55	331321	AA278355	Hs.87929 ESTs	6.1	
	331337	AA287662	Hs.118630 ESTs	9.2	
	331348	AA400586	Hs.88143 ESTs	9.9	
	331359	AA416979	Hs.81897 ESTs	4.3	
	331383	AA454543	Hs.43543 ESTs	4.6	
60	331422	F10802	Hs.237339 ESTs; Moderately similar to III ALU SUB	4.9	
	331442	H77381	Hs.41223 ESTs	7.5	
	331468	N21680	Hs.43455 ESTs	6.4	
	331479	N27154	Hs.44076 ESTs	6.5	
	331490	N32912	Hs.291039 ESTs; Weakly similar to hypothetical 43.	12.5	
65	331493	N34357	Hs.93817 ESTs	4.6	
	331561	N62780	Hs.48703 ESTs	9.2	
	331615	N92352	Hs.5472 ESTs	4.8	
	331659	W48868	Hs.334305 ESTs	8.7	
	331698	Z38907	Hs.65949 KIAA0888 protein	10.3	
	331811	AA404500	Hs.187958 ESTs	4.8	

	331848	AA417039	Hs.98268	signal recognition particle 72kD	7.5
	331873	AA429445	Hs.98540	ESTs	6.5
	331889	AA431407	Hs.98802	Homo sapiens Chromosome 16 BAC clone CTT	33.6
5	331967	AA460158	Hs.99589	KIAA1028 protein	6.8
	331974	AA464518	Hs.105322	ESTs	5.3
	332043	AA490831	Hs.201591	ESTs	10.8
	332076	AA599477	Hs.291156	ESTs	4.4
	332173	F08281	Hs.100725	ESTs	5.5
	332247	N58172		ESTs	14.2
10	332249	N62098	Hs.184140	ESTs	7.2
	332325	T78428	Hs.339687	ESTs	5.6
	332396	AA340504		ESTs; Weakly similar to similar to human	21.2
	332434	N75542	Hs.237731	transcription factor 4	15.3
15	332493	N95485	Hs.56729	ESTs; Highly similar to GTP-binding prot	7.1
	332522	L38503	Hs.178357	glutathione S-transferase theta 2	6.6
	332526	AA281753	Hs.17731	inositol 1,4,5-triphosphate receptor; ty	5.8
	332530	M31682	Hs.19280	inhibin; beta B (activin AB beta polypep	5.5
	332533	M99487	Hs.325825	folate hydrolase (prostate-specific memb	38.1
	332538	N48715	Hs.20991	ESTs	6.5
20	332546	D84454	Hs.22587	solute carrier family 35 (UDP-galactose	4.8
	332594	AA279313	Hs.32851	methyl CpG binding protein 2	5.6
	332610	AA412405	Hs.40513	ESTs; Weakly similar to BETA GALACTOSIDA	5.6
	332661	N85742	Hs.6390	ESTs	6.9
	332687	T94885	Hs.75725	carboxypeptidase E	24.3
25	332712	D26070	Hs.79306	inositol 1,4,5-triphosphate receptor; ty	9.9
	332716	L00058	Hs.79630	v-myc avian myelocytomatosis viral oncog	5.6
	332726	R72029	Hs.83428	synaptophysin-like protein	5
	332781	AA233258		ESTs; Weakly similar to D1007.5 [C.elega	4.5
30	332787			CH22_FGENES.6_2	30.8
	332798			CH22_FGENES.6_5	66.8
	332799			CH22_FGENES.6_6	19.8
	332833			CH22_FGENES.38_7	5.6
	332890			CH22_FGENES.54_1	5.5
	332884			CH22_FGENES.54_6	4.9
35	333168			CH22_FGENES.94_1	4.7
	333169			CH22_FGENES.94_2	4.4
	333452			CH22_FGENES.157_1	4.8
	333456			CH22_FGENES.157_5	4.3
	333458			CH22_FGENES.157_7	4.8
40	333611			CH22_FGENES.217_6	4.7
	333621			CH22_FGENES.219_5	5.5
	333814			CH22_FGENES.282_2	7.1
	333849			CH22_FGENES.290_8	6.2
	333949			CH22_FGENES.303_5	4.3
45	333951			CH22_FGENES.303_7	4.9
	333955			CH22_FGENES.303_11	5.8
	334150			CH22_FGENES.339_1	5.1
	334223			CH22_FGENES.360_4	20.3
	334297			CH22_FGENES.372_3	9.4
50	334443			CH22_FGENES.387_2	4.6
	334444			CH22_FGENES.387_4	5.6
	334447			CH22_FGENES.387_7	13.1
	334570			CH22_FGENES.405_11	5.4
	334749			CH22_FGENES.427_1	5.3
55	334777			CH22_FGENES.430_9	4.7
	334960			CH22_FGENES.485_29	5.2
	335179			CH22_FGENES.504_9	8.8
	335293			CH22_FGENES.527_6	4.7
	335550			CH22_FGENES.576_11	5.1
60	335581			CH22_FGENES.581_19	5.7
	335588			CH22_FGENES.581_25	4.3
	335809			CH22_FGENES.617_8	6.2
	335810			CH22_FGENES.617_7	5.8
	335822			CH22_FGENES.619_7	7.1
65	335824			CH22_FGENES.619_11	8.5
	335853			CH22_FGENES.626_5	4.3
	335886			CH22_FGENES.632_4	4.3
	336034			CH22_FGENES.678_5	6.8
	336441			CH22_FGENES.827_7	7.6

	336624	CH22_FGENES.6-3	43.3
	336625	CH22_FGENES.6-4	37.9
	336679	CH22_FGENES.43-7	5.3
	337577	CH22_C65E1.GENSCAN.8-1	4.9
5	338255	CH22_EM:AC005500.GENSCAN.276-3	13.4
	338260	CH22_EM:AC005500.GENSCAN.279-10	4.6
	338561	CH22_EM:AC005500.GENSCAN.421-5	4.6
	338562	CH22_EM:AC005500.GENSCAN.421-6	4.3
	338759	CH22_EM:AC005500.GENSCAN.517-6	5.1
10	338763	CH22_EM:AC005500.GENSCAN.517-16	5.5
	338764	CH22_EM:AC005500.GENSCAN.517-17	7.1

TABLE 3A shows the accession numbers for those primekeys lacking unigeneID's for Table 3. For each probeset we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

10	Pkey: CAT number: Accession:	Unique Eos probeset identifier number Gene cluster number Genbank accession numbers	
15	Pkey	CAT number	Accession
	123619	371681_1	AA602884 AA609200
	116722	143512_1	Z24878 AA494098 F13654 AA494040 AA143127
	103677	41847_1	Z83806 AJ132081 AJ132090
20	125992	1589048_1	H48372 W01626
	109342	genbank_AA213620	AA213620
	125154	genbank_W38419	W38419
	101447	entrez_M21305	M21305
	124357	genbank_N22401	N22401
25	108910	genbank_AA136590	AA136590
	322278	47271_1	W69304 AF086283 W89200
	315084	350959_1	AI821085 AW973464 AA554802 AI821831 AA657438 AA640756 AA650339
	324019	262782_1	AW177009 AI381610
	324330	300543_1	AA884766 AW974271 AA592975 AA447312
30	324628	338411_1	AI685464 AW971336 AA513587 AA525142
	303029	37699_1	AF199613 AF108756
	324804	398093_1	AI692552 AI393343 AI800510 AI377711 F24263 AA661876
	324961	378239_1	AA613792 AW182329 T05304 AW858385
	329362	c_x_hs	
35	336624	CH22_4071FG_6_3_	
	336625	CH22_4072FG_6_4_	
	336679	CH22_4157FG_43_7_	
	338255	CH22_6856FG_LINK_EM:AC00	
	338260	CH22_6863FG_LINK_EM:AC00	
40	329829	c16_p2	
	329960	c16_p2	
	338561	CH22_7284FG_LINK_EM:AC00	
	338562	CH22_7285FG_LINK_EM:AC00	
	338759	CH22_7581FG_LINK_EM:AC00	
45	338763	CH22_7585FG_LINK_EM:AC00	
	338764	CH22_7586FG_LINK_EM:AC00	
	333168	CH22_400FG_94_1_LINK_EM:A	
	333169	CH22_401FG_94_2_LINK_EM:A	
	333452	CH22_702FG_157_1_LINK_EM:	
50	333458	CH22_706FG_157_5_LINK_EM:	
	333458	CH22_708FG_157_7_LINK_EM:	
	333611	CH22_872FG_217_6_LINK_EM:	
	333821	CH22_882FG_219_5_LINK_EM:	
	333814	CH22_1083FG_282_2_LINK_EM	
55	333849	CH22_1118FG_290_8_LINK_EM	
	335179	CH22_2515FG_504_9_LINK_EM	
	333949	CH22_1225FG_303_5_LINK_EM	
	333951	CH22_1227FG_303_7_LINK_EM	
	333955	CH22_1231FG_303_11_LINK_E	
60	335293	CH22_2835FG_527_6_LINK_EM	
	326816	c20_hs	
	326897	c21_hs	
	335550	CH22_2905FG_578_11_LINK_E	
	335581	CH22_2938FG_581_19_LINK_E	
65	335586	CH22_2944FG_581_25_LINK_E	

	328492	c_7_hs	
	335809	CH22_3181FG_617_6_LINK_EM	
	335810	CH22_3182FG_617_7_LINK_EM	
	335822	CH22_3195FG_619_7_LINK_EM	
5	335824	CH22_3187FG_619_11_LINK_E	
	335853	CH22_3228FG_626_5_LINK_EM	
	335888	CH22_3261FG_632_4_LINK_EM	
	330020	c16_p2	
	330211	c_5_p2	
10	337577	CH22_5864FG_LINK_C65E1.G	
	307848	AI364185	
	332797	CH22_13FG_6_2_LINK_C4G1.G	
	332788	CH22_14FG_6_5_LINK_C4G1.G	
	332799	CH22_15FG_6_6_LINK_C4G1.G	
15	334150	CH22_1429FG_339_1_LINK_EM	
	332933	CH22_154FG_38_7_LINK_C20H	
	332980	CH22_204FG_54_1_LINK_EM:A	
	332984	CH22_208FG_54_6_LINK_EM:A	
	334223	CH22_1507FG_360_4_LINK_EM	
20	334287	CH22_1588FG_372_3_LINK_EM	
	327098	c21_hs	
	334443	CH22_1742FG_387_2_LINK_EM	
	334444	CH22_1743FG_387_4_LINK_EM	
	334447	CH22_1746FG_387_7_LINK_EM	
25	334570	CH22_1875FG_405_11_LINK_E	
	334749	CH22_2061FG_427_1_LINK_EM	
	334777	CH22_2089FG_430_9_LINK_EM	
	336034	CH22_3418FG_678_5_LINK_DJ	
	334960	CH22_2281FG_465_29_LINK_E	
30	336441	CH22_3881FG_827_7_LINK_DJ	
	330551	9851_2	U39840 NM_004496 AW135807 BE087458 BE087567 AA177116 AW195705 AW750756 AI811008 AI694151 BE348594 AW971075 AI347950 AI201455 AI073898 AA652680 AA613671 AI318364 AA507550 AA893692 AI032599 AA991871 AI269801 AW948974 T74639 AA532907 AW949173 BE379594 AI192455 AL039862 AI744012 AI761735 AW243181 AI743687 AI928223 AI423022 AI627855 AI638059 AI651571 AW802044 AI826995 AI431733 AI539125 AA863056 AW270910 AI768930 AW008835 AW815183 AW591147 AI695294 AI672106 AA506358 AI308080 AA011556 AA962437 AI935488 BE218625 AI004356 AW151394 AI218466 N66178 AI419784 AW242519 AW946907 D60374 AA989263 AI698789 AA470460 AI824167 AA669097 AA513815 AA026798 AA676526 AA704429 AA704269 AW118292 AA579216 N58172 AW579842 BE156562 BE156690 BE156489 BE081033 AK001559 BE149402 M85387 AW367811 AW367798 R17370 AI908947 AA382932 R58449 H18732 AA371231 AW962899 AA713530 AW892948 R53463 H11063 AW068542 Z40761 BE176212 BE178155 W23952 W92188 AW374883 AA303497 AW954769 AA036808 BE168063 AW382073 AW382085 AL041475 H80748 AI078161 BE463983 AI805213 AI761264 W94885 N94502 AI623772 AI419532 AI810302 AI634190 AW002516 AW150777 AI352312 AI367474 AW204807 AI675502 AI337028 AW134715 BE328451 AI123157 AI560020 AI300745 AI608631 AI248873 AA742484 AW051635 H18846 AI245045 AA507111 AI640510 AI925594 AA115747 AA143035 AA151106 AK001764 BE313896 AA380189 AA380151 AA194996 AW118089 AA495871 AW975219 AW085598 AI378909 AW992310 AW992409 AI911857 AA657643 AI804471 AI242589 AI623968 R09556 AI129100 AI206500 AA680094 AA677784 AI023178 AI277519 AA424742 AI240654 AA232846 AI804273 AI382376 AA001729 W90790 BE090656 AW295015 AI674596 AI431734 AI420517 AW769185 AI128355 AI192474 AI820001 AA001929 AA706925 AI076676 AI499119 AI200493 AI695919 AI376217 W69195 W69261 AW305099 W90320 BE048357 AI658856 AA838534 AA233258 AI753393 AA709227 AI674387 AI872618
35	330786	53973_3	
	332247	372969_1	
40	332396	20265_1	
	332781	32044_1	
45			
50			

TABLE 3B shows the genomic positioning for those primekeys lacking unigene ID's and accession numbers in Table 3. For each predicted exon, we have listed the genomic sequence source used for prediction. Nucleotide locations of each predicted exon are also listed.

5

10 Pkey: Unique number corresponding to an Eos probeset
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
 Strand: Indicates DNA strand from which exons were predicted.
 Nt_position: Indicates nucleotide positions of predicted exons.

15	Pkey	Ref	Strand	Nt_position
	333611	Dunham, I. et al.	Plus	6548368-6548507
	333621	Dunham, I. et al.	Plus	8597414-8597560
	333814	Dunham, I. et al.	Plus	7894165-7894252
20	333849	Dunham, I. et al.	Plus	8018323-8018472
	333949	Dunham, I. et al.	Plus	8589634-8589791
	333951	Dunham, I. et al.	Plus	8592501-8592637
	333955	Dunham, I. et al.	Plus	8597414-8597560
	334150	Dunham, I. et al.	Plus	10529221-10529854
	334297	Dunham, I. et al.	Plus	13420934-13421058
25	334443	Dunham, I. et al.	Plus	14298981-14299056
	334444	Dunham, I. et al.	Plus	14308433-14308492
	334447	Dunham, I. et al.	Plus	14308764-14308824
	334570	Dunham, I. et al.	Plus	14994868-14994943
	334777	Dunham, I. et al.	Plus	16259586-16260166
30	335179	Dunham, I. et al.	Plus	21634405-21634526
	335581	Dunham, I. et al.	Plus	24976198-24976334
	335586	Dunham, I. et al.	Plus	24990333-24990497
	335609	Dunham, I. et al.	Plus	26310772-26310909
	335810	Dunham, I. et al.	Plus	26314767-26314849
35	335822	Dunham, I. et al.	Plus	26364087-26364196
	335824	Dunham, I. et al.	Plus	26376860-26376942
	335886	Dunham, I. et al.	Plus	26934235-26934364
	336034	Dunham, I. et al.	Plus	29014404-29014590
	336441	Dunham, I. et al.	Plus	34187606-34187663
40	337577	Dunham, I. et al.	Plus	595377-595678
	338260	Dunham, I. et al.	Plus	15458919-15459257
	332797	Dunham, I. et al.	Minus	216964-216798
	332798	Dunham, I. et al.	Minus	232147-231974
	332799	Dunham, I. et al.	Minus	232421-232307
45	332933	Dunham, I. et al.	Minus	2035790-2035681
	332980	Dunham, I. et al.	Minus	5136165-5136019
	332894	Dunham, I. et al.	Minus	2632606-2632457
	333168	Dunham, I. et al.	Minus	3729896-3729788
	333169	Dunham, I. et al.	Minus	3730864-3730787
50	333452	Dunham, I. et al.	Minus	5136165-5136019
	333456	Dunham, I. et al.	Minus	2631933-2631797
	333458	Dunham, I. et al.	Minus	5143942-5143808
	334223	Dunham, I. et al.	Minus	12734365-12734269
55	334749	Dunham, I. et al.	Minus	16090686-16090106
	334960	Dunham, I. et al.	Minus	20160968-20160795
	335293	Dunham, I. et al.	Minus	22316408-22316275
	335550	Dunham, I. et al.	Minus	24668714-24668658
	335853	Dunham, I. et al.	Minus	26614629-26614506
	336824	Dunham, I. et al.	Minus	227714-227577
60	336825	Dunham, I. et al.	Minus	229124-229024
	336679	Dunham, I. et al.	Minus	2035790-2035681
	338255	Dunham, I. et al.	Minus	15242264-15242231
	338561	Dunham, I. et al.	Minus	22311966-22311858
	338562	Dunham, I. et al.	Minus	22312594-22312465
65	338759	Dunham, I. et al.	Minus	26582475-26582199
	338763	Dunham, I. et al.	Minus	26628148-26628009
	338764	Dunham, I. et al.	Minus	26641232-26641101

	329960	5091594	Minus	1031-1162
	329929	6165201	Minus	156410-156553
	330020	6671887	Plus	172397-172491
	326816	6552458	Plus	198354-198436
5	326897	5867660	Minus	71389-72147
	327098	6682516	Minus	1061684-1062361
	330211	6013592	Plus	59158-59215
	328492	5868455	Minus	46094-46241
10	329382	5868837	Minus	65688-68173

TABLE 4: shows a preferred subset of the Accession numbers for genes found in Table 3 which are differentially expressed in prostate tumor tissue compared to normal prostate tissue.

5

10	Pkey:	Unique Eos probeset identifier number			
	ExAccn:	Exemplar Accession number, Genbank accession number			
	UnigeneID:	Unigene number			
	Unigene Title:	Unigene gene title			
	R1:	Ratio of tumor to normal body tissue			
15	Pkey	ExAccn	UnigeneID	Unigene Title	R1
20	100819	HG4020-HT4290	Hs.2387	Transglutaminase	10.5
	102698	U75272	Hs.1867	progastricsin (pepsinogen C)	10.8
	102869	X02544	Hs.572	orosomucoid 1	22.6
	105370	AA236478	Hs.22791	ESTs; Weakly similar to transmembrane pr	10.3
	105645	AA282138	Hs.11325	ESTs	14
25	106094	AA419461	Hs.23317	ESTs	10.9
	109014	AA156790	Hs.262036	ESTs	15.3
	109562	F01811	Hs.187931	ESTs; Moderately similar to voltage-gate	10.8
	113021	T23855	Hs.129836	KIAA1028 protein	10.8
	114124	Z38595	Hs.125019	ESTs; Highly similar to KIAA0886 protein	21.3
30	122791	AA460158	Hs.129836	KIAA1028 protein	12.4
	124352	N21828	Hs.102406	ESTs	10.2
	301042	AI659131	Hs.197733	ESTs	24.9
	302005	AI869668	Hs.123119	ESTs	36.8
	302410	NM_004917	Hs.218366	EST cluster (not in UniGene) with exon h	26.8
35	302881	AA508353	Hs.105314	relaxin 1 (H1)	78.8
	303344	AA255977	Hs.250646	ESTs; Highly similar to ubiquitin-conjug	19.5
	303753	AW503733	Hs.9414	ESTs	13
	310431	AI420227	Hs.149358	ESTs	72.9
	311251	AI655862	Hs.197698	ESTs	41.3
40	311596	AI682088	Hs.79375	ESTs	26.4
	312153	AA759250	Hs.118625	cytochrome b-561	11
	312521	AA033609	Hs.239884	ESTs	11.2
	313676	AA861697	Hs.120591	EST cluster (not in UniGene)	13.4
	314171	AI821895	Hs.193481	ESTs	29.4
45	314907	AI672225	Hs.222886	ESTs	19.3
	315051	AW282425	Hs.163484	EST	15.5
	315052	AA876910	Hs.134427	ESTs	20
	317548	AI654187	Hs.195704	ESTs	14.2
	317869	AW295184	Hs.129142	ESTs; Weakly similar to DEOXYRIBONUCLEAS	13.8
50	318428	AI949409	Hs.194591	ESTs	12.3
	318524	AW291511	Hs.159066	ESTs	25.9
	319080	Z45131	Hs.23023	ESTs	18.9
	319763	AA460775	Hs.6295	ESTs	14.3
	320324	AF071202	Hs.139336	ATP-binding cassette; sub-family C (CFTR	56.2
55	321441	AW297633	Hs.118498	ESTs	14.7
	322303	W07459	Hs.157601	EST cluster (not in UniGene)	22
	322782	AA056060	Hs.202577	EST cluster (not in UniGene)	18.4
	322818	AW043782	Hs.283616	ESTs	10.7
	323287	AA639902	Hs.104215	ESTs	24.7
60	324603	AW016378	Hs.292934	ESTs	24.2
	324617	AA508552	Hs.195839	ESTs	54
	324658	AI694767	Hs.129179	ESTs	22
	324691	AI217963	Hs.293341	ESTs; Weakly similar to Pro- $\alpha 2$ (XII) [H.sa	10.6
	324696	AA841092	Hs.257339	ESTs	10.2
65	324718	AI557019	Hs.116467	ESTs	34.4
	330211		CH.05_p2 gi5013592		12.6
	330430	HG2261-HT2352	Hs.321110	Antigen, Prostate Specific, Alt. Splice	13.8
	330706	AA121140	Hs.177576	ESTs; Moderately similar to kynurenine a	14.5
	330762	AA449677	Hs.15251	Human DNA sequence from clone 437M21 on	18.5
	330882	AA148579	Hs.91202	ESTs	15.3
	330949	H01458	Hs.142696	ESTs	10.3

5	331099	R36671	Hs.14846	ESTs	11.8
	331151	R82331	Hs.268838	ESTs	13
	331889	AA431407	Hs.98802	Homo sapiens Chromosome 16 BAC clone CIT	33.6
	332247	N58172		ESTs	14.2
	332396	AA340504		ESTs; Weakly similar to similar to human	21.2
10	332533	M99487	Hs.325825	folate hydrolase (prostate-specific memb	38.1
	332697	T94885	Hs.75725	carboxypeptidase E	24.3
	332797			CH22_FGENES.6_2	30.8
	332798			CH22_FGENES.6_5	66.8
	332799			CH22_FGENES.6_6	19.8
	334223			CH22_FGENES.360_4	20.3
	336624			CH22_FGENES.6-3	43.3
	336625			CH22_FGENES.6-4	37.9

TABLE 4A shows the accession numbers for those primekeys lacking unigeneID's for Table 4. For each probeset we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

10	Pkey:	Unique Eos probeset Identifier number
	CAT number:	Gene cluster number
	Accession:	Genbank accession numbers
15	Pkey	CAT number
		Accession
	336624	CH22_4071FG_6_3_
	336625	CH22_4072FG_6_4_
	330211	c_5_p2
20	332797	CH22_13FG_6_2_LINK_C4G1.G
	332798	CH22_14FG_6_5_LINK_C4G1.G
	332799	CH22_15FG_6_6_LINK_C4G1.G
	334223	CH22_1507FG_360_4_LINK_EM
25	332247	372969_1
	332396	20265_1
30		AA669097 AA513815 AA026798 AA676526 AA704429 AA704269 AW118292 AA578216 N58172 AW579842 BE156582 BE156690 BE156489 BE081033 AK001559 BE149402 M85387 AW367811 AW367798 R17370 AI908947 AA382932 R58449 H18732 AA371231 AW962899 AA713530 AW892948 R53483 H11063 AW068542 Z40761 BE176212 BE176155 W23952 W92188 AW374883 AA303497 AW954769 AA036808 BE168083 AW382073 AW382085 AL041475 H80748 AI078161 BE463983 AI805213 AI761264 W94885 N94502 AI623772 AJ419532 AI810302 AI634190 AW002516 AW160777 AI352312 AI367474 AW204807 AI675502 AI337026 AW134715 BE328451 AI123157 AI560020 AI300745 AI608631 AI248873 AA742484 AW051635 H18646 AI245045 AA507111 AI640510 AI925594 AA115747 AA143035 AA151106

TABLE 4B shows the genomic positioning for those primekeys lacking unigene ID's and accession numbers in Table 4. For each predicted exon, we have listed the genomic sequence source used for prediction. Nucleotide locations of each predicted exon are also listed.

10 Pkey: Unique number corresponding to an Eos probeset
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
 Strand: Indicates DNA strand from which exons were predicted.
 Nt_position: Indicates nucleotide positions of predicted exons.

15	Pkey	Ref	Strand	Nt_position
	332797	Dunham, I. et al.	Minus	216964-216798
	332798	Dunham, I. et al.	Minus	232147-231974
	332799	Dunham, I. et al.	Minus	232421-232307
20	334223	Dunham, I. et al.	Minus	12734365-12734269
	336624	Dunham, I. et al.	Minus	227714-227577
	336625	Dunham, I. et al.	Minus	229124-229024
	330211	6013592	Plus	59158-59215

TABLE 5: 1170 GENES UP-REGULATED IN PROSTATE CANCER COMPARED TO NORMAL ADULT TISSUES

- 5 Table 5 shows 1170 genes up-regulated in prostate cancer compared to normal adult tissues. These were selected from 59680 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" prostate cancer to "average" normal adult tissues was greater than or equal to 3.44. The "average" prostate cancer level was set to the 85th percentile amongst 73 prostate cancers. The "average" normal adult tissue level was set to the 85th percentile
- 10 amongst 162 non-malignant tissues. In order to remove gene-specific background levels of non-specific hybridization, the 7.5th percentile value amongst the 162 non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

15	Pkey:	Unique Eos probeset identifier number			
	ExAccn:	Exemplar Accession number, Genbank accession number			
	UnigeneID:	Unigene number			
	Unigene Title:	Unigene gene title			
	R1:	Ratio of tumor to normal tissue			
20	Pkey	ExAccn	UnigeneID	Unigene Title	R1
	446057	AA420227	Hs.149358	ESTs, Weakly similar to A46010 X-linked	86.42
	400302	N48056	Hs.1915	folate hydrolase (prostate-specific memb	66.46
	414569	AF109298	Hs.118258	prostate cancer associated protein 1	58.36
25	417407	AA923278	Hs.290905	ESTs, Weakly similar to protease [H.sapi	56.16
	431579	AW971082	Hs.222888	ESTs, Weakly similar to TRHY_HUMAN TRICH	53.38
	409361	NM_005982	Hs.54416	sine oculis homeobox (Drosophila) homolo	48.28
	409731	AA125985	Hs.56145	thymosin, beta, identified in neuroblast	45.24
	400298	AA032279	Hs.61635	six transmembrane epithelial antigen of	43.48
30	420154	AI093155	Hs.95420	JM27 protein	41.12
	433466	AA508353	Hs.105314	relaxin 1 (H1)	39.88
	400298	AA305627	Hs.139336	ATP-binding cassette, sub-family C (CFTR	38.42
	400292	AA250737	Hs.72472	ESTs	38.00
	432887	AI926047	Hs.162859	ESTs	36.48
35	439178	AI446444	Hs.190394	ESTs, Weakly similar to B28096 line-1 pr	36.45
	430722	AW968543	Hs.203270	ESTs, Weakly similar to ALU1_HUMAN ALU S	33.20
	437052	AA861697	Hs.120591	ESTs	33.02
	418398	AI755805	Hs.26691	ESTs	32.68
	434036	AI659131	Hs.197733	hypothetical protein MGC2849	32.44
40	407709	AA456135	Hs.23023	ESTs	32.10
	426747	AA535210	Hs.171995	kallikrein 3, (prostate specific antigen	31.80
	407168	R45175		ESTs	31.72
	440260	AI972867	Hs.7130	copine IV	30.52
	421513	X00949	Hs.105314	relaxin 1 (H1)	30.10
45	416370	N90470	Hs.203697	ESTs, Weakly similar to I38022 hypotheti	29.68
	407122	H20276	Hs.31742	ESTs	29.24
	400287	S39329	Hs.181350	kallikrein 2, prostatic	28.90
	432244	AI669873	Hs.200574	ESTs	28.74
	451939	U80456	Hs.27311	single-minded (Drosophila) homolog 2	28.74
50	415989	AI267700	Hs.111128	ESTs	28.34
	418961	AW967646	Hs.23023	ESTs	27.34
	425628	NM_004476	Hs.1915	folate hydrolase (prostate-specific memb	27.32
	458509	AA654650	Hs.282906	ESTs	27.24
	448290	AK002107	Hs.20843	Homo sapiens cDNA FLJ11245 fis, clone PL	27.16
55	428336	AA503115	Hs.183752	microseminoprotein, beta-	26.17
	450096	AI882088	Hs.223368	holocarboxylase synthetase (biotin-prop	25.60
	400299	X07730	Hs.171995	kallikrein 3, (prostate specific antigen	24.91
	437571	AA760894	Hs.153023	ESTs	24.74
	453160	AI263307	Hs.146228	H2B histone family, member L	24.66
60	453096	AW294631	Hs.11325	ESTs	24.46
	425075	AA506324	Hs.1852	acid phosphatase, prostate	24.23
	407202	N58172	Hs.109370	ESTs	24.18

	424846	AU077324	Hs.1832	neuropeptide Y	23.57
	453370	AI470523	Hs.182358	ATP-binding cassette, sub-family C (CFTR	23.16
	422805	AA438989	Hs.121017	H2A histone family, member A	22.52
	444917	R68851	Hs.144997	ESTs	22.28
5	408826	AF216077	Hs.48376	Homo sapiens clone HB-2 mRNA sequence	22.02
	413597	AW302885	Hs.117183	ESTs	21.76
	426429	X73114	Hs.169849	myosin-binding protein C, slow-type	21.32
	435981	H74319	Hs.188620	ESTs	21.12
	432866	AA650114		ESTs	21.07
10	418848	AI820961	Hs.193465	ESTs	21.08
	405685				20.90
	443271	BE568568	Hs.195704	ESTs	19.88
	418819	AA228776	Hs.191721	ESTs	19.94
	420757	X78592	Hs.99915	androgen receptor (dihydrotestosterone r	19.72
15	418994	AA296520	Hs.89546	selectin E (endothelial adhesion molecu	19.56
	429918	AW873986	Hs.119383	ESTs	19.04
	415539	AI733981	Hs.72472	ESTs	18.43
	450382	AA397658	Hs.60257	Homo sapiens cDNA FLJ13598 fis, clone PL	18.34
	418829	AA516531	Hs.55999	NK homeobox (Drosophila), family 3, A	18.28
20	428984	AL050102	Hs.227209	hypothetical protein FLJ21617	17.82
	443822	AI087412	Hs.143611	ESTs, Weakly similar to 2004399A chromos	17.66
	431676	AI685464	Hs.292638	gb:tt88f04.x1 NCI_CGAP_Pr28 Homo sapiens	17.64
	410330	AW023630	Hs.46786	ESTs	17.52
	432441	AW292425	Hs.163484	ESTs	17.41
25	452782	AB037765	Hs.30652	KIAA1344 protein	17.39
	445472	AB006631	Hs.12784	Homo sapiens mRNA for KIAA0283 gene, par	17.00
	414565	AA502972	Hs.183390	hypothetical protein FLJ13590	16.82
	430487	D87742	Hs.241552	KIAA0268 protein	16.72
	431716	D89053	Hs.268012	fatty acid-Coenzyme A ligase, long-chain	16.60
30	419538	AA603305		gb:np12d11.s1 NCI_CGAP_Pr3 Homo sapiens	16.50
	439677	R82331	Hs.164599	ESTs	16.46
	449625	NM_014253	Hs.23798	odx (odd Oz/ten-m, Drosophila) homolog 1	16.32
	408430	S79876	Hs.44928	dipeptidylpeptidase IV (CD26, adenosine	16.28
	447033	AI357412	Hs.157601	ESTs	16.02
35	453006	AI362575	Hs.167133	ESTs	15.74
	431474	AL133990	Hs.190642	ESTs	15.70
	420218	AW958037	Hs.22437	ribosomal protein L4	15.64
	408000	L11690	Hs.620	bullous pemphigoid antigen 1 (230/240kD)	15.54
40	416208	AW291168	Hs.41295	ESTs, Weakly similar to MUC2_HUMAN MUCIN	15.48
	430226	BE245562	Hs.2551	adrenergic, beta-2-, receptor, surface	15.40
	415263	AA948033	Hs.130853	ESTs	15.38
	432437	W07088	Hs.293685	ESTs	15.28
	428398	AI249368	Hs.98558	ESTs	15.21
	429900	AA460421	Hs.30875	ESTs	14.90
45	449156	AF103907	Hs.171353	prostate cancer antigen 3	14.89
	411096	U80034	Hs.68583	mitochondrial intermediate peptidase	14.81
	435974	U29690	Hs.37744	Homo sapiens beta-1 adrenergic receptor	14.76
	444484	AK002126	Hs.11260	hypothetical protein FLJ11264	14.78
50	422728	AW937828	Hs.103262	ESTs, Weakly similar to ZN91_HUMAN ZINC	14.60
	418601	AA279490	Hs.86368	calmeglin	14.56
	448999	AF178274	Hs.22791	transmembrane protein with EGF-like and	14.55
	445885	AI734009	Hs.127699	KIAA1603 protein	14.44
	452712	AW838616		gb:RCS-LT0054-140200-013-D01 LT0054 Homo	14.22
55	432189	AA527941		gb:nh30c04.s1 NCI_CGAP_Pr3 Homo sapiens	14.12
	424565	AW102723	Hs.75295	guanylate cyclase 1, soluble, alpha 3	13.78
	429290	AF203032	Hs.198760	neurofilament, heavy polypeptide (200kD)	13.57
	419284	AA877104	Hs.293672	ESTs, Weakly similar to ALUB_HUMAN IIII	13.40
	416445	AL043004	Hs.300678	KIAA0135 protein	13.32
60	407275	AI384186		gb:xw34h07.x1 NCI_CGAP_UI4 Homo sapiens	13.24
	408369	R38438	Hs.182575	solute carrier family 15 (H+/peptide tra	13.21
	446720	AI439138	Hs.140548	ESTs	13.06
	434988	AI418055	Hs.161160	ESTs	13.02
	448172	N75276	Hs.135904	ESTs	12.98
65	416182	NM_004354	Hs.79069	cyclin G2	12.94
	420544	AA677577	Hs.98732	Homo sapiens Chromosome 16 BAC clone CIT	12.79
	445413	AA151342	Hs.12677	CGI-147 protein	12.64
	452588	AA889120	Hs.110637	homeo box A10	12.62
	407819	R42185	Hs.274803	ESTs	12.60
	433444	AW875324	Hs.128816	ESTs	12.60

	421059	AI654133	Hs.30212	thyroid receptor interacting protein 15	12.30
	420077	AW512260	Hs.87767	ESTs	12.24
	453930	AA419466	Hs.36727	hypothetical protein FLJ10903	12.22
	441610	AW576148	Hs.148376	ESTs	12.20
5	451009	AA013140	Hs.115707	ESTs	12.18
	433764	AW753676	Hs.39982	ESTs	12.16
	440286	U29589	Hs.7138	cholinergic receptor, muscarinic 3	12.04
	443912	R37257	Hs.184780	ESTs	11.82
	419528	AI821895	Hs.193481	ESTs	11.91
10	423073	BE252822	Hs.123119	MAD (mothers against decapentaplegic, Dr	11.87
	452784	BE463857	Hs.151258	hypothetical protein FLJ21062	11.86
	414422	AA147224	Hs.71814	ESTs	11.78
	450203	AF097894	Hs.301528	L-kynurenine/alpha-aminoadipate aminotra	11.68
	436679	AI127483	Hs.120451	ESTs, Weakly similar to unnamed protein	11.60
15	440901	AA909358	Hs.128612	ESTs	11.60
	448045	AJ297438	Hs.20168	prostate stem cell antigen	11.51
	433887	AW204232	Hs.279522	ESTs	11.50
	434980	AW770553	Hs.293840	sterol O-acyltransferase (acyl-Coenzyme	11.38
	425905	AB032859	Hs.161700	novel C3HC4 type Zinc finger (ring finger)	11.33
20	434680	T11738	Hs.127574	ESTs	11.32
	449650	AF055575	Hs.297647	calcium channel, voltage-dependent, L ty	11.18
	431173	AW871188	Hs.294068	ESTs	11.16
	434539	AW748078	Hs.214410	ESTs, Weakly similar to MUC2_HUMAN MUCIN	11.16
	410037	AB020725	Hs.58009	KIAA0918 protein	11.14
25	417708	N74382	Hs.50495	ESTs	11.14
	458332	AI000341	Hs.220491	ESTs	11.12
	420381	D50640	Hs.301782	phosphodiesterase 3B, cGMP-inhibited	11.10
	425665	AK001050	Hs.159066	hypothetical protein FLJ10188	11.08
	425710	AF030880	Hs.159275	solute carrier family, member 4	11.08
30	428728	NM_016625	Hs.191381	hypothetical protein	11.04
	407021	U52077		gb:Human mariner1 transposase gene, comp	11.02
	410733	D84284	Hs.66052	CD38 antigen (p45)	11.02
	401714				10.90
	434485	AI623511	Hs.118567	ESTs	10.89
35	415786	AW419198	Hs.257824	hypothetical protein FLJ13782	10.87
	452340	NM_002202	Hs.505	ISL1 transcription factor, LIM/homeodoma	10.85
	453628	AW243307	Hs.170187	hypothetical protein	10.72
	408063	BE086548	Hs.42346	calneurin-binding protein calsardin-1	10.67
	417687	AI826596	Hs.250691	ESTs	10.64
40	434666	AF151103	Hs.112259	T cell receptor gamma locus	10.53
	432374	W68815	Hs.301885	Homo sapiens cDNA FLJ11346 fis, clone PL	10.50
	428819	AL135623	Hs.193914	KIAA0575 gene product	10.48
	413409	AI638418	Hs.21745	DEAD/H (Asp-Glu-Ala-Asp/His) box polypep	10.44
	428775	AA434579	Hs.143691	ESTs	10.21
45	436556	AI364997	Hs.7572	ESTs	10.20
	441690	R81733	Hs.33108	ESTs	10.14
	419852	AW503756	Hs.286184	hypothetical protein U551D2.5	10.10
	421991	NM_014918	Hs.110488	KIAA0990 protein	10.04
	423698	AA329796	Hs.1098	DKFZp434J1813 protein	10.02
50	452039	AI922888	Hs.172510	ESTs	10.00
	433043	W57554	Hs.125019	ESTs	9.98
	433927	AI557019	Hs.116467	small nuclear protein PRAC	9.97
	445424	AB028945	Hs.12696	cortactin SH3 domain-binding protein	9.96
	432240	AI694787	Hs.129179	Homo sapiens cDNA FLJ13581 fis, clone PL	9.88
55	433104	AL043002	Hs.128246	ESTs, Moderately similar to unnamed prot	9.84
	452744	AI267652	Hs.30504	Homo sapiens mRNA; cDNA DKFZp434E082 (fr	9.82
	431217	NM_013427	Hs.250830	Rho GTPase activating protein 6	9.75
	427398	AW390020	Hs.20415	chromosome 21 open reading frame 11	9.70
	446896	T15767	Hs.22452	Homo sapiens mRNA for KIAA1737 protein,	9.70
60	421470	R27496	Hs.1378	annexin A3	9.64
	406554				9.60
	401424				9.58
	407802	AL117474	Hs.41181	Homo sapiens mRNA; cDNA DKFZp727C191 (fr	9.56
	423545	AF000692	Hs.129781	chromosome 21 open reading frame 5	9.54
65	439024	R96698	Hs.35598	ESTs	9.51
	431548	AI834273	Hs.9711	novel protein	9.48
	409262	AK000831	Hs.52258	hypothetical protein FLJ20624	9.45
	446271	D82484	Hs.100469	ESTs	9.42
	448692	AW013907	Hs.224276	methylcrotonoyl-Coenzyme A carboxylase 2	9.26

	414140	AA281279	Hs.23317	hypothetical protein FLJ14681	9.24
	435980	AF274571	Hs.129142	deoxyribonuclease II beta	9.24
	421246	AW582862	Hs.300961	CGI-47 protein	9.20
	427304	AA761526	Hs.163853	ESTs	9.16
5	442914	AW188551	Hs.99519	hypothetical protein FLJ14007	9.16
	413627	BE182082	Hs.246973	ESTs	9.14
	439699	AF086534	Hs.187561	ESTs, Moderately similar to ALU1_HUMAN A	9.10
	437718	AI927288	Hs.196779	ESTs	9.07
	439820	AL360204	Hs.283853	Homo sapiens mRNA full length insert cDN	9.06
10	447342	AI199268	Hs.18322	Homo sapiens, Similar to RIKEN cDNA 2010	9.05
	448223	BE300091	Hs.118699	hypothetical protein FLJ12969	9.04
	410001	AB041036	Hs.57771	kallikrein 11	9.03
	424012	AW388377	Hs.137569	tumor protein 63 kDa with strong homolog	9.03
	441781	AW372449	Hs.175982	hypothetical protein FLJ21159	9.02
15	448206	BE622585	Hs.3731	ESTs, Moderately similar to I38022 hypot	9.02
	414269	AA298489		olfactory receptor, family 51, subfamily	8.99
	442081	AA401863	Hs.22380	ESTs	8.98
	420092	AA814043	Hs.88045	ESTs	8.85
	411630	U42349	Hs.71119	Putative prostate cancer tumor suppresso	8.80
20	421863	AI952677	Hs.108972	Homo sapiens mRNA; cDNA DKFZp434P228 (fr	8.80
	454141	AW138413	Hs.182356	ATP-binding cassette, sub-family C (CFTR	8.80
	418278	AI088489	Hs.83937	hypothetical protein	8.78
	428330	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin,	8.76
	432415	T16971	Hs.289014	ESTs, Weakly similar to A43932 mucin 2 p	8.75
25	424906	AI566088	Hs.153716	Homo sapiens mRNA for Hmob33 protein, 3'	8.74
	415245	N59650	Hs.27252	ESTs	8.72
	442409	BE208843	Hs.129544	hypothetical protein MGC15438	8.70
	404571				8.68
	418033	W68180	Hs.259855	elongation factor-2 kinase	8.64
30	456497	AW967956	Hs.123648	ESTs, Weakly similar to AF108460 1 ubinu	8.66
	405876				8.54
	448807	AI571940	Hs.7549	ESTs	8.52
	445372	N36417	Hs.144828	ESTs	8.48
	425171	AW732240	Hs.300615	ESTs	8.44
35	419968	X04430	Hs.93913	interleukin 6 (interferon, beta 2)	8.38
	407385	AA610150	Hs.272072	ESTs, Weakly similar to I38022 hypotheti	8.31
	433172	AB037841	Hs.102652	hypothetical protein ASH1	8.30
	422631	BE218919	Hs.118793	hypothetical protein FLJ10688	8.27
	412719	AW016610	Hs.129911	ESTs	8.24
40	418849	AW474547	Hs.53565	Homo sapiens PIG-M mRNA for mannosyltran	8.22
	444922	AI921750	Hs.144871	Homo sapiens cDNA FLJ13752 fis, clone PL	8.22
	427674	NM_003528	Hs.2178	H2B histone family, member Q	8.20
	432101	AI918950	Hs.11092	EphA3	8.17
45	416288	H51299		gb:yp07c06.s1 Soares breast 3NhbSt Homo	8.15
	404915				8.08
	440108	AA864968	Hs.127699	KIAA1603 protein	8.07
	442861	AA243837	Hs.57787	ESTs	8.06
	452259	AA317439	Hs.28707	signal sequence receptor, gamma (translo	8.06
50	443250	AI041530	Hs.132107	ESTs	8.06
	437267	AW511443	Hs.258110	ESTs	8.04
	452891	N75582	Hs.212875	ESTs, Weakly similar to DYH9_HUMAN CILI	8.02
	422219	AW978073		regulator of mitotic spindle assembly 1	8.00
	453049	BE537217	Hs.30343	ESTs	8.00
55	439731	AI953135	Hs.45140	hypothetical protein FLJ14084	7.98
	408554	AA836381	Hs.7323	nuclear receptor co-repressor/HDAC3 comp	7.94
	421154	AA284333	Hs.287631	Homo sapiens cDNA FLJ14269 fis, clone PL	7.94
	430107	AA465283	Hs.105069	ESTs	7.94
	433404	T32882	Hs.102720	ESTs	7.93
60	450813	AI739625	Hs.203376	ESTs	7.90
	416239	AL038450	Hs.48948	ESTs	7.85
	448212	AI475858		gb:tc87d07.x1 NCI_CGAP_CLL1 Homo sapiens	7.82
	449532	W74653	Hs.271593	ESTs, Moderately similar to A47582 B-cel	7.82
	413930	M86153	Hs.75618	RAB11A, member RAS oncogene family	7.80
	458191	AI420611	Hs.127832	ESTs	7.80
65	444858	AI189738	Hs.208275	ESTs, Weakly similar to ALUA_HUMAN IIII	7.78
	457488	AI732230	Hs.181737	ESTs	7.78
	407235	D20569	Hs.169407	SAC2 (suppressor of actin mutations 2, y	7.76
	433759	AA680003	Hs.109363	Homo sapiens cDNA: FLJ23603 fis, clone L	7.74
	433805	AA706910	Hs.112742	ESTs	7.74

	426485	NM_006207	Hs.170040	platelet-derived growth factor receptor-	7.72
	446028	R44714	Hs.108795	Homo sapiens cDNA FLJ13136 fis, clone NT	7.72
	418555	AI417215	Hs.87159	hypothetical protein FLJ12577	7.70
	447489	AW262580	Hs.147674	protocadherin beta 18	7.70
5	419839	U24577	Hs.93304	phospholipase A2, group VII (platelet-ac	7.68
	416857	AA188775	Hs.292453	ESTs	7.68
	413801	M62246	Hs.35406	ESTs, Highly similar to unnamed protein	7.66
	425480	AB023198	Hs.158135	KIAA0981 protein	7.66
	420120	AL049610	Hs.95243	transcription elongation factor A (SII)-	7.64
10	424099	AF071202	Hs.139336	ATP-binding cassette, sub-family C (CFTR	7.64
	446307	T50083	Hs.9094	ESTs	7.63
	429220	AW207208	Hs.138319	ESTs	7.59
	420345	AW295230	Hs.25231	ESTs	7.54
	429208	AA447890	Hs.190478	ESTs	7.54
15	447247	AW369351	Hs.287855	Homo sapiens cDNA FLJ13090 fis, clone NT	7.53
	440995	T57773	Hs.10263	ESTs	7.53
	448706	AW291095	Hs.21814	interleukin 20 receptor, alpha	7.52
	410227	AB009284	Hs.61152	exostoses (multiple)-like 2	7.49
	431618	AA508552	Hs.195839	ESTs, Weakly similar to I38022 hypotheti	7.48
20	434217	AW014795	Hs.23349	ESTs	7.44
	431487	N71831	Hs.256398	Homo sapiens mRNA; cDNA DKFZp434E0528 (f	7.42
	448519	AW175685	Hs.244334	Homo sapiens protein mRNA, complete cds	7.42
	446791	AI632278	Hs.34981	ESTs	7.40
	419743	AW408762	Hs.127478	Homo sapiens clone 24416 mRNA sequence	7.39
25	445855	BE247129	Hs.145569	ESTs	7.36
	425211	M18667	Hs.1867	progastricsin (pepsinogen C)	7.35
	419131	AA406293	Hs.301622	ESTs	7.34
	400294	N95798	Hs.179809	Homo sapiens protein mRNA, complete cds	7.33
	441738	AW292779	Hs.169799	ESTs	7.28
30	427701	AA411101	Hs.221750	nuclear autoantigenic sperm protein (his	7.24
	457733	AW974812	Hs.291971	ESTs	7.24
	418432	M14156	Hs.85112	Insulin-like growth factor 1 (somatomedi	7.22
	441201	AW118822	Hs.128757	ESTs	7.21
	419953	BE267154	Hs.125752	ESTs	7.20
35	419991	AJ000098	Hs.94210	eyes absent (Drosophila) homolog 1	7.20
	425018	BE245277	Hs.154196	E4F transcription factor 1	7.20
	424560	AA158727	Hs.150555	protein predicted by clone 23733	7.18
	435390	AA879001	Hs.182221	ESTs	7.14
	420658	AW965215	Hs.130707	ESTs	7.12
40	408291	AB023191	Hs.44131	KIAA0974 protein	7.10
	409110	AA191493	Hs.48778	niban protein	7.10
	414485	V27026	Hs.182625	VAMP (vesicle-associated membrane protei	7.10
	430039	BE253012	Hs.153400	ESTs, Weakly similar to ALU1_HUMAN ALU S	7.10
	450832	AW970602	Hs.105421	ESTs	7.10
45	417153	X57010	Hs.81343	collagen, type II, alpha 1 (primary oste	7.08
	412446	AI768015	Hs.82127	ESTs	7.07
	412953	Z45794	Hs.238809	ESTs	7.06
	418051	AW192535	Hs.19479	ESTs	7.06
	421566	NM_000399	Hs.1395	early growth response 2 (Krox-20 (Drosop	7.04
50	446999	AA151520	Hs.279525	hypothetical protein MGC4485	7.04
	440529	AW207640	Hs.16478	Homo sapiens cDNA: FLJ21718 fis, clone C	7.04
	441111	AI806867	Hs.126594	ESTs	7.01
	451027	AW518204	Hs.40808	ESTs	7.00
	408432	AW195262		gbxn67b05.x1 NCL CGAP_CML1 Homo sapiens	7.00
55	432223	AA333283	Hs.285336	Homo sapiens, clone IMAGE:3460280, mRNA	7.00
	444805	AB007899	Hs.12017	homolog of yeast ubiquitin-protein ligas	6.99
	414212	AA138569	Hs.295940	KIAA0187 gene product	6.98
	431725	X65724	Hs.2839	Norrie disease (pseudoglioma)	6.98
	449685	AW296669	Hs.66095	ESTs	6.97
60	447313	U92981	Hs.18081	Homo sapiens clone DT1P1B6 mRNA, CAG rep	6.96
	424590	AW966399	Hs.46821	hypothetical protein FLJ20086	6.94
	449655	AI021887	Hs.59970	ESTs	6.82
	419563	AA528235	Hs.193162	Homo sapiens cDNA FLJ11983 fis, clone HE	6.80
	434163	AW974720	Hs.25208	group XII secreted phospholipase A2	6.89
65	415809	Z32789	Hs.46601	ESTs	6.86
	425782	U66468	Hs.158525	cell growth regulatory with EF-hand doma	6.85
	417958	AA767382	Hs.193417	ESTs	6.84
	427408	AA583206	Hs.2156	RAR-related orphan receptor A	6.79
	445873	AA250970	Hs.251948	poly(A)-binding protein, cytoplasmic 1-1	6.74

	410718	AI920783	Hs.191435	ESTs	6.74
	432363	AA534489		gb:mf76g11.s1 NCL CGAP_Co3 Homo sapiens	6.74
	438521	AW203986	Hs.213003	ESTs	6.73
5	435604	AA625279	Hs.26892	uncharacterized bone marrow protein BM04	6.73
	419083	AI478560	Hs.98613	Homo sapiens cDNA FLJ12282 fis, clone MA	6.72
	418245	AA088767	Hs.83883	transmembrane, prostate androgen induced	6.70
	420714	BE172704	Hs.222746	KIAA1610 protein	6.70
	412707	AW206373	Hs.16443	Homo sapiens cDNA: FLJ21721 fis, clone C	6.67
	421896	N62293	Hs.45107	ESTs	6.66
10	411078	AI222020	Hs.182364	CocoaCrisp	6.66
	452465	AA610211	Hs.34244	ESTs	6.66
	422763	AA033699	Hs.63938	ESTs, Moderately similar to MAS2_HUMAN M	6.66
	444618	AV653785	Hs.300171	ELL-RELATED RNA POLYMERASE II, ELONGATIO	6.64
	450164	AI239923	Hs.30098	ESTs	6.63
15	431060	AF039307	Hs.249171	homeo box A11	6.62
	408031	AA081395	Hs.42173	Homo sapiens cDNA FLJ10366 fis, clone NT	6.62
	420285	AA258124	Hs.293878	ESTs, Moderately similar to ZN91_HUMAN Z	6.62
	444670	H58373	Hs.37494	hypothetical protein MGC5370	6.62
	444489	AI151010	Hs.157774	ESTs	6.60
20	445685	AW779829	Hs.263436	gb:hn88a05.x1 NCL CGAP_Kd11 Homo sapien	6.60
	435677	AA694142	Hs.293728	ESTs, Weakly similar to TSGA RAT TESTIS	6.59
	452221	C21322	Hs.11577	hypothetical protein FLJ22242	6.59
	431510	AA580082	Hs.112264	ESTs	6.58
	415874	AF081622	Hs.78893	KIAA0244 protein	6.54
25	418405	AI668282	Hs.11898	ESTs, Highly similar to KIAA1370 protein	6.54
	452768	AW069459	Hs.61539	ESTs	6.54
	401451				6.52
	416269	W26333		ESTs	6.52
	431778	AL080276	Hs.268562	regulator of G-protein signalling 17	6.51
30	409089	NM_014781	Hs.50421	KIAA0203 gene product	6.50
	442833	AA328153	Hs.88201	ESTs, Weakly similar to A Chain A, Cryst	6.50
	431992	NM_002742	Hs.2891	protein kinase C, mu	6.49
	418833	AW974899	Hs.292776	ESTs	6.48
	429183	AA884766		gb:am20a10.s1 Soares_NFL_T_GBC_S1 Homo s	6.46
35	430403	AF039390	Hs.241382	tumor necrosis factor (ligand) superfamily	6.46
	443058	AW451642	Hs.16732	ESTs	6.46
	418564	AA831143	Hs.179809	Homo sapiens prostelin mRNA, complete cds	6.44
	432674	AA841092	Hs.257339	ESTs, Weakly similar to I38022 hypotheti	6.44
	423600	AI633559	Hs.29076	ESTs	6.44
40	404253				6.42
	433610	AA806822	Hs.112547	ESTs	6.42
	421552	AF026692	Hs.105700	secreted frizzled-related protein 4	6.41
	407118	AA156790	Hs.262036	ESTs, Weakly similar to Z223_HUMAN ZINC	6.40
	408608	N78738	Hs.136102	KIAA0853 protein	6.40
45	421452	AI925946	Hs.104530	fetal hypothetical protein	6.40
	433285	AW975944	Hs.237396	ESTs	6.40
	434926	BE543269	Hs.50252	mitochondrial ribosomal protein L32	6.40
	446189	H85224	Hs.214013	ESTs	6.40
	416806	NM_000288	Hs.76993	peroxisomal biogenesis factor 7	6.38
50	416467	H57685	Hs.37467	ESTs	6.36
	453403	BE466639	Hs.61779	Homo sapiens cDNA FLJ13591 fis, clone PL	6.34
	429769	NM_004917	Hs.218366	kallikrein 4 (protease, enamel matrix, p	6.34
	423642	AW452650	Hs.157148	hypothetical protein MGC13204	6.32
	425843	BE313280	Hs.159627	death associated protein 3	6.32
55	439221	AA737106	Hs.32250	ESTs, Moderately similar to I78885 serin	6.32
	428194	AA765603	Hs.180877	H3 histone, family 3B (H3.3B)	6.30
	431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta	6.30
	439368	AF100143	Hs.6540	fibroblast growth factor 13	6.30
	452769	AW081826	Hs.242561	ESTs	6.30
60	416838	D54745	Hs.80247	cholecystokinin	6.30
	436962	AW377314	Hs.5364	DKFZP564D52 protein	6.29
	433383	AF034837	Hs.192731	double-stranded RNA specific adenosine d	6.29
	418638	AW749855		gb:QV4-BT0534-281299-053-c05 BT0534 Homo	6.28
	450728	AW162923	Hs.25363	presenilin 2 (Alzheimer disease 4)	6.25
65	440293	AI004193	Hs.22123	ESTs	6.24
	453745	AA952989	Hs.63908	hypothetical protein MGC14726	6.24
	426595	AW871980	Hs.62402	p21/Cdc42/Rac1-activated Kinase 1 (yeast	6.24
	444412	AI147652	Hs.216381	Homo sapiens clone HH409 unknown mRNA	6.24
	413384	NM_000401	Hs.75334	exostoses (multiple) 2	6.22

	426320	W47595	Hs.169300	transforming growth factor, beta 2	6.22
	423349	AF010258	Hs.127428	homeo box A9	6.20
	429165	AW009888	Hs.118258	prostate cancer associated protein 1	6.18
	424800	AL035588	Hs.153203	MyoD family inhibitor	6.18
5	409564	AA045857	Hs.54943	fractura callus 1 (rat) homolog	6.16
	438786	W67821	Hs.109590	genethonin 1	6.16
	425451	AF242769	Hs.157461	mesenchymal stem cell protein DSC54	6.14
	451683	AI872360	Hs.208293	ESTs	6.14
	413623	AA825721	Hs.246973	ESTs	6.12
10	452232	AW020603	Hs.271688	radial spoke protein 3	6.12
	453390	AA862496	Hs.28482	ESTs	6.12
	435542	AA687376	Hs.269533	ESTs	6.12
	420424	AB033036	Hs.87594	KIAA1210 protein	6.11
	407103	AA424861	Hs.256301	hypothetical protein MGC13170	6.10
15	409734	BE161684	Hs.56155	hypothetical protein	6.10
	432688	BE223007	Hs.152460	Homo sapiens cDNA FLJ12909 fis, clone NT	6.10
	438361	AA805666	Hs.146217	Homo sapiens cDNA: FLJ23077 fis, clone L	6.10
	411479	AW848047		gb:U3-CT0214-291299-052-A12 CT0214 Homo	6.10
	438849	W28948	Hs.10762	ESTs	6.08
20	452726	AF188527	Hs.61661	ESTs, Weakly similar to AF174605 1 F-box	6.08
	445895	D29954	Hs.13421	KIAA0056 protein	6.08
	440774	AI420611	Hs.127832	ESTs	6.07
	422583	AA410506	Hs.118578	KIAA0874 protein	6.06
25	427500	AW970017	Hs.293948	ESTs, Weakly similar to S65657 alpha-1C-	6.04
	443848	AI085198	Hs.298699	ESTs	6.04
	410566	AA373210	Hs.43047	Homo sapiens cDNA FLJ13585 fis, clone PL	6.02
	417845	AL117461	Hs.82719	Homo sapiens mRNA; cDNA DKFZp586F1822 (f	6.02
	430273	AI311127	Hs.125522	ESTs	6.02
	434782	AA649253	Hs.132458	ESTs	6.01
30	442490	AW965078	Hs.30212	thyroid receptor interacting protein 15	6.01
	420026	AI831180	Hs.166676	ESTs	6.00
	437782	AI370878	Hs.123163	exportin 1 (CRM1, yeast, homolog)	6.00
	447359	NM_012093	Hs.18268	adenylate kinase 5	6.00
35	447713	AI420733	Hs.207083	ESTs	6.00
	451073	AI758905	Hs.208063	ESTs	6.00
	451640	AA195601	Hs.28771	Human DNA sequence from clone 747H23 on	6.00
	410889	X91662	Hs.65744	twist (Drosophila) homolog (acrocephalos	5.97
	441222	AI277237	Hs.44208	hypothetical protein FLJ23153	5.96
	447732	AI758398	Hs.161318	ESTs	5.96
40	437756	AA767537	Hs.197096	ESTs	5.95
	408829	NM_008042	Hs.48384	heparan sulfate (glucosamine) 3-O-sulfot	5.94
	453911	AW503857	Hs.4007	Sarcolemma-associated protein	5.94
	414085	AA114016	Hs.75748	aldehyde dehydrogenase 1 family, member	5.93
	408875	NM_015434	Hs.48604	DKFZP434B168 protein	5.92
45	439451	AF086270	Hs.278554	heterochromatin-like protein 1	5.92
	423853	AB011537	Hs.133466	sift (Drosophila) homolog 1	5.91
	453060	AW294092	Hs.21594	hypothetical protein MGC15754	5.91
	420407	AA814732	Hs.145010	lipopolysaccharide-specific response 5-II	5.91
	450480	X82125	Hs.25040	zinc finger protein 239	5.90
50	408448	AW450669	Hs.45068	hypothetical protein DKFZp434I143	5.88
	421039	NM_003478	Hs.101299	cullin 5	5.88
	451684	AF218751	Hs.26813	CDA14	5.88
	438063	AK000028	Hs.250867	ribosomal protein S24	5.88
55	410507	AA355288	Hs.271408	transitional epithelia response protein	5.86
	420179	N74530	Hs.21168	ESTs	5.84
	453878	AW984440	Hs.19025	DC32	5.84
	452270	AW975014	Hs.26	ferrochelatase (protoporphyrin)	5.83
	435867	AA954229	Hs.114052	ESTs	5.82
60	417683	AW566008	Hs.239154	ankyrin repeat, family A (RFXANK-like),	5.82
	432005	AA524190	Hs.120777	ESTs, Weakly similar to ELL2_HUMAN RNA P	5.81
	408815	AA833930	Hs.288036	tRNA isopentenylpyrophosphate transferas	5.80
	437880	R50393	Hs.278438	KIAA1474 protein	5.80
	425856	AA384908	Hs.98927	hypothetical protein FLJ13993	5.79
	400301	X03635	Hs.1657	estrogen receptor 1	5.78
65	446261	AA313893	Hs.13399	hypothetical protein FLJ12615 similar to	5.78
	410141	R07775	Hs.287657	Homo sapiens cDNA: FLJ21291 fis, clone C	5.77
	427258	AA400091	Hs.39421	ESTs	5.76
	419108	AA389724	Hs.191264	ESTs, Weakly similar to ALU7_HUMAN ALU S	5.76
	442029	AW956698	Hs.14458	neural precursor cell expressed, develop	5.76

	407783	AW996872	Hs.172028	a disintegrin and metalloproteinase doma	5.75
	434408	AI031771	Hs.132586	ESTs	5.74
	415077	L41607	Hs.934	glucosaminyl (N-acetyl) transferase 2, I	5.74
5	432435	BE218886	Hs.282070	ESTs	5.74
	433313	W20128	Hs.298039	ESTs	5.73
	431740	N75450	Hs.183412	ESTs, Moderately similar to AF116721 67	5.73
	412991	AW949013		gb:QV4-FT0005-110500-201-e12 FT0005 Homo	5.72
	418852	BE537037	Hs.273294	hypothetical protein FLJ20069	5.72
10	418882	NM_004996	Hs.89433	ATP-binding cassette, sub-family C (CFTR	5.72
	446867	AB007891	Hs.16349	KIAA0431 protein	5.72
	437866	AA156781	Hs.83992	metallothionein 1E (functional)	5.72
	410232	AW372451	Hs.61184	CGI-79 protein	5.70
	414452	AA454038	Hs.29032	ESTs	5.70
15	422762	AL031320	Hs.119976	Human DNA sequence from clone RP1-20N2 o	5.70
	428730	AA625947	Hs.25750	ESTs	5.70
	431571	AW500486	Hs.180610	splicing factor proline/glutamine rich (5.70
	433393	AF038564	Hs.96074	Itchy (mouse homolog) E3 ubiquitin prote	5.70
	450616	AL133067	Hs.25214	hypothetical protein	5.70
20	443774	AL117428	Hs.9740	DKFZP434A236 protein	5.69
	446100	AW967109	Hs.13804	hypothetical protein dJ462023.2	5.69
	419168	AI336132	Hs.33718	Homo sapiens cDNA FLJ12641 fis, clone NT	5.68
	416653	AA768553	Hs.77498	metallothionein 1E (functional)	5.67
	452679	Z42387	Hs.4299	transmembrane, prostate androgen induced	5.66
25	450244	AA007534	Hs.125062	ESTs	5.66
	408621	AI970672	Hs.46838	chromosome 11 open reading frame 8	5.65
	450325	AI935962	Hs.26289	ESTs	5.65
	439671	AW162840	Hs.6641	kinesin family member 5C	5.64
	452387	AI680772	Hs.4316	trinucleotide repeat containing 12	5.64
30	413992	W26276	Hs.136075	RNA, U2 small nuclear	5.63
	444151	AW972917	Hs.128749	alpha-methylacyl-CoA racemase	5.63
	417791	AW965339	Hs.111471	ESTs	5.62
	410198	AI936442	Hs.59838	hypothetical protein FLJ10808	5.60
	415123	D60925		ESTs	5.60
35	429170	NM_001394	Hs.2359	dual specificity phosphatase 4	5.60
	434415	BE177494		gb:RC6-HT0596-270300-011-C05 HT0596 Homo	5.60
	440738	AI004650	Hs.225674	WD repeat domain 9	5.60
	443830	AI142095	Hs.143273	ESTs	5.60
	448603	AI655662	Hs.197698	ESTs	5.60
40	414342	AA742181	Hs.75912	KIAA0257 protein	5.59
	422634	NM_016010	Hs.118821	CGI-62 protein	5.58
	435047	AA454985	Hs.54973	cadherin-like protein VR20	5.55
	400268				5.55
	452055	AI377431	Hs.293772	hypothetical protein MGC10858	5.54
45	437073	AI885608	Hs.94122	ESTs	5.54
	434072	H70854	Hs.283059	Homo sapiens PRO1082 mRNA, complete cds	5.53
	418339	AA839902	Hs.104215	ESTs, Moderately similar to SPCN_HUMAN S	5.52
	434551	BE387162	Hs.280858	ESTs, Highly similar to A35661 DNA excis	5.52
	439569	AW602166	Hs.222399	CEGP1 protein	5.51
50	441102	AA973905	Hs.16003	intermediate filament protein syncoilin	5.50
	448310	AI480316		gb:tm26h09.x1 Soares_NFL_T_GBC_S1 Homo s	5.50
	413173	BE076928	Hs.70980	ESTs	5.48
	436246	AW450863	Hs.119991	ESTs	5.48
	449300	AI656959	Hs.222165	ESTs	5.48
55	452823	AB012124	Hs.30696	transcription factor-like 5 (basic helix	5.48
	451403	AA885569	Hs.15727	Homo sapiens cDNA FLJ14511 fis, clone NT	5.46
	417061	AI675944	Hs.188691	Homo sapiens cDNA FLJ12033 fis, clone HE	5.44
	429126	AW172356	Hs.99083	ESTs	5.44
	431316	AA502663	Hs.145037	ESTs	5.44
	439192	AW970538	Hs.105413	ESTs	5.44
60	431938	AA938471	Hs.115242	specific granule protein (28 kDa); cyste	5.44
	451552	AA047233	Hs.33810	ESTs	5.43
	416991	N38389	Hs.295091	KIAA0226 gene product	5.42
	427638	AA06411	Hs.208341	ESTs, Weakly similar to KIAA0989 protein	5.42
	427718	AI798680	Hs.25933	ESTs	5.42
65	438710	AA833907	Hs.178724	ESTs, Weakly similar to ALU1_HUMAN ALU S	5.42
	406076	AL380179	Hs.137011	Homo sapiens mRNA; cDNA DKFZp547P134 (fr	5.40
	431263	AW129203	Hs.13743	ESTs	5.40
	421264	AL039123	Hs.103042	microtubule-associated protein 1B	5.38
	421685	AF189723	Hs.106778	ATPase, Ca++ transporting, type 2C, memb	5.37

	408460	AA054726	Hs.285574	ESTs	5.38
	409081	AW970386	Hs.269423	ESTs	5.38
	421987	AJ133161	Hs.286131	CGI-101 protein	5.38
5	428002	AA418703		gb:zv98c03.s1 Soares_NhHMPu_S1 Homo sapi	5.38
	441217	AJ922183	Hs.213246	ESTs	5.38
	426006	R49031	Hs.22827	ESTs	5.35
	422806	BE314767	Hs.1581	glutathione S-transferase theta 2	5.34
	432281	AK001239	Hs.274263	hypothetical protein FLJ10377	5.32
10	451982	F13036	Hs.27373	Homo sapiens mRNA; cDNA DKFZp564O1763 (f	5.32
	421129	BE439899	Hs.89271	ESTs	5.31
	444042	NM_004915	Hs.10237	ATP-binding cassette, sub-family G (WHIT	5.31
	410150	AW382942	Hs.8774	ESTs	5.30
	423952	AW877787	Hs.136102	KIAA0853 protein	5.30
15	452822	X85689	Hs.288617	hypothetical protein FLJ22621	5.30
	447752	M73700	Hs.347	lactotransferrin	5.29
	441766	R53790	Hs.23294	hypothetical protein FLJ14393	5.29
	431359	AW993522	Hs.292934	ESTs	5.27
	427212	AW293849	Hs.58279	ESTs, Weakly similar to ALU7_HUMAN ALU S	5.27
20	449916	T60525	Hs.299221	pyruvate dehydrogenase kinase, isoenzyme	5.27
	454014	AW016670	Hs.233275	ESTs	5.27
	419714	AA758751	Hs.98216	ESTs	5.26
	428845	AL157579	Hs.153610	KIAA0751 gene product	5.26
	417333	AL157545	Hs.42179	bromodomain and PHD finger containing, 3	5.24
	419986	AJ345455	Hs.78915	GA-binding protein transcription factor,	5.24
25	407182	AA312551	Hs.230157	ESTs	5.22
	420111	AA255652		gb:zs21h11.r1 NCLCGAP_GCB1 Homo sapiens	5.22
	428058	AJ821625	Hs.191602	ESTs	5.22
	459551	AJ472808		gb:ij70a07.x1 Soares_NSF_F8_9W_OT_PA_P_S	5.22
30	432524	AJ458020	Hs.293287	ESTs	5.22
	436207	AA334774	Hs.12845	hypothetical protein MGC13159	5.22
	410870	U81599	Hs.66731	homeo box B13	5.22
	451418	BE387790	Hs.26369	hypothetical protein FLJ20287	5.22
	409757	NM_001898	Hs.123114	cystatin SN	5.21
35	441124	T87717	Hs.119563	ESTs	5.21
	428593	AW207440	Hs.185973	degenerative spermatocyte (homolog Dros	5.21
	436401	AJ087958	Hs.29088	ESTs	5.20
	437113	AA744893		gb:ny26c10.s1 NCLCGAP_GCB1 Homo sapiens	5.20
	450947	AJ745400	Hs.204662	ESTs	5.20
40	453279	AW893940	Hs.59698	ESTs	5.20
	445467	AJ239832	Hs.15817	ESTs, Weakly similar to ALU4_HUMAN ALU S	5.19
	448944	AB014605	Hs.22599	atrophin-1 interacting protein 1; activ	5.19
	412198	AA937111	Hs.69165	ESTs	5.18
	422646	H87863	Hs.151380	ESTs, Weakly similar to T16584 hypotheti	5.18
45	438988	AF085888	Hs.269307	ESTs	5.18
	453954	AW118336	Hs.75251	DEAD/H (Asp-Glu-Ala-Asp/His) box binding	5.18
	447541	AK000288	Hs.18800	hypothetical protein FLJ20281	5.18
	434029	AA621763	Hs.170434	Homo sapiens cDNA FLJ14242 fis, clone OV	5.16
	459294	AW977286	Hs.169531	RBP1-like protein	5.16
50	429441	AJ224172	Hs.204096	lipophilin B (uteroglobin family member)	5.16
	424692	AA429834	Hs.151791	KIAA0092 gene product	5.15
	427359	AW020782	Hs.79881	Homo sapiens cDNA: FLJ23006 fis, clone L	5.15
	419872	AJ422851	Hs.148162	ESTs	5.15
	429422	AK001494	Hs.202596	Homo sapiens cDNA FLJ10632 fis, clone NT	5.14
55	448902	Z45998	Hs.22543	Homo sapiens mRNA; cDNA DKFZp76111912 (f	5.14
	459055	N23235	Hs.30567	ESTs, Weakly similar to B34087 hypotheti	5.14
	431318	AA502700	Hs.293147	ESTs, Moderately similar to A46010 X-link	5.14
	452953	AJ932884	Hs.271741	ESTs, Weakly similar to A46010 X-linked	5.13
	428372	AK000684	Hs.183887	hypothetical protein FLJ22104	5.12
60	434401	AJ864131	Hs.71119	Putative prostate cancer tumor suppresso	5.12
	416434	AW163045	Hs.79334	nuclear factor, interleukin 3 regulated	5.11
	410268	AA316181	Hs.61635	six transmembrane epithelial antigen of	5.10
	417517	AF001178	Hs.82238	POP4 (processing of precursor, S. cerev	5.10
	453816	NM_003462	Hs.33846	dynal, axonemal, light intermediate pol	5.10
65	427958	AA418000	Hs.98280	potassium intermediate/small conductance	5.09
	407945	X69208	Hs.606	ATPase, Cu++ transporting, alpha polypep	5.08
	425154	NM_001851	Hs.154850	collagen, type IX, alpha 1	5.08
	412863	AA121673	Hs.59757	zinc finger protein 281	5.06
	420807	AA280627	Hs.57848	ESTs	5.06
	430568	AA769221	Hs.270847	delta-tubulin	5.06

	433887	AA743991		gbny57g01.s1 NCL_CGAP_Pr18 Homo sapiens	5.06
	438375	AW015940	Hs.232234	ESTs	5.06
	418092	R45154	Hs.106604	ESTs	5.06
5	418576	AW968159	Hs.289104	Alu-binding protein with zinc finger dom	5.05
	413328	Y15723	Hs.75285	guanylate cyclase 1, soluble, alpha 3	5.04
	414271	AK000275	Hs.75871	protein kinase C binding protein 1	5.04
	432729	AK000292	Hs.278732	hypothetical protein FLJ20285	5.04
	433433	AI692623	Hs.121513	Homo sapiens clone Z'3-1 placenta expres	5.04
	439662	H87552	Hs.269060	ESTs	5.04
10	439743	AL389558	Hs.283858	Homo sapiens mRNA full length insert cDN	5.04
	417511	AL049178	Hs.82223	chordin-like	5.02
	437814	AI088192	Hs.135474	ESTs, Weakly similar to DDX9_HUMAN ATP-D	5.02
	426342	AF093419	Hs.169378	multiple PDZ domain protein	5.02
	429782	NM_005754	Hs.220689	Ras-GTPase-activating protein SH3-domain	5.02
15	429975	AI167145	Hs.165538	ESTs	5.02
	436209	AW850417	Hs.254020	ESTs, Moderately similar to unnamed prot	5.02
	438571	AW020775	Hs.55022	ESTs	5.02
	450223	AA418204	Hs.241493	natural killer-tumor recognition sequenc	5.02
	408267	AW380525	Hs.267705	tubulin-specific chaperone e	5.01
20	417730	Z44761		gbHSC28F061 normalized infant brain cDN	5.00
	425465	L18964	Hs.1904	protein kinase C, iota	5.00
	430599	NM_004855	Hs.247118	phosphatidylinositol glycan, class B	5.00
	450961	AW978813	Hs.250867	metallothionein 1E (functional)	5.00
	451386	AB029006	Hs.26334	spastic paraplegia 4 (autosomal dominant	5.00
25	420380	AA840891	Hs.102406	ESTs	4.99
	424947	R77852	Hs.239625	ESTs, Weakly similar to alternatively sp	4.99
	442653	BE269247	Hs.170226	gb:601185486F1 NIH_MGC_8 Homo sapiens cd	4.98
	457211	AW972565	Hs.32399	ESTs, Weakly similar to S51797 vasodilat	4.97
	425851	NM_001490	Hs.159642	glucosaminyl (N-acetyl) transferase 1, c	4.97
30	446279	AA490770	Hs.182382	ESTs	4.96
	433377	AI752713	Hs.43845	ESTs	4.96
	450218	R02018	Hs.168640	ankylosis, progressive (mouse) homolog	4.96
	412715	NM_000947	Hs.74519	primase, polypeptide 2A (58kD)	4.94
	448164	R61680	Hs.26904	ESTs, Moderately similar to Z195_HUMAN Z	4.94
35	420121	AW968271	Hs.191534	ESTs, Weakly similar to ALU1_HUMAN ALU S	4.94
	421689	N87820	Hs.106826	KIAA1696 protein	4.93
	445808	AV655234	Hs.298083	ESTs, Moderately similar to PC4259 ferri	4.92
	418533	BE244053	Hs.79362	retinoblastoma-like 2 (p130)	4.92
	418049	AA211487	Hs.190488	Homo sapiens, Similar to nuclear localiz	4.92
40	436039	AW023323	Hs.121070	ESTs	4.92
	432653	N62096	Hs.293185	ESTs, Weakly similar to JC7328 amino aci	4.91
	420324	AF163474	Hs.96744	prostate androgen-regulated transcript 1	4.91
	403047				4.91
45	436889	AA764852	Hs.291567	ESTs	4.90
	431117	AF003522	Hs.250500	delta (Drosophila)-like 1	4.90
	427617	D42063	Hs.179825	RAN binding protein 2	4.88
	428804	AK000713	Hs.193738	hypothetical protein FLJ20706	4.88
	433050	AI093930	Hs.163440	Homo sapiens cDNA: FLJ21000 fis, clone C	4.88
	418575	AA225313	Hs.222886	ESTs, Weakly similar to TRHY_HUMAN TRICH	4.86
50	432615	AA557191	Hs.55028	ESTs, Weakly similar to I54374 gene NF2	4.86
	412652	AI801777	Hs.6774	ESTs	4.86
	432473	AI202703	Hs.152414	ESTs	4.86
	449071	NM_005872	Hs.22960	breast carcinoma amplified sequence 2	4.86
	450654	AJ245587	Hs.25275	Kruppel-type zinc finger protein	4.85
55	418866	T65754	Hs.100489	gb:yc11c07.s1 Stratagene lung (937210) H	4.85
	407598	R86913		gb:yc30f05.r1 Soares fetal liver spleen	4.84
	456516	BE172704	Hs.222746	KIAA1610 protein	4.84
	426501	AW043782	Hs.293616	ESTs	4.84
	448730	AB032983	Hs.21894	KIAA1157 protein	4.84
60	458339	AW976853	Hs.172843	ESTs	4.83
	422083	NM_001141	Hs.111256	arachidonate 15-lipoxygenase, second typ	4.82
	420159	AI572490	Hs.89785	Homo sapiens cDNA: FLJ21245 fis, clone C	4.82
	424103	NM_001918	Hs.139410	dihydrolipoamide branched chain transacy	4.82
	448535	W15267	Hs.23672	low density lipoprotein receptor-related	4.82
65	422048	NM_012445	Hs.288126	spondin 2, extracellular matrix protein	4.82
	416737	AF154335	Hs.79691	LIM domain protein	4.82
	419972	AL041465	Hs.294038	golgin-67	4.81
	420235	AA258758	Hs.31178	ESTs	4.81
	423412	AF109300	Hs.147924	prostate cancer associated protein 5	4.80

	429598	AA811257	Hs.269710	ESTs	4.80
	457114	AI821625	Hs.191602	ESTs	4.80
	421828	AW891965	Hs.289109	histone deacetylase 3	4.79
5	424602	AK002055	Hs.301129	hypothetical protein FLJ11193	4.78
	428364	AA426565	Hs.160541	ESTs, Moderately similar to ALU1_HUMAN A	4.78
	452335	AW188944	Hs.61272	ESTs	4.78
	410765	AI694972	Hs.66180	nucleosome assembly protein 1-like 2	4.77
	421040	AA715026	Hs.135280	ESTs	4.76
10	421518	AI056382	Hs.208819	ESTs	4.76
	452560	BE077084		ESTs	4.76
	409752	AW963990		gb:EST376063 MAGE resequences, MAGH Homo	4.75
	439703	AF086538	Hs.188245	ESTs	4.75
	418836	AI655499	Hs.161712	ESTs	4.74
	450642	R39773	Hs.7130	copine IV	4.74
15	419879	Z17805	Hs.93564	Homer, neuronal immediate early gene, 2	4.74
	411440	AW749402		gb:QV4-BT0383-261299-061-c08 BT0383 Homo	4.74
	450649	NM_001429	Hs.297722	E1A binding protein p300	4.74
	408738	NM_014785	Hs.47313	KIAA0258 gene product	4.73
20	435020	AW505076	Hs.301855	DiGeorge syndrome critical region gene 8	4.72
	411624	BE145964		KIAA0594 protein	4.72
	439360	AA448488	Hs.55346	ribosomal protein L44	4.72
	440491	R35252	Hs.24944	ESTs, Weakly similar to 2109260A B cell	4.72
	442611	BE077155	Hs.177537	hypothetical protein DKFZp761B1514	4.72
25	443555	N71710	Hs.21398	ESTs, Moderately similar to A Chain A, H	4.72
	453800	BE300741	Hs.288416	hypothetical protein FLJ13340	4.72
	457528	AW973791	Hs.292784	ESTs	4.72
	416795	AI497778	Hs.168053	HBV pX associated protein-8	4.71
	407302	R74206	Hs.268755	ESTs, Weakly similar to I78885 serine/th	4.71
30	404721				4.70
	426261	AW242243	Hs.168670	peroxisomal farnesylated protein	4.70
	431924	AK000850	Hs.272203	Homo sapiens cDNA FLJ20843 fis, clone AD	4.70
	435256	AF193768	Hs.13872	cytokine-like protein C17	4.70
	438295	AI394151	Hs.37932	ESTs	4.70
35	442655	AW027457	Hs.30323	ESTs, Weakly similar to B34087 hypotheti	4.70
	415788	AW628686	Hs.78851	KIAA0217 protein	4.69
	442760	BE075297	Hs.10067	ESTs, Weakly similar to A43932 mucin 2 p	4.69
	432432	AA541323	Hs.115831	ESTs	4.68
	454398	AA463437	Hs.11556	Homo sapiens cDNA FLJ12566 fis, clone NT	4.68
40	452741	BE382914	Hs.30503	Homo sapiens cDNA FLJ11344 fis, clone PL	4.67
	424853	BE549737	Hs.132967	Human EST clone 122887 mariner transpos	4.67
	419706	C04649	Hs.77899	tropomyosin 1 (alpha)	4.66
	412088	AI689498	Hs.108932	ESTs	4.65
	416276	U41060	Hs.79136	LIV-1 protein, estrogen regulated	4.64
45	429281	AA830856	Hs.29808	Homo sapiens cDNA: FLJ21122 fis, clone C	4.64
	448207	AI475490	Hs.170577	ESTs	4.64
	408374	AW025430	Hs.155591	forkhead box F1	4.64
	447162	BE328091	Hs.157396	ESTs, Weakly similar to A46010 X-linked	4.64
	451900	AB023199	Hs.27207	KIAA0982 protein	4.63
50	421437	AW821252	Hs.104336	hypothetical protein	4.63
	418624	AI734080	Hs.104211	ESTs	4.63
	426172	AA371307	Hs.125056	ESTs	4.62
	439831	AW136488	Hs.25545	ESTs	4.61
	452994	AW962597	Hs.31305	KIAA1547 protein	4.61
55	457726	AI217477	Hs.194591	ESTs	4.60
	434629	AA789081	Hs.4029	glioma-amplified sequences-41	4.60
	403764				4.58
	410659	AI080175	Hs.68826	ESTs	4.58
60	432383	AK000144	Hs.274449	Homo sapiens cDNA FLJ20137 fis, clone CO	4.58
	451246	AW189232	Hs.39140	cutaneous T-cell lymphoma tumor antigen	4.58
	433234	AB040928	Hs.65366	KIAA1495 protein	4.57
	424983	AI742434	Hs.169911	ESTs	4.56
	437812	AI582291	Hs.16848	ESTs, Weakly similar to O4HUD1 debrisqu	4.56
	438447	AI082883	Hs.167593	hypothetical protein FLJ13409; KIAA1711	4.55
65	434715	BE005346	Hs.116410	ESTs	4.55
	447673	AI823987	Hs.182285	ESTs	4.54
	408897	N50204	Hs.283709	Epipolysaccharide specific response-7 p	4.54
	436845	AW023424	Hs.156520	ESTs	4.54
	421247	BE391727	Hs.102910	general transcription factor IIF, polype	4.53
	450377	AB033091	Hs.24936	KIAA1265 protein	4.53

5	433644	AW342028	Hs.256112	gb:hb75d03.x1 NCL_CGAP_Ut2 Homo sapiens	4.53
	408321	AW405882	Hs.44205	coristatin	4.53
	439225	AA192689	Hs.45032	ESTs	4.52
	440348	AW015802	Hs.47023	ESTs	4.52
	446351	AW444551	Hs.258532	x 001 protein	4.52
10	451212	AW902872	Hs.287334	ESTs	4.52
	430294	AI538226	Hs.135184	guanine nucleotide binding protein 4	4.52
	435005	U80743	Hs.4316	trinucleotide repeat containing 12	4.52
	448072	AI459308	Hs.24908	ESTs	4.50
	403721				4.50
15	451018	AW985589	Hs.247324	mitochondrial ribosomal protein S14	4.50
	453070	AK001465	Hs.31575	SEC63, endoplasmic reticulum translocon	4.49
	417412	X16898	Hs.82112	interleukin 1 receptor, type I	4.48
	439735	AI635388	Hs.142848	hypothetical protein	4.48
	435683	AI023707	Hs.134273	ESTs	4.48
20	424036	AA770688	Hs.81948	H2A histone family, member L	4.48
	426386	AA748850	Hs.174877	bladder cancer overexpressed protein	4.48
	408622	AA056060	Hs.202577	Homo sapiens cDNA FLJ12166 fis, clone MA	4.47
	444269	AI590346	Hs.148220	ESTs	4.47
	430187	AI799909	Hs.158989	ESTs	4.48
25	427761	AA412205	Hs.140986	ESTs	4.48
	430261	AA305127	Hs.237225	hypothetical protein HT023	4.48
	444169	AV648170	Hs.58758	ESTs	4.44
	430598	AK001784	Hs.247112	hypothetical protein FLJ10902	4.44
	412903	BE007967	Hs.155785	ESTs	4.44
30	417048	AI088775	Hs.55498	geranylgeranyl diphosphate synthase 1	4.44
	442710	AI015831	Hs.23210	ESTs	4.44
	457413	AA743462	Hs.165337	ESTs	4.44
	400303	AA242758	Hs.79138	LIV-1 protein, estrogen regulated	4.42
	443268	AI800271	Hs.129445	hypothetical protein FLJ12496	4.42
35	438209	AL120659	Hs.6111	aryl-hydrocarbon receptor nuclear trans	4.42
	431724	AA514535	Hs.283704	ESTs	4.41
	412280	AW205118	Hs.272814	hypothetical protein DKFZp434E1723	4.40
	440801	AA906368	Hs.190535	ESTs	4.40
	452959	AI933416	Hs.189674	ESTs	4.40
40	453861	AI026838	Hs.30120	ESTs, Weakly similar to NUCL_HUMAN NUCLE	4.40
	417421	AL138201	Hs.82120	nuclear receptor subfamily 4, group A, m	4.40
	447270	AC002551	Hs.331	general transcription factor IIIC, polyp	4.38
	433641	AF080229		gb:Human endogenous retrovirus K clone 1	4.38
	447078	AW885727	Hs.301570	ESTs	4.38
45	424242	AA337476		hypothetical protein MGC13102	4.37
	408170	AW204516	Hs.31835	ESTs	4.36
	448757	AI386784	Hs.48820	TATA box binding protein (TBP)-associate	4.36
	420021	AA252848	Hs.293557	ESTs	4.36
	448684	AI659790	Hs.253302	ESTs	4.36
50	453867	AI929383	Hs.108196	hypothetical protein DKFZp434N185	4.36
	458712	AI347502	Hs.173066	hypothetical protein FLJ20781	4.36
	417251	AW015242	Hs.99488	ESTs, Weakly similar to YK54_YEAST HYPOT	4.35
	434423	NM_006769	Hs.3844	UIM domain only 4	4.35
	423427	AL137612	Hs.285848	KIAA1454 protein	4.34
55	415715	F30364		ESTs	4.33
	404561				4.32
	422969	AA782536	Hs.122647	N-myristoyltransferase 2	4.32
	423685	BE350494	Hs.49753	uveal autoantigen with coiled coil domai	4.32
	443977	AL120986	Hs.150627	ESTs, Weakly similar to I38022 hypotheti	4.32
60	425071	NM_013989	Hs.154424	deiodinase, iodothyronine, type II	4.32
	431583	AL042813	Hs.262476	S-adenosylmethionine decarboxylase 1	4.31
	411379	AI816344	Hs.12554	ESTs, Weakly similar to NPL4_HUMAN NUCLE	4.30
	421476	AW953805	Hs.21887	ESTs	4.30
	425178	H16097	Hs.161027	ESTs	4.30
65	439262	AA832333	Hs.124399	ESTs	4.30
	442818	AK001741	Hs.8739	hypothetical protein FLJ10879	4.30
	421977	W94197	Hs.110165	ribosomal protein L26 homolog	4.29
	437114	AA836841	Hs.163085	ESTs	4.28
	420185	N44348	Hs.300784	Homo sapiens cDNA FLJ11177 fis, clone PL	4.28
	418330	BE409405	Hs.94722	ESTs	4.27
	419750	AL079741	Hs.183114	Homo sapiens cDNA FLJ14236 fis, clone NT	4.26
	437085	AL038450	Hs.103238	ESTs	4.26
	455276	BE176479		gb:RC3-HT0585-160300-022-b09 HT0585 Homo	4.24

	416292	AA179233	Hs.42390	nasopharyngeal carcinoma susceptibility	4.24
	423740	Y07701	Hs.132243	aminopeptidase puromycin sensitive	4.24
	442023	AI187878	Hs.144549	ESTs	4.24
	426764	AA732524	Hs.151464	ESTs, Weakly similar to ALUC_HUMAN IIII	4.23
5	454058	AI273419	Hs.135145	hypothetical protein FLJ13984	4.23
	456511	AA282330	Hs.145668	ESTs	4.22
	448330	AL036449	Hs.207163	ESTs	4.22
	424701	NM_005923	Hs.151988	mitogen-activated protein kinase kinase	4.21
	432621	AI298501	Hs.12807	ESTs, Weakly similar to T46428 hypotheti	4.20
10	445707	AI248720	Hs.114390	ESTs	4.20
	419910	AA662913	Hs.190173	ESTs, Weakly similar to A46010 X-linked	4.20
	424085	NM_002914	Hs.139228	replication factor C (activator 1) 2 (40	4.20
	440749	W22335	Hs.7392	hypothetical protein MGC3199	4.20
	442787	W93048	Hs.227203	hypothetical protein MGC2747	4.20
15	443414	R54584	Hs.25209	ESTs	4.20
	443556	AA256769	Hs.94949	methylmalonyl-CoA epimerase	4.20
	444170	AW613879	Hs.102408	ESTs	4.20
	446751	AA766998	Hs.85874	Human DNA sequence from clone RP11-16L21	4.20
	421041	N35914	Hs.14691	ESTs, Moderately similar to I38022 hypot	4.19
20	447476	BE293466	Hs.20880	ESTs, Weakly similar to I38022 hypotheti	4.19
	448543	AW897741	Hs.21380	Homo sapiens mRNA; cDNA DKFZp586P1124 (f	4.18
	410294	AB014515	Hs.288891	KIAA0615 gene product	4.18
	433607	AA602004	Hs.23260	ESTs	4.18
	435552	AI666636	Hs.193480	ESTs, Moderately similar to ALU6_HUMAN A	4.18
25	447124	AW976438	Hs.17428	RBP1-like protein	4.18
	453308	AW959731	Hs.32538	ESTs	4.17
	439328	W07411	Hs.118212	ESTs, Moderately similar to ALU3_HUMAN A	4.16
	430473	AW130690	Hs.299842	ESTs	4.16
	437257	AI283085	Hs.290931	ESTs, Weakly similar to YFJ7_YEAST HYPOT	4.16
30	438018	AK001160	Hs.5999	hypothetical protein FLJ10298	4.16
	443857	AI089292	Hs.287621	hypothetical protein FLJ14069	4.15
	446711	AF169892	Hs.12450	protocadherin 9	4.15
	419103	Z40229	Hs.96423	hypothetical protein FLJ23033	4.14
	405403				4.14
35	407378	AA299264		ESTs, Moderately similar to I38022 hypot	4.14
	408986	AW298602	Hs.197687	ESTs	4.14
	418727	AA227609	Hs.94834	ESTs	4.14
	434400	AI478211	Hs.186896	Homo sapiens cDNA FLJ11417 fis, clone HE	4.14
	438578	AA811244	Hs.164168	ESTs	4.14
40	450459	AI697193	Hs.299254	Homo sapiens cDNA: FLJ23597 fis, clone L	4.14
	429887	AW366286	Hs.145696	splicing factor (CC1.3)	4.13
	448148	NM_016578	Hs.20509	HBV pX associated protein-8	4.13
	450316	W84446	Hs.17850	hypothetical protein MGC4643	4.12
	417531	NM_003157	Hs.1087	serine/threonine kinase 2	4.12
45	431592	R69016	Hs.293871	hypothetical protein MGC10895s	4.12
	432483	AA548518	Hs.186783	ESTs	4.12
	433613	AA836126	Hs.5669	ESTs	4.12
	434739	AA804487	Hs.144130	ESTs	4.12
	438259	AW205969	Hs.131808	ESTs	4.12
50	425810	AI923627	Hs.31903	ESTs	4.10
	432672	AW973775	Hs.130760	myosin phosphatase, target subunit 2	4.10
	433345	AI681545	Hs.152982	hypothetical protein FLJ13117	4.10
	432712	AB016247	Hs.288031	sterol-C5-desaturase (fungal ERG3, delta	4.09
55	453020	AL162039	Hs.31422	Homo sapiens mRNA; cDNA DKFZp434M229 (fr	4.09
	412045	AA099802	Hs.4299	transmembrane, prostate androgen induced	4.09
	435114	AA775483	Hs.288936	mitochondrial ribosomal protein L9	4.08
	443204	AW205878	Hs.29643	Homo sapiens cDNA FLJ13103 fis, clone NT	4.08
	445459	AI478629	Hs.158465	likely ortholog of mouse putative IKK re	4.08
	438938	H46212	Hs.137221	ESTs	4.07
60	454119	BE549773	Hs.40510	uncoupling protein 4	4.06
	411000	N40449	Hs.201619	ESTs, Weakly similar to S38383 SEB48 pro	4.06
	418928	AA232658	Hs.87070	UDP-glucose:glycoprotein glucosyltransfe	4.06
	424432	AB037821	Hs.146858	protocadherin 10	4.06
	449673	AA002064	Hs.18920	ESTs	4.06
65	429299	AI620463	Hs.89197	hypothetical protein MGC13102	4.06
	422174	AL049325	Hs.112493	Homo sapiens mRNA; cDNA DKFZp564D036 (fr	4.05
	455497	AA112573	Hs.285691	Homo sapiens protein mRNA, complete cds	4.05
	415138	C18358	Hs.78045	tissue factor pathway inhibitor 2	4.04
	402791				4.04

	426792	AL044854	Hs.172329	KIAA0576 protein	4.04
	438660	U95740	Hs.6349	Homo sapiens, clone IMAGE:3010666, mRNA,	4.04
	442768	AL048534	Hs.48458	ESTs, Weakly similar to ALU8_HUMAN ALU S	4.04
	447668	AF155655	Hs.18885	CGI-116 protein	4.04
5	428342	AF739168	Hs.131798	Homo sapiens cDNA FLJ13458 fis, clone PL	4.04
	453439	AF572438	Hs.32976	guanine nucleotide binding protein 4	4.02
	453857	AL080235	Hs.35861	DKFZP586E1621 protein	4.02
	428249	AA130914	Hs.183291	zinc finger protein 268	4.02
	432015	AL157504	Hs.159115	Homo sapiens mRNA; cDNA DKFZp586O0724 (f	4.02
10	445495	BE622641	Hs.38489	ESTs, Weakly similar to I38022 hypotheti	4.02
	451746	M86178		ESTs	4.02
	452211	AB985513	Hs.233420	ESTs	4.02
	453048	AA284040	Hs.219441	ESTs, Highly similar to CA5B_HUMAN CARBO	4.02
	456038	AA203285	Hs.294141	ESTs, Weakly similar to alternatively sp	4.02
15	452449	AW068658	Hs.20943	ESTs	4.02
	407204	FA1933	Hs.140237	ESTs, Weakly similar to ALU1_HUMAN ALU S	4.01
	428046	AW812785	Hs.155381	ESTs, Moderately similar to I38022 hypot	4.01
	438520	AA706319	Hs.99416	ESTs	4.01
	443292	AK000213	Hs.9186	hypothetical protein	4.01
20	432715	AA247152	Hs.200483	ESTs, Weakly similar to KIAA1074 protein	4.00
	403797				4.00
	418347	AA216419	Hs.268295	gb:nc16e03.s1 NCL_CGAP_Pr1 Homo sapiens	4.00
	419459	AW291128	Hs.278422	DKFZP586G1122 protein	4.00
	420911	U77413	Hs.100293	O-linked N-acetylglucosamine (GlcNAc) tr	4.00
25	425176	AW015644	Hs.301430	TEA domain family member 1 (SV40 transcr	4.00
	447505	AL049266	Hs.18724	Homo sapiens mRNA; cDNA DKFZp564F083 (fr	4.00
	453773	AL133761		gb:DKFZp761C1413_r1 761 (synonym: hamy2)	4.00
	434384	AA631910	Hs.162849	ESTs	3.99
	422471	AA311027	Hs.271894	ESTs, Weakly similar to I38022 hypotheti	3.99
30	427386	AW836261	Hs.177488	ESTs	3.98
	433394	AF077753	Hs.93810	cerebral cavernous malformations 1	3.98
	441269	AW015206	Hs.178784	ESTs	3.97
	419829	AB020695	Hs.91662	KIAA0888 protein	3.96
	435008	AF150262	Hs.162888	ESTs	3.96
35	456649	RT4441	Hs.117176	poly(A)-binding protein, nuclear 1	3.96
	418723	AA504428	Hs.10487	Homo sapiens, clone IMAGE:3954132, mRNA,	3.96
	428738	NM_000380	Hs.182803	xeroderma pigmentosum, complementation g	3.95
	430456	AA314998	Hs.241503	hypothetical protein	3.95
	422017	NM_003877	Hs.110776	STAT induced STAT inhibitor-2	3.95
40	409960	BE261944	Hs.153028	hexokinase 1	3.95
	455309	AW894017		gb:RC4-NN0027-150400-012-g04 NN0027 Homo	3.95
	450295	AF765732	Hs.201194	ESTs	3.94
	456660	AA909249	Hs.112282	solute carrier family 30 (zinc transport	3.94
	410908	AA121688	Hs.10592	ESTs	3.94
45	447145	AA761073	Hs.182943	TRAF family member-associated NFKB activ	3.94
	449318	AW236021	Hs.108788	Homo sapiens, Similar to RIKEN cDNA 5730	3.94
	449869	W57990	Hs.60059	Homo sapiens cDNA FLJ11478 fis, clone HE	3.94
	411897	AW182924	Hs.128790	ESTs	3.93
	437531	AF00752	Hs.112259	T cell receptor gamma locus	3.93
50	452238	F01811	Hs.187931	ESTs	3.93
	410488	AW235094	Hs.183424	zinc finger protein	3.92
	424882	AF379461	Hs.153636	far upstream element (FUSE) binding prot	3.92
	428269	H15302	Hs.168950	Homo sapiens mRNA; cDNA DKFZp566A1046 (f	3.92
	427043	AA397679	Hs.298460	ESTs	3.92
55	440404	AF015881	Hs.125616	mitochondrial ribosomal protein S5	3.92
	452762	AW501435	Hs.171409	v-akt murine thymoma viral oncogene homo	3.92
	453058	AW612293	Hs.288684	Homo sapiens cDNA FLJ11750 fis, clone HE	3.92
	423583	AL122055	Hs.129836	KIAA1028 protein	3.92
	408001	AA048458	Hs.95296	ESTs	3.92
60	419197	N48921	Hs.27441	KIAA1615 protein	3.91
	428695	AF355847	Hs.189999	purinergic receptor (family A group 5)	3.91
	401747				3.91
	410011	AB020641	Hs.57856	PFTAIR protein kinase 1	3.91
	432205	AF06583	Hs.125291	ESTs	3.91
65	447857	AA081218	Hs.58608	Homo sapiens cDNA FLJ14206 fis, clone NT	3.91
	446494	AA483276	Hs.288908	WW Domain-Containing Gene	3.91
	409828	AL137163	Hs.57549	hypothetical protein dJ473B4	3.90
	411588	BE336654	Hs.70937	H3 histone family, member A	3.90
	424790	AL119344	Hs.13328	ESTs, Weakly similar to 2004399A chromos	3.90

	425707	AF115402	Hs.11713	ET4-like factor 5 (ets domain transcript	3.90
	431325	AW026751	Hs.5794	ESTs, Weakly similar to 2109280A B cell	3.89
	451806	NM_003729	Hs.27076	RNA 3'-terminal phosphate cyclase	3.89
	401045				3.89
5	433023	AW864783	Hs.34161	thrombospondin 1	3.89
	452160	BE378541	Hs.278815	cysteine sulfinic acid decarboxylase-rel	3.89
	437372	AA323968	Hs.283631	hypothetical protein DKFZp547G183	3.89
	417067	AJ001417	Hs.81086	solute carrier family 22 (extraneuronal	3.88
	410467	AF102548	Hs.63931	dachshund (Drosophila) homolog	3.88
10	422660	AW297582	Hs.237062	hypothetical protein FLJ22548 similar to	3.88
	431930	AB035301	Hs.272211	cadherin 7, type 2	3.88
	453047	AW023798	Hs.288025	ESTs	3.88
	433891	AA613782		gbnc97h03.s1 NCL_CGAP_Pr2 Homo sapiens	3.88
	401785				3.88
15	431088	AA491824	Hs.166881	ESTs	3.88
	451952	AL120173	Hs.301663	ESTs	3.87
	422089	AA523172	Hs.103135	ESTs, Weakly similar to SFR4_HUMAN SPLIC	3.87
	452277	AL049013	Hs.28783	KIAA1223 protein	3.87
	438279	AA805166	Hs.165165	HIV-1 rev binding protein 2	3.86
20	458229	AI928602	Hs.177	phosphatidylinositol glycan, class H	3.86
	406414				3.86
	417183	AI922189	Hs.288390	hypothetical protein FLJ22795	3.85
	413174	AA723584	Hs.191343	ESTs	3.85
25	433332	AJ367347	Hs.127809	Homo sapiens clone TCCCTA00151 mRNA sequ	3.85
	411089	AA456454	Hs.118637	cell division cycle 2-like 1 (PITSLRE pr	3.85
	412494	AL133900	Hs.782	ADP-ribosylation factor domain protein 1	3.84
	413530	AA130158	Hs.18977	ESTs, Moderately similar to ALU8_HUMAN A	3.84
	459592	AL037421	Hs.208746	ESTs, Moderately similar to pot. ORF I [3.84
	418329	AW247430	Hs.84152	cystathionine-beta-synthase	3.83
30	451488	AW503398	Hs.210047	ESTs, Moderately similar to I38022 hypot	3.83
	434804	AA649530		gbns44f05.s1 NCL_CGAP_Alv1 Homo sapiens	3.83
	401819				3.82
	424179	F30712		Homo sapiens, clone IMAGE:4285740, mRNA	3.82
35	424850	AA151057	Hs.153498	chromosome 18 open reading frame 1	3.82
	426472	BE246138	Hs.30853	ESTs	3.82
	426625	T78300	Hs.171409	serologically defined colon cancer antig	3.82
	427585	D31152	Hs.179729	collagen, type X, alpha 1 (Schmid metaph	3.82
	427756	AI376540	Hs.15574	ESTs	3.82
40	444701	AI916512	Hs.198394	ESTs	3.82
	423052	M28214	Hs.123072	RAB3B, member RAS oncogene family	3.82
	429259	AA420450	Hs.292911	ESTs, Highly similar to S60712 band-6-pr	3.82
	416111	AA033813	Hs.79018	chromatin assembly factor 1, subunit A (3.82
	433586	T83301		gbnd78d06.s1 Soares fetal liver spleen	3.81
45	438527	AI969251	Hs.143237	RAB7, member RAS oncogene family-like 1	3.81
	410297	AA148710	Hs.159441	tumican	3.81
	429898	AW117322	Hs.42366	ESTs	3.81
	409079	W87707	Hs.82065	interleukin 6 signal transducer (gp130,	3.80
	419423	D26488	Hs.90315	KIAA0007 protein	3.80
50	429643	AA455889	Hs.187548	FYVE-finger-containing Rab5 effector pro	3.80
	431499	NM_001514	Hs.258561	general transcription factor IIB	3.80
	445060	AA830811	Hs.88808	ESTs	3.80
	449419	R34910	Hs.119172	ESTs	3.80
	450584	AA040403	Hs.60371	ESTs	3.80
55	426137	AL040683	Hs.167031	DKFZP566D133 protein	3.79
	420185	AL044058	Hs.158047	ESTs	3.79
	410076	T05387	Hs.7891	ESTs	3.78
	444078	BE246919	Hs.10290	U5 snRNP-specific 40 kDa protein (hPrp8-	3.78
	417318	AW953937	Hs.12891	ESTs	3.78
	414684	AA587775	Hs.68295	multi-PDZ-domain-containing protein	3.78
60	410275	U85658	Hs.61796	transcription factor AP-2 gamma (activat	3.77
	410503	AW875746	Hs.188662	KIAA1702 protein	3.77
	434170	AA626509	Hs.122329	ESTs	3.77
	421838	AW881089	Hs.108806	Homo sapiens mRNA; cDNA DKFZp566M0947 (f	3.77
65	425268	AI807883	Hs.156932	Homo sapiens cDNA FLJ20653 fis, clone KA	3.76
	431698	AA259068	Hs.287819	protein phosphatase 1, regulatory (inhib	3.76
	411890	AW963824	Hs.31707	ESTs, Weakly similar to YEW4_YEAST HYPOT	3.76
	430291	AV660345	Hs.238128	CGL-49 protein	3.76
	448779	BE042877	Hs.177135	ESTs	3.76
	452682	AA456183	Hs.155606	progesterone membrane binding protein	3.75

5	452598	AJ831594	Hs.68647	ESTs, Weakly similar to ALU7_HUMAN ALU S	3.75
	439498	AA908731	Hs.58297	CLLL8 protein	3.75
	440258	AJ741633	Hs.125350	ESTs	3.74
	456848	AL121087	Hs.296406	KIAA0685 gene product	3.74
	415082	AA160000	Hs.137396	ESTs, Weakly similar to JC5238 galactosyl	3.74
10	420653	AJ224532	Hs.88550	ESTs	3.74
	431637	AJ878330	Hs.265980	hypothetical protein FLJ10563	3.74
	440411	N30258	Hs.156971	hypothetical protein DKFZp434G1415	3.74
	405917				3.74
	419440	AB020689	Hs.90419	KIAA0882 protein	3.74
15	451230	BE546208	Hs.26090	hypothetical protein FLJ20272	3.73
	428597	NM_003816	Hs.2442	a disintegrin and metalloproteinase doma	3.73
	430144	AJ732722	Hs.187694	ERGL protein; ERGIC-53-like protein	3.72
	438394	BE378823	Hs.27693	peptidylprolyl isomerase (cyclophilin)-1	3.72
	440527	AV657117	Hs.184184	ESTs, Moderately similar to S65657 alpha	3.72
20	449433	AJ672096	Hs.9012	ESTs, Weakly similar to S26650 DNA-bind	3.72
	458228	BE503227	Hs.134759	ESTs	3.72
	448653	BE614599	Hs.106823	hypothetical protein MGC14797	3.72
	415075	L27479	Hs.77889	Friedreich ataxia region gene X123	3.72
	433544	AJ793211	Hs.165372	ESTs, Moderately similar to ALU1_HUMAN A	3.71
25	418293	AJ224483	Hs.16063	hypothetical protein FLJ21877	3.71
	449897	AW819842	Hs.24135	transmembrane protein vezatin; hypotheti	3.71
	420297	AJ628272	Hs.88323	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.70
	423065	R96158	Hs.194606	Homo sapiens, clone MGC:5406, mRNA, comp	3.70
	429340	N35938	Hs.199429	Homo sapiens mRNA; cDNA DKFZp434M2216 (f	3.70
30	437777	AA768098	Hs.189079	ESTs	3.70
	440351	AF030933	Hs.7179	RAD1 (S. pombe) homolog	3.70
	443603	BE502601	Hs.134289	ESTs, Weakly similar to KIAA1063 protein	3.70
	446965	BE242873	Hs.16677	WD repeat domain 15	3.70
	412350	AJ658306	Hs.73826	protein tyrosine phosphatase, non-recept	3.70
35	433852	AJ378329	Hs.128629	ESTs	3.70
	433142	AL120697	Hs.110640	ESTs	3.69
	419994	AA282881	Hs.190057	ESTs	3.69
	412628	AJ972402	Hs.173902	hypothetical protein MGC2648	3.69
	431416	AA532718	Hs.178604	ESTs	3.69
40	439444	AJ277652	Hs.54578	ESTs, Weakly similar to I38022 hypotheti	3.68
	414709	AA704703	Hs.77031	Sp2 transcription factor	3.68
	447397	BE247676	Hs.18442	E-1 enzyme	3.68
	405718				3.68
	425217	AU076696	Hs.155174	CDC5 (cell division cycle 5, S. pombe, h	3.68
45	442242	AV647908	Hs.90424	Homo sapiens cDNA: FLJ23285 fs, clone H	3.68
	424690	BE538356	Hs.151777	eukaryotic translation initiation factor	3.68
	421734	AJ318624	Hs.107444	Homo sapiens cDNA FLJ20562 fs, clone KA	3.67
	427221	L15409	Hs.174007	von Hippel-Lindau syndrome	3.67
	439884	AJ720078	Hs.291997	ESTs, Weakly similar to A47582 B-cell gr	3.66
50	402408				3.66
	426327	W03242	Hs.44898	Homo sapiens clone TCCCTA00151 mRNA sequ	3.66
	427119	AW880582	Hs.114574	ESTs	3.66
	427356	AW023482	Hs.97849	ESTs	3.66
	452946	X95425	Hs.31092	EphA5	3.66
55	419078	M93119	Hs.89584	Insulinoma-associated 1	3.66
	416295	AJ064824	Hs.193385	ESTs	3.65
	427144	X95097	Hs.2126	vasoactive intestinal peptide receptor 2	3.65
	447500	AJ381800	Hs.159212	ESTs	3.65
	453127	AJ696871	Hs.294110	ESTs	3.65
60	423396	AJ382555	Hs.127950	bromodomain-containing 1	3.65
	419346	AJ830417		polybromo 1	3.64
	441540	C01367	Hs.127128	ESTs	3.64
	448501	AJ302616	Hs.150819	ESTs	3.64
	459527	AW977556	Hs.291735	ESTs, Weakly similar to I78885 serine/th	3.63
65	446320	AF126245	Hs.14791	acyl-Coenzyme A dehydrogenase family, me	3.63
	435706	W31254	Hs.7045	GL004 protein	3.63
	400110				3.62
	410313	R10305	Hs.185683	ESTs	3.62
	414713	BE485243	Hs.12664	ESTs	3.62
	436279	AW900372	Hs.180793	ESTs, Weakly similar to S65657 alpha-1C-	3.62
	439818	AL360137	Hs.19934	Homo sapiens mRNA full length insert cDN	3.62
	451797	AW663858	Hs.56120	small inducible cytokine subfamily E, me	3.62
	451294	AJ457338	Hs.29894	ESTs	3.62

	434194	AF118847	Hs.283940	Homo sapiens PRO1550 mRNA, partial cds	3.62
	404939				3.62
	408101	AW988504	Hs.123073	CDC2-related protein kinase 7	3.62
	435846	AA700870	Hs.14304	ESTs	3.61
5	432833	N51075	Hs.47181	ESTs	3.61
	427276	AA400269	Hs.49598	ESTs	3.61
	433495	AW373784	Hs.71	alpha-2-glycoprotein 1, zinc	3.60
	403137				3.60
	404165				3.60
10	409571	AA504249	Hs.187585	ESTs	3.60
	410561	BE540255	Hs.6994	Homo sapiens cDNA: FLJ22044 fis, clone H	3.60
	412824	BE018422	Hs.75258	H2A histone family, member Y	3.60
	434228	Z42047	Hs.283978	Homo sapiens PRO2751 mRNA, complete cds	3.60
	436797	AA731491	Hs.178518	hypothetical protein MGC14879	3.60
15	437182	AW005505	Hs.5484	thyroid hormone receptor coactivating pr	3.60
	437444	H46008	Hs.31518	ESTs	3.60
	404210				3.59
	446157	BE270828	Hs.131740	Homo sapiens cDNA: FLJ22562 fis, clone H	3.59
	437587	AI591222	Hs.122421	Human DNA sequence from clone RP1-187J11	3.58
20	423147	AA987927	Hs.131740	Homo sapiens cDNA: FLJ22562 fis, clone H	3.57
	452226	AA024898	Hs.298002	ESTs	3.56
	443775	AF281664	Hs.204732	matrix metalloproteinase 26	3.56
	452501	AB037781	Hs.29718	hypothetical protein FLJ10980	3.56
	428647	AA830050	Hs.124344	ESTs	3.56
25	422443	NM_014707	Hs.116753	histone deacetylase 7B	3.55
	447966	AA340605	Hs.105887	ESTs, Weakly similar to Homolog of rat Z	3.55
	420892	AW975076	Hs.172589	nuclear phosphoprotein similar to S. cer	3.55
	420230	AL034344	Hs.288020	forkhead box C1	3.55
	418428	Y12490	Hs.85092	thyroid hormone receptor interactor 11	3.54
30	428949	AA442153	Hs.104744	hypothetical protein DKFZp434J0617	3.54
	444929	AI685841	Hs.161354	ESTs	3.54
	433339	AF018226	Hs.8038	glioblastoma overexpressed	3.54
	424369	R87622	Hs.26714	KIAA1831 protein	3.54
	433002	AF048730	Hs.279908	cyclin T1	3.53
35	435425	H18263	Hs.31418	ESTs	3.53
	415621	AI648602	Hs.131189	ESTs	3.53
	416974	AF010233	Hs.80667	RALBP1 associated Eps domain containing	3.53
	405793				3.52
	409770	AW498536		gb:U1-HF-BR0p-ajl-o-12-0-ULr1 NIH_MGC_5	3.52
40	425305	AA363025	Hs.155572	Human clone 23801 mRNA sequence	3.52
	428939	AW236550	Hs.131814	ESTs	3.52
	438388	AA806349	Hs.44698	ESTs	3.52
	443703	AV646177	Hs.213021	ESTs	3.52
	457940	AL360159	Hs.30445	Homo sapiens TRIPartite motif protein ps	3.52
45	402444				3.52
	409643	AW450866	Hs.257359	ESTs	3.51
	418250	U29926	Hs.83918	adenosine monophosphate deaminase (isofo	3.51
	432745	AI821826	Hs.269507	gbm178f05.x5 NCL CGAP_Pr3 Homo sapiens	3.51
	414222	AL135173	Hs.878	sorbitol dehydrogenase	3.51
50	430061	AB037817	Hs.230188	KIAA1386 protein	3.51
	421491	H99999	Hs.42738	ESTs	3.50
	422384	AA224077	Hs.42438	Sm protein F	3.50
	434565	T52172		ESTs	3.50
	438379	N23018	Hs.171391	C-terminal binding protein 2	3.50
55	439741	BE378646	Hs.6904	Homo sapiens mRNA full length insert cDN	3.50
	447311	R37010	Hs.33417	Homo sapiens cDNA: FLJ22806 fis, clone K	3.50
	447805	AW627832	Hs.19614	gemin4	3.50
	454265	H03556	Hs.300849	ESTs, Weakly similar to thyroid hormone	3.50
	418838	AW385224	Hs.35198	ectonucleotide pyrophosphatase/phosphodi	3.50
60	448904	AW512213	Hs.42500	ADP-ribosylation factor-like 5	3.50
	408617	BE003760	Hs.55209	Homo sapiens mRNA; cDNA DKFZp434K0514 (f	3.49
	434075	AW003418	Hs.160804	ESTs	3.49
	444190	AI878918	Hs.10526	cysteine and glycine-rich protein 2	3.49
	435017	AA336522	Hs.12854	angiotensin II, type I receptor-associat	3.48
65	423445	NM_014324	Hs.128749	alpha-methylacyl-CoA racemase	3.48
	420271	AI954365	Hs.42892	ESTs	3.48
	443684	AI681307	Hs.166674	ESTs	3.48
	444168	AW379879		gb:RC1-HT0256-081199-011-101 HT0256 Homo	3.48
	446074	AA079799	Hs.28263	hypothetical protein FLJ11898	3.48

	452582	AL137407	Hs.29911	Homo sapiens mRNA; cDNA DKFZp434M232 (tr	3.48
	431542	H63010	Hs.5740	ESTs	3.48
	432697	AW975050	Hs.293892	ESTs, Weakly similar to ALU4_HUMAN ALU S	3.48
5	435572	AW975339	Hs.239828	ESTs, Weakly similar to GAG2_HUMAN RETRO	3.47
	407192	AA609200		gbaf12a02.s1 Soares_testis_NHT Homo sap	3.47
	413435	X51405	Hs.75380	carboxypeptidase E	3.46
	447210	AF035269	Hs.17752	phosphatidylserine-specific phospholipase	3.46
	447958	AW796524	Hs.58644	Homo sapiens microsomal signal peptidase	3.46
	425312	AA354940	Hs.145958	ESTs	3.46
10	442007	AA301118	Hs.142838	nucleolar phosphoprotein Nopp34	3.46
	417455	AW007066	Hs.18949	ESTs, Weakly similar to CA2B_HUMAN COLLA	3.45
	426931	NM_003416	Hs.2078	zinc finger protein 7 (KOX 4, clone HF.1	3.45
	408739	W01556	Hs.238797	ESTs, Moderately similar to I38022 hypot	3.45
	436024	AI800041	Hs.180555	ESTs	3.45
15	408418	AW963897	Hs.44743	KIAA1435 protein	3.45
	409151	AA306105	Hs.50785	SEC22, vesicle trafficking protein (S. c	3.44
	418626	AW289508	Hs.135230	ESTs	3.44
	420560	AW207748	Hs.59115	ESTs	3.44
	420686	AI850339	Hs.40782	ESTs	3.44
20	428870	AA436631	Hs.36049	ESTs	3.44
	436754	AI061288	Hs.133437	ESTs	3.44
	437860	AI669586	Hs.222194	ESTs	3.44
	452300	AW628045	Hs.28896	Homo sapiens mRNA full length insert cDN	3.44
25	421887	AW161450	Hs.109201	CGI-86 protein	3.44

TABLE 5A shows the accession numbers for those primekeys lacking a unigeneID in Tables 5, 6, and 7. For each probeset we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

Pkey: CAT number: Accession:	Unique Eos probeset identifier number	
	Gene cluster number	Genbank accession numbers
Pkey	CAT number	Accession
407596	1003489_1	R86913 R86901 H25352 R01370 H43764 AW044451 W21298
408432	1058667_1	AW195262 R27888 AW811262
409752	115301_1	AW963990 AA078186 AW749482 AA077468 BE151571 AA376917
409770	1154048_1	AW499536 AW499553 AW502138 AW499537 AW502136 AW501743
411440	124577_1	AW749402 AW749403 Z45743 R80376 AA093358
411479	1247077_1	AW848047 AW848202 AW848631 AW848142 AW848702 AW848121 AW848632 AW848140 AW848571
		AW848009 AW848067 AW848069 AW848905 AW848214
411624	1252166_1	BE145964 BE146286 AW854564
412991	134248_1	AW949013 AA126111
414269	143133_1	AA298489 AA137165
415123	1523390_1	D60925 D60828 D80767
415715	1548818_1	F30364 F36559 T15435
416288	1585983_1	H51299 H44619 H46391 R86024 H51892 T72744
416289	1586037_1	W26333 R05358 H44682
417730	1695795_1	Z44761 R25801 R11926 R35604
418636	177402_1	AW749855 AA225995 AW750208 AW750206
419348	184129_1	AI830417 AA236612
419536	185688_1	AA603305 AA244095 AA244183
420111	190755_1	AA255652 AA280911 AW967920 AA262684
422219	213547_1	AW978073 AW978072 AA807550 AA306567
424179	236389_1	F30712 F35665 AW263888 AI904014 AI904018 AA336927 AA336502
424242	237181_1	AA337476 AW966227 AA450376 AW960222 AA381051
428002	285602_1	AA418703 AA418711 BE071915 BE071920 BE071912
429163	300543_1	AA884766 AW974271 AA592975 AA447312
432189	342819_1	AA527941 AI810608 AI620190 AA635266
432340	345248_1	AA534222 AA632632 T81234
432363	345469_1	AA534489 AW970240 AW970323
432968	356839_1	AA650114 AW974148 AA572946
433586	370470_1	T85301 AW517087 AA601054 BE073959
433641	37186_1	AF080229 AF080231 AF080230 AF080232 AF080233 AF080234 BE550633 AI636743 AW614951 BE467547
		AI680833 AI633818 N29988 U87592 U87593 U87590 U87591 S48404 U87587 AA463992 AW206802 AI970376
		AI583718 AI672574 N25695 AW665466 AI818326 AA126128 AI480345 AW013827 AA248638 AI214968
		AA204735 AA207155 AA206262 AA204833 AW003247 AW496808 AI080480 AI631703 AI651023 AI867418
		AW818140 AA502500 AI206199 AI871282 AI352545 BE501030 AI652535 BE485762 AA206331 AW451866
		AA471088 AA206342 AA204834 AA206100 AW021661 AA332922 N66048 AA703396 H92278 AW139734
		H92683 U87589 U87595 H69001 U87594 BE466420 AI624817 BE466611 AI206344 AA574397 AA348354
		AI493192
433687	373061_1	AA743991 AA804852 AW272737
433891	376239_1	AA613792 AW182329 T05304 AW858385
434415	385931_1	BE177494 AW276909 AA632849
434565	38898_1	T52172 AF147324 T52248
434804	393481_1	AA649530 AA659316 H64973
437113	433234_1	AA744693 AW750059
444168	593829_1	AW379879 AI126285 H12014
448212	755089_1	AI475858 AW969013
448310	757918_1	AI480316 AW847535
451746	883303_1	M86178 AI813822 D56893

452560	922216_1	BE077084 AW139963 AW863127 AW806209 AW806204 AW806205 AW806206 AW806211 AW806212 AW806207 AW806208 AW806210 AI907497
452712	928309_1	AW838616 AW838660 BE144343 AI914520 AW888910 BE184854 BE184784
453773	980699_1	AL133761 AL133767
5 455278	1272541_1	BE176479 BE176678 BE176357 BE176550 AW886079 BE176676 BE176615 BE176555 BE176489 BE176610 BE176362
455309	1278153_1	AW894017 AW893956 AW894032

TABLE 5B shows the genomic positioning for those primekeys lacking unigene ID's and accession numbers in Tables 5, 6, and 7. For each predicted exon, we have listed the genomic sequence source used for prediction. Nucleotide locations of each predicted exon are also listed.

10	Pkey:	Unique number corresponding to an Eos probeset		
	Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1989) 402:489-495.		
	Strand:	Indicates DNA strand from which exons were predicted.		
	Nt_position:	Indicates nucleotide positions of predicted exons.		
15				
	Pkey	Ref	Strand	Nt_position
20	401045	8117619	Plus	90044-60184,91111-91345
	401424	8176894	Plus	24223-24428
	401451	6634068	Minus	119926-121272
	401714	6715702	Plus	96484-66681
	401747	9789672	Minus	118596-118816,119119-119244,119609-119761,120422-120990,130161-130381,130468-130593,131097-131258,131866-131932,132451-132575,133580-134011
25	401785	7249180	Minus	165776-165996,166189-166314,166408-166569,167112-167268,167387-167469,168634-168842
	401819	7467933	Minus	28217-28488
	402408	9796239	Minus	110326-110491
	402444	9796614	Plus	28391-28517
	402791	6137008	Minus	51038-51207
30	403047	3540153	Minus	59793-59968
	403137	9211494	Minus	92349-92572,92958-93084,93579-93712,93949-94072,94591-94748,95214-95337
	403721	7528046	Minus	156847-157366
	403764	7717105	Minus	118692-118853
	403797	8099896	Minus	123065-125008
35	404165	9826489	Minus	69025-69128
	404210	5006246	Plus	169926-170121
	404253	9367202	Minus	55675-56055
	404561	9795980	Minus	69039-70100
	404571	7249169	Minus	112450-112848
40	404721	9856648	Minus	173763-174294
	404915	7341766	Minus	100915-101087
	404939	6862697	Plus	175318-175478
	405403	6850244	Minus	37491-37670,40951-41031
	405685	4508129	Minus	37956-38097
45	405718	9795467	Plus	113080-113266
	405783	1405887	Minus	89197-89453
	405876	6758747	Plus	39694-40031
	405917	7712162	Minus	106829-107213
	406414	9256407	Plus	49593-49850
50	406554	7711566	Plus	106956-107121

TABLE 6:286 GENES ENCODING EXTRACELLULAR OR CELL SURFACE PROTEINS UP-REGULATED IN PROSTATE CANCER COMPARED TO NORMAL ADULT TISSUES

Table 6 shows 286 genes up-regulated in prostate cancer compared to normal adult tissues that are likely to be extracellular or cell-surface proteins. These were selected as for Table 5 and the predicted protein contained a structural domain that is indicative of extracellular localization (e.g. egf, 7tm domains).

	Pkey: ExAccn: UnigeneID: Unigene Title: R1:	Unique Eos probeset Identifier number Exemplar Accession number, Genbank accession number Unigene number Unigene gene title Ratio of tumor to normal tissue			
10	Pkey	ExAccn	UnigeneID	Unigene Title	R1
	409361	NM_005982	Hs.54416	sine oculis homeobox (Drosophila) homolo	48.28
	409731	AA125985	Hs.56145	thymosin, beta, identified in neuroblast	45.24
	400298	AA032279	Hs.61635	six transmembrane epithelial antigen of	43.48
15	420154	AI093155	Hs.95420	JM27 protein	41.12
	426747	AA535210	Hs.171995	kallikrein 3, (prostate specific antigen	31.80
	400289	X07730	Hs.171995	kallikrein 3, (prostate specific antigen	24.91
	425075	AA506324	Hs.1852	acid phosphatase, prostate	24.23
	424846	AU077324	Hs.1832	neuropeptide Y	23.57
20	405685				20.80
	420757	X78592	Hs.99915	androgen receptor (dihydrotestosterone r	19.72
	418994	AA296520	Hs.89546	selectin E (endothelial adhesion molecul	19.56
	452782	AB037765	Hs.30652	KIAA1344 protein	17.39
	445472	AB006631	Hs.12784	Homo sapiens mRNA for KIAA0293 gene, par	17.00
25	414565	AA502972	Hs.183390	hypothetical protein FLJ13590	16.82
	431716	D89053	Hs.268012	fatty-acid-Coenzyme A ligase, long-chain	16.60
	408430	S78976	Hs.44926	dipeptidylpeptidase IV (CD26, adenosine	16.28
	408000	L11690	Hs.620	bulbous pemphigoid antigen 1 (230/240kD)	15.54
	430226	BE245562	Hs.2551	adrenergic, beta-2-, receptor, surface	15.40
30	444484	AK002126	Hs.11260	hypothetical protein FLJ11264	14.76
	418601	AA279490	Hs.86368	calmeglin	14.56
	448999	AF179274	Hs.22791	transmembrane protein with EGF-like and	14.55
	416182	NM_004354	Hs.79069	cyclin G2	12.94
	420544	AA677577	Hs.98732	Homo sapiens Chromosome 16 BAC clone CIT	12.79
35	445413	AA151342	Hs.12677	CGI-147 protein	12.64
	453930	AA419466	Hs.36727	hypothetical protein FLJ10903	12.22
	440286	U28589	Hs.7138	cholinergic receptor, muscarinic 3	12.04
	452784	BE463857	Hs.151258	hypothetical protein FLJ21062	11.86
	450203	AF097994	Hs.301528	L-tryptophan/alpha-aminoadipate aminotra	11.68
40	448045	AJ297436	Hs.20166	prostate stem cell antigen	11.51
	449650	AF055575	Hs.23838	calcium channel, voltage-dependent, L ty	11.18
	420381	D50640	Hs.337616	phosphodiesterase 3B, cGMP-inhibited	11.10
	425665	AK001050	Hs.159066	hypothetical protein FLJ10188	11.08
	425710	AF030880	Hs.159275	solute carrier family, member 4	11.08
45	428728	NM_016625	Hs.191381	hypothetical protein	11.04
	407021	U52077		gbHuman mariner1 transposase gene, comp	11.02
	410733	D84284	Hs.66052	CD38 antigen (p45)	11.02
	452340	NM_002202	Hs.505	ISL1 transcription factor, LIM/homeodoma	10.85
	428819	AL135623	Hs.193914	KIAA0575 gene product	10.48
50	421991	NM_014918	Hs.110488	KIAA0990 protein	10.04
	431217	NM_013427	Hs.250830	Rho GTPase activating protein 6	9.75
	421470	R27498	Hs.1378	annexin A3	9.64
	409282	AK000631	Hs.52256	hypothetical protein FLJ20624	9.45
	435980	AF274571	Hs.129142	deoxyribonuclease II beta	9.24
55	421246	AW582962	Hs.102897	CGI-47 protein	9.20
	410001	AB041036	Hs.57771	kallikrein 11	9.03
	441791	AW372449	Hs.175982	hypothetical protein FLJ21159	9.02

	404571				8.68
	456497	AW967956	Hs.123648	ESTs, Weakly similar to AF108460 1 ubinu	8.58
	418968	X04430	Hs.93913	Interleukin 6 (interferon, beta 2)	8.36
	433172	AB037841	Hs.102652	hypothetical protein ASH1	8.30
5	422631	BE218919	Hs.118793	hypothetical protein FLJ10688	8.27
	427674	NM_003528	Hs.2178	H2B histone family, member Q	8.20
	404915				8.08
	452259	AA317439	Hs.28707	signal sequence receptor, gamma (transio	8.06
	452891	N75582	Hs.212875	ESTs, Weakly similar to DYH9_HUMAN CILIA	8.02
10	439731	A1953135	Hs.45140	hypothetical protein FLJ14084	7.98
	419839	U24577	Hs.93304	phospholipase A2, group VII (platelet-ac	7.68
	420120	AL049610	Hs.95243	transcription elongation factor A (SII)-	7.64
	424099	AF071202	Hs.139336	ATP-binding cassette, sub-family C (CFTR	7.64
	448706	AW291095	Hs.21814	interleukin 20 receptor, alpha	7.52
15	410227	AB009284	Hs.61152	exostoses (multiple)-like 2	7.49
	425211	M18667	Hs.1867	progastricsin (pepsinogen C)	7.35
	441736	AW292779	Hs.169799	ESTs	7.28
	419991	AJ000098	Hs.94210	eyes absent (Drosophila) homolog 1	7.20
	425018	BE245277	Hs.154196	E4F transcription factor 1	7.20
20	424580	AA158727	Hs.150555	protein predicted by clone 23733	7.18
	409110	AA181493	Hs.48778	riban protein	7.10
	421566	NM_000399	Hs.1395	early growth response 2 (Krox-20 (Drosop	7.04
	431725	X65724	Hs.2839	Norris disease (pseudoglioma)	6.98
	425782	U66468	Hs.159525	cell growth regulatory with EF-hand doma	6.85
25	427408	AA583206	Hs.2158	RAR-related orphan receptor A	6.79
	435604	AA625279	Hs.26882	uncharacterized bone marrow protein BMO4	6.73
	415874	AF091622	Hs.78893	KIAA0244 protein	6.54
	401451				6.52
	431778	AL080276	Hs.268562	regulator of G-protein signalling 17	6.51
30	409089	NM_014781	Hs.50421	KIAA0203 gene product	6.50
	431992	NM_002742	Hs.2891	protein kinase C, mu	6.49
	404253				6.42
	421552	AF026692	Hs.105700	secreted frizzled-related protein 4	6.41
	418806	NM_000288	Hs.79993	peroxisomal biogenesis factor 7	6.38
35	431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta	6.30
	439366	AF100143	Hs.6540	fibroblast growth factor 13	6.30
	416836	D54745	Hs.80247	cholecystokinin	6.30
	433383	AF034837	Hs.192731	double-stranded RNA specific adenosine d	6.29
	450728	AW162923	Hs.25363	presenilin 2 (Alzheimer disease 4)	6.25
40	413384	NM_000401	Hs.75334	exostoses (multiple) 2	6.22
	423349	AF010258	Hs.127428	homeo box A9	6.20
	424800	AL035588	Hs.153203	MyoD family inhibitor	6.18
	425451	AF242769	Hs.157461	mesenchymal stem cell protein DSC54	6.14
	447359	NM_012093	Hs.18268	adenylate kinase 5	6.00
45	410889	X91682	Hs.66744	twist (Drosophila) homolog (acrocephalos	5.97
	408829	NM_006042	Hs.48384	heparan sulfate (glucosamine) 3-O-sulfot	5.84
	453911	AW503857	Hs.4007	Sarcolemmal-associated protein	5.94
	408875	NM_015434	Hs.48604	DKFZP434B168 protein	5.82
	450480	X82125	Hs.25040	zinc finger protein 239	5.90
50	451684	AF216751	Hs.26813	CDA14	5.88
	400301	X03835	Hs.1657	estrogen receptor 1	5.78
	415077	L41807	Hs.934	glucosaminyl (N-acetyl) transferase 2, I	5.74
	418852	BE537037	Hs.273294	hypothetical protein FLJ20069	5.72
	448867	AB007891	Hs.16349	KIAA0431 protein	5.72
55	410232	AW372451	Hs.61184	CGI-79 protein	5.70
	422762	AL031320	Hs.118976	Human DNA sequence from clone RP1-20N2 o	5.70
	450616	AL133067	Hs.302689	hypothetical protein	5.70
	408621	A1970672	Hs.46638	chromosome 11 open reading frame 8	5.65
	439671	AW162840	Hs.6641	kinesin family member 5C	5.64
60	410196	A1936442	Hs.59838	hypothetical protein FLJ10808	5.60
	429170	NM_001394	Hs.2358	dual specificity phosphatase 4	5.60
	440738	A1004650	Hs.225674	WD repeat domain 9	5.60
	414342	AA742181	Hs.75912	KIAA0257 protein	5.59
	422634	NM_016010	Hs.118821	CGI-62 protein	5.56
65	400268				5.55
	439569	AW602166	Hs.222399	CEGP1 protein	5.51
	452823	AB012124	Hs.30696	transcription factor-like 5 (basic helix	5.48
	431938	AA838471	Hs.54431	specific granule protein (28 kDa); cyste	5.44
	427638	AA406411	Hs.208341	ESTs, Weakly similar to KIAA0989 protein	5.42

5	421264	AL039123	Hs.103042	microtubule-associated protein 1B	5.38
	421685	AF189723	Hs.106778	ATPase, Ca++ transporting, type 2C, memb	5.37
	421987	AI133161	Hs.286131	CGI-101 protein	5.36
	422806	BE314767	Hs.1581	glutathione S-transferase theta 2	5.34
	432281	AK001239	Hs.274263	hypothetical protein FLJ10377	5.32
	451982	F13036	Hs.27373	Homo sapiens mRNA; cDNA DKFZp564O1763 (I	5.32
	444042	NM_004915	Hs.10237	ATP-binding cassette, sub-family G (WHIT	5.31
	447752	M73700	Hs.105938	lactotransferrin	5.29
	451418	BE387790	Hs.26369	hypothetical protein FLJ20287	5.22
10	428593	AW207440	Hs.185973	degenerative spermatocyte (homolog Dros	5.21
	447541	AK000288	Hs.18800	hypothetical protein FLJ20281	5.18
	459294	AW877286	Hs.17428	RBP1-like protein	5.16
	424692	AA429834	Hs.151791	KIAA0092 gene product	5.15
15	416434	AW163045	Hs.79334	nuclear factor, interleukin 3 regulated	5.11
	410268	AA316181	Hs.61635	six transmembrane epithelial antigen of	5.10
	417517	AF001176	Hs.82238	POP4 (processing of precursor, S. cerev	5.10
	453616	NM_003462	Hs.33846	dynein, axonemal, light intermediate pol	5.10
	427958	AA418000	Hs.98280	potassium intermediate/small conductance	5.09
20	407945	X69208	Hs.606	ATPase, Cu++ transporting, alpha polypep	5.08
	418578	AW868159	Hs.289104	Alu-binding protein with zinc finger dom	5.05
	413328	Y15723	Hs.75295	guanylate cyclase 1, soluble, alpha 3	5.04
	432729	AK000292	Hs.278732	hypothetical protein FLJ20285	5.04
	426342	AF093419	Hs.169378	multiple PDZ domain protein	5.02
25	429782	NM_005754	Hs.220589	Ras-GTPase-activating protein SH3-domain	5.02
	436209	AW850417	Hs.254020	ESTs, Moderately similar to unnamed prot	5.02
	430599	NM_004855	Hs.247118	phosphatidylinositol glycan, class B	5.00
	451386	AB029006	Hs.26334	spastic paraplegia 4 (autosomal dominant	5.00
	457211	AW972565	Hs.32399	ESTs, Weakly similar to S51797 vasodilat	4.97
30	425851	NM_001490	Hs.159642	glucosaminyl (N-acetyl) transferase 1, c	4.97
	421689	N87820	Hs.106826	KIAA1696 protein	4.93
	416533	BE244053	Hs.79362	retinoblastoma-like 2 (p130)	4.92
	432653	N62096	Hs.293185	ESTs, Weakly similar to JC7328 amino ac	4.91
	403047				4.91
35	431117	AF003522	Hs.250500	delta (Drosophila)-like 1	4.90
	427617	D42063	Hs.199179	RAN binding protein 2	4.88
	428804	AK000713	Hs.193736	hypothetical protein FLJ20706	4.88
	449071	NM_005872	Hs.22960	breast carcinoma amplified sequence 2	4.88
	407596	R66913		gb.yq30f05.r1 Soares fetal liver spleen	4.84
40	456516	BE172704	Hs.222746	KIAA1610 protein	4.84
	458339	AW976853	Hs.172843	ESTs	4.83
	422083	NM_001141	Hs.111258	arachidonate 15-lipoxygenase, second typ	4.82
	449535	W15267	Hs.23672	low density lipoprotein receptor-related	4.82
	422048	NM_012445	Hs.288128	spondin 2, extracellular matrix protein	4.82
	424602	AK002055	Hs.151048	hypothetical protein FLJ11193	4.78
45	410765	AI694972	Hs.66180	nucleosome assembly protein 1-like 2	4.77
	419879	Z17805	Hs.93564	Homer, neuronal immediate early gene, 2	4.74
	450649	NM_001429	Hs.25272	E1A binding protein p300	4.74
	411624	BE145964	Hs.103283	KIAA0594 protein	4.72
	404721				4.70
50	426261	AW242243	Hs.168670	peroxisomal farnesylated protein	4.70
	416276	U41060	Hs.79136	LIV-1 protein, estrogen regulated	4.64
	408374	AW025430	Hs.155591	forkhead box F1	4.64
	451900	AB023199	Hs.27207	KIAA0982 protein	4.63
55	421437	AW821252	Hs.104336	hypothetical protein	4.63
	434629	AA789081	Hs.4029	glioma-amplified sequence-41	4.60
	403764				4.58
	421247	BE391727	Hs.102910	general transcription factor IIH, polype	4.53
	403721				4.50
60	453070	AK001465	Hs.31575	SEC63, endoplasmic reticulum translocon	4.49
	417412	X16896	Hs.82112	interleukin 1 receptor, type I	4.48
	439735	AI635386	Hs.142848	hypothetical protein	4.48
	430261	AA305127	Hs.237225	hypothetical protein HT023	4.46
	430598	AK001764	Hs.247112	hypothetical protein FLJ10902	4.44
65	400303	AA242758	Hs.79136	LIV-1 protein, estrogen regulated	4.42
	438209	AL120659	Hs.6111	aryl-hydrocarbon receptor nuclear trans	4.42
	417421	AL138201	Hs.82120	nuclear receptor subfamily 4, group A, m	4.40
	447270	AC002551	Hs.331	general transcription factor IIIC, polyp	4.38
	434423	NM_006769	Hs.3844	LIM domain only 4	4.35
	404561				4.32

5	422869	AA782538	Hs.122647	N-myristoyltransferase 2	4.32
	423685	BE350484	Hs.49753	uveal autoantigen with coiled coil domain	4.32
	425071	NM_013989	Hs.154424	deiodinase, iodothyronine, type II	4.32
	431583	AL042613	Hs.262476	S-adenosylmethionine decarboxylase 1	4.31
	442818	AK001741	Hs.8739	hypothetical protein FLJ10879	4.30
	423740	Y07701	Hs.293007	aminopeptidase puromycin sensitive	4.24
	424701	NM_005923	Hs.151988	mitogen-activated protein kinase kinase	4.21
	424085	NM_002914	Hs.139226	replication factor C (activator 1) 2 (40	4.20
10	410294	AB014515	Hs.323712	KIAA0615 gene product	4.18
	447124	AW976438	Hs.17428	RBP1-like protein	4.18
	438018	AK001160	Hs.5999	hypothetical protein FLJ10298	4.16
	443857	AF089292	Hs.287621	hypothetical protein FLJ14069	4.15
	446711	AF169682	Hs.12450	protocadherin 9	4.15
	405403				4.14
15	448148	NM_016578	Hs.20509	HBV pX associated protein-8	4.13
	417531	NM_003157	Hs.1087	serine/threonine kinase 2	4.12
	433345	AF681545	Hs.152982	hypothetical protein FLJ13117	4.10
	432712	AB016247	Hs.269031	sterol-C5-desaturase (fungal ERG3, delta	4.09
	435114	AA776483	Hs.288936	mitochondrial ribosomal protein L9	4.08
20	445459	AF78629	Hs.158465	likely ortholog of mouse putative IKK re	4.08
	402791				4.04
	438860	U95740	Hs.6349	Homo sapiens, clone IMAGE:3010668, mRNA,	4.04
	447568	AF155655	Hs.18885	CGI-118 protein	4.04
25	452211	AF85513	Hs.233420	ESTs	4.02
	443292	AK000213	Hs.9196	hypothetical protein	4.01
	420911	U77413	Hs.100293	O-linked N-acetylglucosamine (GlcNAc) tr	4.00
	428738	NM_000380	Hs.192803	xeroderma pigmentosum, complementation g	3.95
	430458	AA314998	Hs.241503	hypothetical protein	3.95
30	437531	AF00752	Hs.112259	T cell receptor gamma locus	3.93
	428695	AF355647	Hs.189999	purinergic receptor (family A group 5)	3.91
	410011	AB020641	Hs.57856	PFTAIR protein kinase 1	3.91
	446494	AA463276	Hs.288906	WW Domain-Containing Gene	3.91
	409928	AL137163	Hs.57549	hypothetical protein dJ473B4	3.90
	411598	BE336654	Hs.70937	H3 histone family, member A	3.90
35	425707	AF115402	Hs.11713	E74-like factor 5 (ets domain transcript	3.90
	451806	NM_003729	Hs.27076	RNA 3'-terminal phosphate cyclase	3.89
	401045				3.89
	437372	AA323968	Hs.283631	hypothetical protein DKFZp547G183	3.89
40	417067	AJ001417	Hs.81086	solute carrier family 22 (extraneuronal	3.88
	410487	AF102546	Hs.63931	dachshund (Drosophila) homolog	3.88
	431930	AB035301	Hs.272211	cadherin 7, type 2	3.88
	453047	AW023798	Hs.286025	ESTs	3.88
	401785				3.88
45	458229	AF29602	Hs.177	phosphatidylinositol glycan, class H	3.88
	406414				3.86
	412494	AL133900	Hs.792	ADP-ribosylation factor domain protein 1	3.84
	418329	AW247430	Hs.84152	cystathionine-beta-synthase	3.83
	424850	AA151057	Hs.153498	chromosome 18 open reading frame 1	3.82
50	427585	D31152	Hs.179729	collagen, type X, alpha 1 (Schmid metaph	3.82
	423052	M28214	Hs.123072	RAB3B, member RAS oncogene family	3.82
	416111	AA033813	Hs.79018	chromatin assembly factor 1, subunit A (3.82
	419423	D26488	Hs.90315	KIAA0007 protein	3.80
	428643	AA455889	Hs.167279	FYVE-finger-containing Rab5 effector pro	3.80
55	431499	NM_001514	Hs.258561	general transcription factor IIB	3.80
	444078	BE246919	Hs.10280	U5 snRNP-specific 40 kDa protein (hPrp8-	3.78
	430291	AV660345	Hs.238128	CGI-49 protein	3.76
	431637	AF79330	Hs.265960	hypothetical protein FLJ10563	3.74
	440411	N30256	Hs.151093	hypothetical protein DKFZp434G1415	3.74
60	405917				3.74
	451230	BE546208	Hs.26090	hypothetical protein FLJ20272	3.73
	429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase doma	3.73
	415075	L27479	Hs.77889	Friedreich ataxia region gene X123	3.72
	440351	AF030933	Hs.7179	RAD1 (S. pombe) homolog	3.70
65	443603	BE502601	Hs.134289	ESTs, Weakly similar to KIAA1063 protein	3.70
	446965	BE242873	Hs.16677	WD repeat domain 15	3.70
	412350	AF659306	Hs.73826	protein tyrosine phosphatase, non-recept	3.70
	433852	AF78329	Hs.126829	ESTs	3.70
	447397	BE247676	Hs.18442	E-1 enzyme	3.68
	405718				3.68

	425217	AU076696	Hs.155174	CDC5 (cell division cycle 5, <i>S. pombe</i> , h	3.88
	421734	AI318624	Hs.107444	Homo sapiens cDNA FLJ20582 fis, clone KA	3.87
	427221	L15409	Hs.174007	von Hippel-Lindau syndrome	3.87
	402408				3.88
5	452848	X95425	Hs.31092	EphA5	3.68
	419078	M93119	Hs.89584	insulinoma-associated 1	3.68
	427144	X95087	Hs.2126	vasoactive intestinal peptide receptor 2	3.65
	423396	AI382555	Hs.127850	bromodomain-containing 1	3.65
	448320	AF126245	Hs.14781	acyl-Coenzyme A dehydrogenase family, me	3.63
10	404939				3.62
	403137				3.60
	437162	AW005505	Hs.5464	thyroid hormone receptor coactivating pr	3.60
	404210				3.59
	443775	AF291664	Hs.204732	matrix metalloproteinase 26	3.58
15	452501	AB037791	Hs.29716	hypothetical protein FLJ10980	3.58
	422443	NM_014707	Hs.116753	histone deacetylase 7B	3.55
	420230	AL034344	Hs.284188	forkhead box C1	3.55
	418428	Y12490	Hs.85092	thyroid hormone receptor interactor 11	3.54
	433002	AF048730	Hs.279908	cyclin T1	3.53
20	405783				3.52
	457940	AL360159	Hs.306517	Homo sapiens TRipartite motif protein ps	3.52
	402444				3.52
	418250	U29926	Hs.83918	adenosine monophosphate deaminase (iso	3.51
	414222	AL135173	Hs.878	sorbitol dehydrogenase	3.51
25	422384	AA224077	Hs.42438	Sm protein F	3.50
	447805	AW627932	Hs.19614	gem1n4	3.50
	454265	H03558	Hs.300949	ESTs, Weakly similar to thyroid hormone	3.50
	423445	NM_014324	Hs.128749	alpha-methylacyl-CoA racemase	3.48
	413435	X51405	Hs.75360	carboxypeptidase E	3.46
30	447210	AF035269	Hs.17752	phosphatidylserine-specific phospholipas	3.48
	426931	NM_003418	Hs.2076	zinc finger protein 7 (KOX 4, clone HF.1	3.45
	408418	AW963897	Hs.44743	KIAA1435 protein	3.45
	421887	AW161450	Hs.109201	CGI-86 protein	3.44

Table 7: 42 GENES ENCODING SMALL MOLECULE TARGETS UP-REGULATED IN PROSTATE CANCER COMPARED TO NORMAL ADULT TISSUES

5 Table 7 shows 42 genes up-regulated in prostate cancer compared to normal adult tissues that are likely to be small molecule targets. These were selected as for Table 5 and the predicted protein contained a structural domain that is indicative of a drugable structure (e.g. protease, kinase, phosphatase, receptor). The functional domain is indicated for each gene.

10 Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigenelD: Unigene number
 Unigene Title: Unigene gene title
 PSDomain: Protein Structural Domain
 R1: Ratio of tumor vs. normal tissue

	Pkey	ExAccn	UnigenelD	Unigene Title	PSDomain	R1
20	426747	AA535210	Hs.171895	kallikrein 3, (prostate specific antigen	trypsin	31.80
	400299	X07730	Hs.171895	kallikrein 3, (prostate specific antigen	trypsin	24.91
	420757	X78592	Hs.99915	androgen receptor (dihydrotestosterone r	Androgen_recep,hormone_rec,zf-C4	19.72
	408430	S79876	Hs.44926	dipeptidylpeptidase IV (CD26, adenosine	DPPIV_N_term,Peptidase_S9	16.28
	430228	BE245562	Hs.2551	adrenergic, beta-2-, receptor, surface	7tm_1	15.40
25	411096	U80034	Hs.68583	mitochondrial intermediate peptidase	Peptidase_M3	14.81
	440288	U29589	Hs.7138	cholinergic receptor, muscarinic 3	7tm_1	12.04
	420381	D50640	Hs.337616	phosphodiesterase 3B, cGMP-inhibited	PDEase	11.10
	407021	U52077		gbHuman mariner1 transposase gene, comp	SET,Transposase_1	11.02
	401424				arginase	9.58
30	410001	AB041038	Hs.57771	kallikrein 11	trypsin	9.03
	428330	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin,	Peptidase_M10	8.76
	424099	AF071202	Hs.139336	ATP-binding cassette, sub-family C (CFTR	ABC_tran,ABC_membrane	7.64
	419991	AJ000098	Hs.94210	eyes absent (Drosophila) homolog 1	Hydrolase	7.20
	431892	NM_002742	Hs.2891	protein kinase C, mu	pkinase,DAQ_PE-bind,PH	6.49
35	447359	NM_012093	Hs.18268	adenylate kinase 5	adenylatekinase	6.00
	400301	X03635	Hs.1657	estrogen receptor 1	Oest_recep,zf-C4,hormone_rec	5.78
	421685	AF189723	Hs.106778	ATPase, Ca++ transporting, type 2C, memb	E1-E2_ATPase,Hydrolase	5.37
	444042	NM_004915	Hs.10237	ATP-binding cassette, sub-family G (WHIT	ABC_tran	5.31
	447752	M73700	Hs.105938	lactotransferrin	transferrin,7tm_1	5.29
40	407945	X69208	Hs.606	ATPase, Cu++ transporting, alpha polypep	E1-E2_ATPase,Hydrolase,HMA	5.08
	403047				trypsin	4.91
	427617	D42063	Hs.199179	RAN binding protein 2	Ran_BP1,zf-RanBP,TPR,pro_isomerase	4.88
	422083	NM_001141	Hs.111256	arachidonate 15-lipoxygenase, second typ	lipoxygenase,PLAT	4.82
	449535	W15267	Hs.23672	low density lipoprotein receptor-related	ldl_recept_b,ldl_recept_a,EGF	4.82
45	425071	NM_013989	Hs.154424	deiodinase, iodothyronine, type II	T4_deiodinase	4.32
	423740	Y07701	Hs.293007	aminopeptidase puromycin sensitive	Peptidase_M1	4.24
	424701	NM_005923	Hs.151988	mitogen-activated protein kinase kinase	pkinase	4.21
	424085	NM_002914	Hs.139226	replication factor C (activator 1) 2 (40	AAA,Viral_helicase1	4.20
	417531	NM_003157	Hs.1087	serine/threonine kinase 2	pkinase	4.12
50	428695	A355647	Hs.189999	purinergic receptor (family A group 5)	7tm_1	3.91
	410011	AB020641	Hs.57856	PFTAIR protein kinase 1	pkinase	3.91
	424850	AA151057	Hs.153498	chromosome 18 open reading frame 1	ldl_recept_a	3.82
	412350	AI658306	Hs.73826	protein tyrosine phosphatase, non-recept	Y_phosphatase,Band_41,PDZ	3.70
	447397	BE247676	Hs.18442	E-1 enzyme	Hydrolase	3.68
55	452948	X85425	Hs.31092	EphA5	EPH_bnd,fn3,pkinase,SAM	3.66
	427144	X85087	Hs.2128	vasoactive intestinal peptide receptor 2	7tm_2	3.65
	443775	AF291664	Hs.204732	matrix metalloproteinase 26	Peptidase_M10	3.56
	457940	AL380159	Hs.306517	Homo sapiens TRIPartite motif protein ps	SPRY,7tm_1	3.52
	418250	U29326	Hs.83918	adenosine monophosphate deaminase (isofo	A_deaminase	3.51
60	413435	X51405	Hs.75360	carboxypeptidase E	Zn_carbOpept	3.48
	447210	AF035269	Hs.17752	phosphatidylserine-specific phospholipas	lipase	3.48

TABLE 8: 136 GENES SIGNIFICANTLY DOWN-REGULATED IN PROSTATE CANCER COMPARED TO NORMAL PROSTATE

Table 8 shows 136 genes significantly down-regulated in prostate cancer compared to normal prostate. These were selected from 59680 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" normal prostate to "average" prostate cancer tissues was greater than or equal to 2. The "average" normal prostate level was set to the mean amongst 4 normal prostate tissues. The "average" prostate cancer level was set to the 85th percentile amongst 73 tumor samples. In order to remove gene-specific background levels of non-specific hybridization, the 10th percentile value amongst all the tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

Pkey:	Unique Eos probeset identifier number			
ExAccn:	Exemplar Accession number, Genbank accession number			
UnigeneID:	Unigene number			
Unigene Title:	Unigene gene title			
R1:	Ratio of normal prostate to prostate cancer			
Pkey	ExAccn	UnigeneID	Unigene Title	R1
425932	M81650	Hs.1968	semenogelin I	57.69
425545	N98529	Hs.158295	Human mRNA for myosin light chain 3 (MLC	19.70
426752	X69490	Hs.172004	titin	15.25
442082	R41823	Hs.7413	ESTs; calyntenin-2	10.05
407245	X90568	Hs.172004	titin	9.38
422711	D60641	Hs.21739	Homo sapiens mRNA; cDNA DKFZp586I1518 (I	9.05
420813	X51501	Hs.99949	prolactin-induced protein	8.18
411987	AA375975	Hs.183380	*ESTs, Moderately similar to ALU7_HUMAN	7.45
404567				5.62
416030	H15261	Hs.21948	ESTs	5.51
444892	AI620617	Hs.148565	ESTs	5.27
444573	AW043590	Hs.225023	ESTs	5.20
428068	AW016437	Hs.233462	ESTs	5.08
437440	AA846804	Hs.123694	ESTs	4.95
404113				4.75
452279	AA286844	Hs.61260	hypothetical protein FLJ13164	4.75
421058	AW297967	Hs.188181	ESTs	4.63
445592	AV654382	Hs.17947	*ESTs, Weakly similar to K02F3.10 [C.ele	4.53
405163				4.49
405227				4.45
454059	NM_003154	Hs.37048	statherin	4.45
450152	AI138635	Hs.22958	ESTs	4.40
407013	U35637		*gb:Human nebulin mRNA, partial cds	4.03
403612				4.02
440089	AA884468	Hs.135646	ESTs	4.00
408988	AL119844	Hs.49476	Homo sapiens clone TUA8 Cri-du-chat regi	3.98
436726	AA324975	Hs.128993	*ESTs, Weakly similar to KIAA0465 protei	3.95
459367	BE148877		*gb:CM4-HT0244-111189-040-h12 HT0244 Hom	3.95
427318	AF186081	Hs.175783	zinc transporter	3.92
411762	AW880972		*gb:QV0-CT0387-180300-167-h07 CT0387 Hom	3.85
418668	AW407987	Hs.87150	Human clone A9A2BR11 (CAC)n/(GTG)n repea	3.75
458311	AF069478		*gb:AF069478 Homo sapiens astrocytoma II	3.61
403849				3.60
419682	H13139	Hs.82282	paired-like homeodomain transcription fa	3.58
412519	AA198241	Hs.73980	*troponin T1, skeletal, slow	3.51
414206	AW276887	Hs.46609	ESTs	3.45
427419	NM_000200	Hs.177888	histatin 3	3.37
420777	AA280223	Hs.130865	ESTs	3.35
428134	AA421773	Hs.161008	ESTs	3.31
450218	R02018	Hs.188840	*Ank, mouse, homolog of	3.30
433474	AI192185	Hs.147174	*EST, Highly similar to ubiquitin-prote	3.30
418833	AW974899	Hs.292776	ESTs	3.26
400440	X83957	Hs.83870	nebulin	3.16

	413778	AA090235	Hs.75535	*myosin, light polypeptide 2, regulatory	3.08
	423151	AW838068		*gb:QV3-LT0048-010300-109-f02 LT0048 Hom	3.05
	445060	AA830811	Hs.88808	ESTs	2.98
	457065	AI476318	Hs.192480	ESTs	2.85
5	432458	H00093		*gb:ph8f12u_18/1TV Outward Alu-primed hn	2.92
	405678				2.85
	406707	S73840	Hs.931	*myosin, heavy polypeptide 2, skeletal m	2.81
	444105	AW189097	Hs.166597	ESTs	2.78
	433968	AL157518	Hs.90421	PRO2463 protein	2.73
10	438522	AA809431	Hs.258688	ESTs	2.73
	436562	H71937	Hs.169756	*complement component 1, s subcomponent	2.68
	412417	AA102268	Hs.42175	ESTs	2.67
	455590	BE072259		*gb:QV4-BT0536-271289-059-g04 BT0536 Hom	2.65
	415380	F07853	Hs.16085	putative G-protein coupled receptor	2.65
15	428729	AL162331	Hs.191436	hypothetical protein FLJ10619	2.64
	408537	AW207734		*gb:UH-HB12-age-h-01-0-UI.s1 NCI_CGAP_S	2.63
	424706	AA741336	Hs.152108	transcriptional unit N143	2.63
	413212	BE072092		*gb:PM4-BT0532-160200-003-b11 BT0532 Hom	2.63
	406704	M21665	Hs.929	*myosin, heavy polypeptide 7, cardiac mu	2.62
20	437507	AA758538	Hs.246682	ESTs	2.60
	410384	AI933794	Hs.42745	ESTs	2.58
	408074	R20723	Hs.124764	ESTs	2.58
	436653	AA828828	Hs.282402	ESTs	2.52
25	458090	AI282149	Hs.56213	*ESTs, Highly similar to FXD3_HUMAN FORK	2.51
	432003	AI589154	Hs.122972	ESTs	2.50
	436915	AA737400	Hs.142230	ESTs	2.50
	410028	AW576454	Hs.258553	ESTs	2.46
	448920	AW408009	Hs.22580	alkylglycerone phosphate synthase	2.45
	422046	AI638562		*gb:ts50a10.x1 NCI_CGAP_UI1 Homo sapiens	2.44
30	451122	AA015767	Hs.183587	ESTs	2.40
	422646	H87863	Hs.151380	ESTs	2.36
	451237	AW600293		*gb:EST00049 pGEM-T library Homo sapiens	2.36
	400001			AFFX control: BioB-3	2.36
	415935	Z45365		*gb:HSC2NFD81 normalized infant brain cD	2.36
35	439708	AW872527	Hs.59761	ESTs	2.36
	423341	AW242394	Hs.252495	ESTs	2.36
	436486	AA742221	Hs.120633	ESTs	2.35
	407449	AJ002784		gb:Homo sapiens mRNA; fetal brain cDNA 5	2.33
	430573	AA744550	Hs.136345	ESTs	2.32
40	401974				2.31
	443358	AL044498	Hs.133262	*ESTs, Weakly similar to PH0217 reverse	2.31
	430751	NM_012471	Hs.247668	transient receptor potential channel 5	2.25
	439128	AI949371	Hs.153089	ESTs	2.25
	448765	R15337	Hs.21958	*Homo sapiens cDNA FLJ10532 fis, clone N	2.25
45	451130	AI762250	Hs.211347	ESTs	2.24
	405420				2.23
	455029	AW851258		*gb:IL3-CT0220-160200-066-H08 CT0220 Hom	2.23
	438224	AA933999		*gb:con91f04.s1 Soares_NFL_T_GBC_S1 Homo	2.23
50	407764	BE008347		*gb:CM0-BN0154-080400-325-h04 BN0154 Hom	2.23
	413549	BE252470		*gb:601108292F1 NIH_MGC_16 Homo sapiens	2.23
	437010	AA741368	Hs.291434	ESTs	2.23
	435111	AI914279	Hs.213740	ESTs	2.22
	403375				2.21
	455060	AW853441		*gb:RC1-CT0252-030100-023-p09 CT0252 Hom	2.21
55	409792	AW854153		*gb:RC3-CT0254-060400-029-d03 CT0254 Hom	2.20
	421154	AA284333	Hs.287631	*Homo sapiens cDNA FLJ14269 fis, clone P	2.19
	401963				2.18
	435034	AF168711	Hs.159337	x 010 protein	2.18
	448998	AW998989	Hs.105749	KIAA0553 protein	2.18
60	436818	AW297599	Hs.255667	ESTs	2.17
	442252	AI733395	Hs.129124	ESTs	2.17
	419310	AA238233	Hs.188716	ESTs	2.16
	418579	H91800	Hs.124156	ESTs	2.16
	423315	R54109	Hs.26096	ESTs	2.16
65	432744	AA988835	Hs.38664	ESTs	2.15
	424492	AI133482	Hs.165210	ESTs	2.15
	424770	AA425582		*gb:zw46e05.r1 Soares_total_fetus_Nb2HF8	2.15
	437101	AA744518	Hs.120610	ESTs	2.15
	428793	AC004957	Hs.288975	*ESTs, Highly similar to collapsin-2-lik	2.15

	415708	H56475	"gb:yt87d11.r1 Soares_pineal_gland_N3HPG	2.13
	459619			2.12
	427506	AK000134	Hs.179100 hypothetical protein FLJ20127	2.12
	452508	AA804174	Hs.184354 ESTs	2.10
5	410881	AW809157	"gb:RCO-ST0118-041099-031-c07_1 ST0118 Homo sapiens cDNA, mRNA sequence"	2.10
	403087			2.10
	403869			2.10
	445028	D81194	Hs.282499 ESTs	2.10
	447884	H29505	"gb:ym60d10.r1 Soares Infant brain 1N1B Homo sapiens cDNA clone 5', mRNA sequence"	2.10
10	414575	H11257	Hs.295233 ESTs	2.09
	420351	BE218221	Hs.190044 ESTs	2.08
	426998	BE274360	"gb:601121068F1 NIH_MGC_20 Homo sapiens cDNA clone 5', mRNA sequence"	2.08
	405455			2.08
15	423843	AA332652	"gb:EST36627 Embryo, 8 week I Homo sapiens cDNA 5' end similar to similar to monomamine oxidase B, mRNA sequence"	2.08
	406135			2.07
	427046	BE246180	Hs.121385 ESTs	2.07
	403493			2.05
20	444514	Al682905	Hs.270431 "ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMILY J SEQUENCE CONTAMINATION WARNING ENTRY [H.sapiens]"	2.05
	435884	AA701443	Hs.192868 ESTs	2.05
	418629	AB020695	Hs.91662 KIAA0888 protein	2.03
	405900			2.03
	457350	AW974438	Hs.194136 "ESTs, Moderately similar to AF091457 1 zinc finger protein RIN ZF [R.norvegicus]"	2.02
25	400007		AFFX control: BioDn-5	2.01
	406978	M64358	"gb:Human rhom-3 gene, exon."	2.00

TABLE 8A shows the accession numbers for those primekeys lacking a unigeneID in Table 8. For each probeset we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

10	Pkey: CAT number: Accession:	Unique Eos probeset identifier number Gene cluster number Genbank accession numbers
<hr/>		
15	Pkey	CAT number Accessions
	407764	1014849_1 BE008347 BE008320 BE083307 BE083311 AW075968
	408537	1064753_1 AW207734 D60164 D81150 D81078 D61356 AW996804
	409792	1154677_1 AW854153 AW500210 BE145772 AW501310
20	410881	1225682_1 AW809157 AW812181 AW812175 AW812172 AW812161 AW812165
	411762	1256906_1 AW860972 AW862598 AW862599 AW860988 AW860983 AW860899 AW860925 AW860922 AW860986 AW860984 AW860989
	413212	1353792_1 BE072092 BE072106 BE072088 BE072098 BE072103
	413549	1375933_2 BE252470 BE147573
	415708	1548209_1 H56475 F29401 F34552
25	415835	1558511_1 Z45365 R25905 H05203 T77498
	422048	210744_1 AI638562 T16929 H13401 F07773 R55838
	423151	225415_1 AW838068 AW837986 AW838067 AA322487 AW837936
	423843	232510_1 AA332652 AA331633 AW999369 AW902993 BE170475 AA378845 AW964175 AI475221
	424770	243504_1 AA425582 AI880208 AA346646 N22655 AW811775 AW811786
30	426998	274259_-1 BE274360
	432456	347718_2 H00093 H00079 H00070 H00054 H00049 H00063 AW905306 AW905241 AW905410 AW905307 AW905411 AW905240
	AW905210	
		AW905352 AW905304 AW905239 AW905242 AW905243 H00087
35	438224	452856_1 AA933999 AA781181
	447884	740749_1 H29505 R18575 Z43580 T48738 AI435454 BE004683
	451237	863269_1 AW600293 AI787468
	455029	1249374_1 AW851258 AW851435 AW851106 AW851421
	455060	1251259_1 AW853441 BE145228 BE145218 BE145162 BE145283
	455590	1335127_1 BE072259 BE072230 BE007911
40	458311	543550_1 AF069478 AF069479 AF069480

TABLE 8B shows the genomic positioning for those primekeys lacking unigene ID's and accession numbers in table 8. For each predicted exon, we have listed the genomic sequence source used for prediction. Nucleotide locations of each predicted exon are also listed.

5

10 Pkey: Unique number corresponding to an Eos probeset
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA
 sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
 Strand: Indicates DNA strand from which exons were predicted.
 Nt_position: Indicates nucleotide positions of predicted exons.

	Pkey	Ref	Strand	Nt_position
15	401963	3126783	Plus	51382-51521
	401974	3126777	Plus	85330-85683
	403087	8954241	Plus	169511-169795
20	403375	9255944	Minus	92554-92795
	403493	7341425	Plus	157568-159084
	403612	8469060	Minus	94723-94859
	403649	8705159	Minus	27141-27247
	403869	7280046	Minus	34379-34583
25	404113	9588571	Minus	13448-13648
	404567	7249169	Minus	101320-101501
	405163	9966267	Minus	161171-161299
	405227	6731245	Minus	22550-22802
	405420	7211837	Minus	13428-13582
30	405455	7656675	Plus	134112-134671
	405678	4079870	Plus	151821-152027
	405900	6758795	Minus	71181-71535
	406135	9164918	Minus	65489-65715

TABLE 9: 1001 GENES SIGNIFICANTLY UP-REGULATED IN NORMAL PROSTATE COMPARED TO PROSTATE CANCER

Table 9 shows 1001 genes significantly up-regulated in prostate cancer compared to normal prostate. These were selected from 59680 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" normal prostate to "average" prostate cancer tissues was greater than or equal to 8.14. The "average" normal prostate level was set to the mean amongst 4 normal prostate tissues. The "average" prostate cancer level was set to the 85th percentile amongst 73 tumor samples. In order to remove gene-specific background levels of non-specific hybridization, the 10th percentile value amongst all the tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

15	Pkey:	Unique Eos probeset identifier number			
	ExAccn:	Exemplar Accession number, Genbank accession number			
	UnigeneID:	Unigene number			
	Unigene Title:	Unigene gene title			
	R1:	Ratio of prostate cancer to normal prostate			
20	Pkey	ExAccn	UnigeneID	Unigene Title	R1
	451002	AA013299	Hs.8018	ESTs, Weakly similar to ALU3_HUMAN ALU S	1684.00
25	435598	AA689465	Hs.188999	ESTs	738.00
	443576	AI078027	Hs.169338	ESTs	246.86
30	434247	AA928118	Hs.272065	ESTs	245.20
	400452	AK000185		gb:Homo sapiens cDNA FLJ20178 fis, clone	222.00
35	405932				221.33
	427906	AA864330	Hs.166520	ESTs	212.00
40	443685	AI686550	Hs.174481	ESTs	163.20
	451554	AI474868	Hs.193237	ESTs	149.45
45	418323	NM_002118	Hs.1162	major histocompatibility complex, class	126.11
	429480	M36860	Hs.9295	elastin (supraaortic aortic stenosis,	123.27
50	426025	AW138330	Hs.233778	ESTs	120.00
	418917	X02894	Hs.1217	adenosine deaminase	106.75
55	404407				105.71
	442027	AI652928	Hs.128395	ESTs	100.53
60	433704	AA608684	Hs.121705	ESTs, Moderately similar to ALUC_HUMAN I	94.00
	453758	U83527		gb:HSU83527 Human fetal brain (M.Lovett)	89.18
65	415354	F08495		gb:HSU1A8051 normalized infant brain cDN	87.73
	424239	M67439	Hs.143526	dopamine receptor D5	86.82
70	444143	AW747996	Hs.160999	ESTs	86.43
	401672				77.28
75	430590	AW383947	Hs.246381	CD68 antigen	68.47
	411972	BE074959		gb:PMO-BT0582-310100-001-f08 BT0582 Homo	68.00
80	448992	AI766053	Hs.188346	ESTs	61.26
	408828	BE540279		gb:601058857F1 NIH_MGC_10 Homo sapiens c	57.71
85	409653	AW451693	Hs.220826	ESTs	56.40
	402964				54.67
90	422673	N59027		gb:yv59d11.r1 Soares fetal liver spleen	54.00
	422568	AA372275	Hs.279800	Homo sapiens cDNA FLJ11383 fis, clone HE	54.00
95	438907	R32704	Hs.301298	ESTs	52.98
	405172				52.86
100	444897	AW137088	Hs.144857	ESTs	52.32
	458019	AW592931	Hs.256298	ESTs	51.63
105	405275	AB028989	Hs.88500	mitogen-activated protein kinase 8 inter	50.98
	457815	AA703679	Hs.106999	ESTs, Weakly similar to SYT5_HUMAN SYNAP	49.60
110	424385	AA339666		gb:EST44776 Fetal brain I Homo sapiens c	48.90
	407172	T54095		gb:ya92cd5.s1 Stratagene placenta (93722	47.98
115	428202	AA424163	Hs.156895	ESTs	46.83
	435672	AI700148	Hs.283626	ESTs	43.57
120	420283	AA485224	Hs.57734	G protein-coupled receptor kinase-intera	43.00
	417018	AA837098	Hs.269933	ESTs	42.70
125	438854	AF074994	Hs.24240	ESTs	42.67

	406134			42.43	
	457319	AA480895	Hs.201552	ESTs, Weakly similar to T17288 hypotheti	42.31
	409314	AA070268		gb:zm69d04.r1 Stratagene neuroepithelium	42.25
	401124				41.61
5	429318	AI371157	Hs.178538	ESTs	40.00
	420317	AB006628	Hs.96485	KIAA0290 protein	39.64
	457588	AW062439		gb:MR0-CT0060-120899-001-f08 CT0060 Homo	39.60
	417407	AA923278	Hs.290805	ESTs, Weakly similar to protease [H.sapi]	38.73
	430269	BE221682	Hs.178364	ESTs	38.06
10	439802	W79114	Hs.58558	ESTs	36.69
	433686	AA604799	Hs.136528	ESTs, Moderately similar to ALU1_HUMAN A	36.29
	417993	AW963705	Hs.285806	ESTs, Weakly similar to ALU7_HUMAN ALU S	36.18
	428214	AA936282	Hs.120397	ESTs	36.10
	416908	AA333990	Hs.80424	coagulation factor XIII, A1 polypeptide	36.08
15	426264	BE314852	Hs.168694	hypothetical protein FLJ10257	36.00
	415911	H08798	Hs.124952	ESTs	36.00
	457502	AA076049	Hs.274415	Homo sapiens cDNA FLJ10229 fis, clone HE	35.23
	421566	NM_000399	Hs.1395	early growth response 2 (Krox-20 (Drosop	35.20
	401468				34.89
20	458561	AI220150	Hs.211195	ESTs	34.60
	433601	BE350738	Hs.123993	ESTs, Weakly similar to T00366 hypotheti	33.24
	454977	AW848032		gb:IL3-CT0214-231299-053-D11 CT0214 Homo	32.96
	402828				32.93
25	414522	AW518944	Hs.76325	Homo sapiens cDNA: FLJ23125 fis, clone L	31.76
	402842				31.68
	421245	AA285363		gb:HTH280 HTCDL1 Homo sapiens cDNA 5'/3'	31.59
	401631	F05183	Hs.1799	CD1D antigen, d polypeptide	31.28
	408057	AW139565		gb:UH-BI1-aea-d-04-0-ULs1 NCL_CGAP_Su	31.24
	408069	H81795		gb:ys68a10.r1 Soares retina N2b4HR Homo	31.20
30	438694	T87479	Hs.291797	ESTs	31.09
	449156	AF103907	Hs.171353	prostate cancer antigen 3	29.78
	428766	AJ076734	Hs.193665	solute carrier family 28 (sodium-coupled	29.76
	452549	AJ907039		gb:PM-BT134-020499-566 BT134 Homo sapien	29.59
	410129	BE244074	Hs.285531	regulator of Fas-induced apoptosis	29.53
35	414464	AI870175	Hs.13957	ESTs	29.47
	412326	R07568	Hs.73817	Small inducible cytokine A3 (homologous	29.22
	459081	W07808		gb:zb03a12.r1 Soares_fetal_lung_NbHL19W	29.20
	448702	AW102670	Hs.122484	ESTs	29.13
	451939	U80458	Hs.27311	single-minded (Drosophila) homolog 2	28.74
40	443412	W84893	Hs.9305	angiotensin receptor-like 1	28.61
	457324	AB028990	Hs.243901	KIAA1067 protein	28.24
	424247	X14008	Hs.234734	lysosome (renal amyloidosis)	28.18
	457140	AI279950	Hs.178140	ESTs	28.12
	444151	AW972917	Hs.128749	alpha-methylacyl-CoA racemase	28.06
45	457669	AW104257	Hs.123426	ESTs, Weakly similar to putative serine/	27.61
	412429	AV650262	Hs.75765	GRO2 oncogene	27.36
	405495				27.33
	406518				27.25
	407997	AW135429	Hs.243577	ESTs	26.98
50	442115	AW452332	Hs.257554	ESTs	26.36
	409038	T97490	Hs.50002	small inducible cytokine subfamily A (Cy	26.34
	402838				26.32
	449848	AI979284	Hs.200552	ESTs	26.21
	417153	X57010	Hs.81343	collagen, type II, alpha 1 (primary oste	26.20
55	439792	NM_014858	Hs.8684	KIAA0476 gene product	25.91
	450098	AI682088	Hs.223368	ESTs	25.60
	424186	AL133660	Hs.142926	Homo sapiens mRNA; cDNA DKFZp434M0927 (f	25.57
	414248	BE391090	Hs.280278	EST	25.57
	420848	NM_005188	Hs.99980	Cas-Br-M (murine) ecotropic retroviral t	25.48
60	424778	AA251048	Hs.153042	lymphocyte antigen 9	25.42
	409128	AA063426		gb:zf70c08.s1 Soares_pineal_gland_N3HPG	25.25
	443938	AW083491	Hs.31196	ESTs	25.22
	419392	W28573		gb:51f10 Human retina cDNA randomly prim	25.01
	411201	T74588	Hs.8509	ESTs, Weakly similar to CO3_HUMAN COMPLE	24.85
65	422940	BE077458		gb:RC1-BT0606-090500-015-b04 BT0606 Homo	24.78
	437571	AA760894	Hs.153023	ESTs	24.74
	433973	AI014723	Hs.131770	ESTs	24.57
	422416	BE018557	Hs.11900	Human DNA sequence from clone RP4-683P15	24.53
	421552	AF026692	Hs.105700	secreted frizzled-related protein 4	24.49

	443668	U25758	Hs.134584	ESTs	24.49
	424800	AL036588	Hs.153203	MyoD family inhibitor	24.10
	453633	AA357001	Hs.34045	hypothetical protein FLJ20764	24.04
	430565	AL122081	Hs.244343	cadherin related 23	24.00
5	433694	AI208611	Hs.12068	Homo sapiens cDNA FLJ11720 fis, clone HE	23.89
	451045	AA215672		gb:zr96e09.s1 NCL_CGAP_GCB1 Homo sapiens	23.83
	408583	AW449674	Hs.47359	ESTs	23.73
	444040	AF204231	Hs.182982	golgin-67	23.62
	414182	AA136301		gb:zr93g04.s1 Soares_pregnant_uterus_NbH	23.39
10	418678	NM_001327	Hs.167379	cancer/testis antigen	23.20
	408380	AF123050	Hs.44532	diubiquitin	22.68
	456076	BE243877	Hs.76941	ATPase, Na+/K+ transporting, beta 3 poly	22.65
	418299	AA279530	Hs.83968	integrin, beta 2 (antigen CD18 (p95), ly	22.39
	444917	R68651	Hs.144997	ESTs	22.26
15	444381	BE387335	Hs.283713	ESTs	22.08
	415788	AW628686	Hs.78851	KIAA0217 protein	22.04
	410896	AW609837		gb:MR4-STD124-261099-015-b07 STD124 Homo	22.00
	412978	AI431708	Hs.820	homeo box C8	21.95
	458418	AV653846	Hs.128261	Homo sapiens Chromosome 16 BAC clone CIT	21.94
20	454791	BE071874		gb:RC2-BT0522-120200-014-a06 BT0522 Homo	21.84
	408748	JO5500	Hs.47431	spectrin, beta, erythrocytic (includes s	21.26
	416011	H14487		gb:ym18c10.r1 Soares Infant brain 1N1B H	21.24
	440474	AI207936	Hs.7195	gamma-aminobutyric acid (GABA) A recepto	21.14
	447047	AI623698	Hs.246306	Homo sapiens cDNA: FLJ23529 fis, clone L	21.11
25	426793	X89887	Hs.172350	HIR (histone cell cycle regulation defec	21.10
	409841	AW502139		gb:UL-HF-BR0p-ajr-e-05-0-UL.r1 NIH_MGC_5	21.07
	405685				20.90
	457359	AI983207	Hs.192481	ESTs, Weakly similar to SYPH_HUMAN SYNAP	20.84
	423067	AA321355	Hs.285401	ESTs	20.74
30	422355	AW403724	Hs.140	immunoglobulin heavy constant gamma 3 (G	20.73
	401201				20.73
	458278	W28912	Hs.129019	ESTs	20.68
	439097	H66948		gb:yr86d10.r1 Soares fetal liver spleen	20.67
	414875	H42679	Hs.77522	major histocompatibility complex, class	20.66
35	400828				20.66
	451355	NM_004197	Hs.444	serine/threonine kinase 19	20.64
	446982	AW500221	Hs.43616	Homo sapiens mRNA for FLJ00029 protein,	20.61
	417105	X60992	Hs.81228	CD6 antigen	20.61
	405777				20.51
40	424123	AW966158	Hs.58582	Homo sapiens cDNA FLJ12702 fis, clone NT	20.20
	425009	X58288	Hs.154151	protein tyrosine phosphatase, receptor t	20.10
	443271	BE588568	Hs.185704	ESTs	19.98
	421064	AI245432	Hs.101382	tumor necrosis factor, alpha-induced pro	19.98
	418619	AA228776	Hs.191721	ESTs	19.94
45	457595	AA584854		gb:mo09h11.s1 NCL_CGAP_Phe1 Homo sapiens	19.90
	404426				19.84
	412571	U43143	Hs.74049	fms-related tyrosine kinase 4	19.79
	431457	NM_012211	Hs.256297	integrin, alpha 11	19.62
	414002	NM_006732	Hs.75578	FBJ murine osteosarcoma viral oncogene h	19.57
50	418994	AA296520	Hs.89548	Selectin E (endothelial adhesion molecucl	19.56
	437158	AW090198	Hs.4779	KIAA1150 protein	19.52
	437866	AA156781	Hs.83992	ESTs	19.44
	417421	AL138201	Hs.82120	nuclear receptor subfamily 4, group A, m	19.34
	433057	X15675	Hs.296832	Human pTR7 mRNA for repetitive sequence	19.22
55	421730	AW449808	Hs.164036	glucosamine (N-acetyl)-6-sulfatase (Sanf	19.21
	456557	AA284477	Hs.96618	ESTs	18.77
	440806	AI247422	Hs.129968	ESTs	18.76
	439845	AL355743	Hs.56663	Homo sapiens EST from clone 41214, full	18.65
	416155	AI807264	Hs.205442	ESTs, Weakly similar to AF117610 1 inner	18.64
60	437820	AA769062	Hs.16029	ESTs, Weakly similar to alternatively sp	18.62
	450923	AW043951	Hs.38449	ESTs	18.59
	418329	AW247430	Hs.84152	cystathionine-beta-synthase	18.58
	424537	AI673027	Hs.143271	ESTs	18.55
	447742	AF113925	Hs.18405	caspase recruitment domain 4	18.52
65	415251	R42863	Hs.7124	ESTs	18.47
	440770	AA912815	Hs.222078	ESTs	18.40
	407711	AI085846	Hs.25522	ESTs	18.32
	427157	U51168	Hs.173824	thymine-DNA glycosylase	18.28
	409847	AW501751	Hs.279733	ESTs	18.15

5	417240	N57568	Hs.176028	EST	18.13
	435732	AF229178	Hs.123138	leucine rich repeat and death domain con	18.12
	436898	AW977385	Hs.278615	ESTs	18.12
	432485	N90868	Hs.276770	CDW52 antigen (CAMPATH-1 antigen)	17.90
	429490	AJ971131	Hs.293684	ESTs, Weakly similar to alternatively sp	17.82
10	429984	AL050102	Hs.227209	DKFZP586F1019 protein	17.82
	449214	AJ889114	Hs.185863	ESTs	17.75
	433867	AK000598	Hs.3818	hippocalcin-like 1	17.72
	431735	AW977724	Hs.75968	thymosin, beta 4, X chromosome	17.71
	401515				17.67
15	444045	AJ097439	Hs.135548	ESTs	17.58
	442754	AL045825	Hs.210187	ESTs	17.55
	426559	AB001814	Hs.170414	paired basic amino acid cleaving system	17.54
	432415	T16971	Hs.289014	ESTs	17.50
	427829	AJ188225	Hs.127482	ESTs	17.50
20	432516	R08003	Hs.188013	ESTs	17.44
	435259	AA152108	Hs.4859	cyclin L, alpha-6a	17.38
	414989	T81668		gb:yd29c04.r1 Soares fetal liver spleen	17.31
	444880	AW118683	Hs.154150	ESTs	17.30
	417651	R06874	Hs.268628	ESTs	17.27
25	453457	AL037103	Hs.270589	ESTs, Weakly similar to unnamed protein	17.22
	424246	AW452533	Hs.143804	Kaiso	17.22
	419078	M93119	Hs.89584	insulinoma-associated 1	17.18
	417696	BE241624	Hs.82401	CD69 antigen (p60, early T-cell activati	17.14
	431117	AF003522	Hs.250500	delta (Drosophila)-like 1	17.14
30	455254	AW877015		gb:QV2-PT0010-250300-096-112 PT0010 Homo	17.14
	425782	U66468	Hs.159525	cell growth regulatory with EF-hand doma	17.12
	426678	H08170	Hs.113755	ESTs	17.12
	428403	NM_000361	Hs.2030	thrombomodulin	17.01
	426905	AB032859	Hs.161700	KIAA1133 protein	17.00
35	438867	AW451157	Hs.181157	ESTs	16.98
	420940	AA830664	Hs.143974	ESTs	16.94
	459234	AJ940425		gb:CM0-CT0052-150799-024-c04 CT0052 Homo	16.92
	404756				16.91
	422247	U18244	Hs.113602	solute carrier family 1 (high affinity a	16.90
40	420568	F09247	Hs.167399	protocadherin alpha 5	16.88
	443559	AJ078765	Hs.268899	ESTs	16.80
	438703	AJ803373	Hs.31589	ESTs	16.78
	411424	AW845985		gb:RC2-CT0163-200989-002-H08 CT0163 Homo	16.70
	402895				16.69
45	422538	NM_008441	Hs.118131	5,10-methenyltetrahydrofolate synthetase	16.68
	447108	AW449602	Hs.217953	ESTs, Moderately similar to NK-TUMOR REC	16.65
	448520	AB002367	Hs.21355	doublecortin and CaM kinase-like 1	16.54
	438567	AW451855	Hs.153065	ESTs	16.52
	407811	AW190902	Hs.40098	cysteine knot superfamily 1, BMP antagon	16.50
50	410721	R23534	Hs.2730	heterogeneous nuclear ribonucleoprotein	16.50
	437133	AB018319	Hs.5480	KIAA0776 protein	16.40
	408182	AA047854		gb:zf49g04.r1 Soares retina N2b4HR Homo	16.32
	417315	AJ080042	Hs.180450	ribosomal protein S24	16.30
	431840	AA534908	Hs.2880	POU domain, class 5, transcription facto	16.28
55	439882	AA847856	Hs.124565	ESTs	16.20
	418277	AW135221	Hs.130812	ESTs	16.09
	410688	AW786342		gb:PM2-UM0027-230200-002-h02 UM0027 Homo	16.04
	420120	AL049810	Hs.95243	transcription elongation factor A (SII)-	16.04
	428597	NM_003816	Hs.2442	a disintegrin and metalloproteinase doma	16.02
60	447033	AJ357412	Hs.157601	EST - not in UniGene	16.02
	421684	BE281591	Hs.106768	hypothetical protein FLJ10511	15.94
	408599	AA055800	Hs.222933	ESTs	15.93
	446012	AV656098	Hs.172382	hypothetical protein FLJ20001	15.88
	409871	AA076769		gb:7B02B10 Chromosome 7 Fetal Brain cDNA	15.85
65	405934				15.84
	426108	AA622037	Hs.166468	programmed cell death 5	15.84
	416208	AW291168	Hs.41285	ESTs	15.48
	410708	AA534370	Hs.154088	Homo sapiens cDNA: FLJ22756 fls, clone K	15.42
	447342	AJ199268	Hs.19322	ESTs; Weakly similar to III ALU SUBFAM1	15.38
	454563	AW807530		gb:CM0-ST0081-130999-054-d02 ST0081 Homo	15.37
	411507	AW850140		gb:IL3-CT0219-261099-023-D11 CT0219 Homo	15.38
	438170	AJ916685	Hs.194601	ESTs	15.29
	416292	AA178233	Hs.42390	nasopharyngeal carcinoma susceptibility	15.28

	406638	M13861	gb:Human T-cell receptor active beta-cha	15.28
	446688	AW138043	Hs.156307 ESTs	15.25
	434485	AI623511	Hs.118567 ESTs	15.24
5	441188	AW282830	Hs.255609 ESTs	15.22
	444172	BE147740	Hs.104558 ESTs	15.22
	409521	BE244854	Hs.159578 Homo sapiens mRNA for FLJ00020 protein,	15.16
	420748	AA279956	Hs.88672 ESTs	15.14
	422583	AA410506	Hs.118578 H.sapiens mRNA for ribosomal protein L18	15.14
10	424240	AB023185	Hs.143535 calcium/calmodulin-dependant protein kin	15.12
	451118	AI862098	Hs.80640 ESTs	15.12
	437495	BE177778	gb:RC1-HT0598-310300-012-407 HT0598 Homo	15.12
	445467	AI239832	Hs.15617 ESTs, Weakly similar to ALU4_HUMAN ALU S	15.06
	418305	AW006783	Hs.6686 ESTs	15.03
	402812			15.02
15	436851	AA732480	Hs.283581 ESTs	15.00
	400991			15.00
	415752	BE314524	Hs.78776 Human putative transmembrane protein (nm	14.96
	428900	AA460421	Hs.30875 ESTs	14.90
	403883			14.84
20	430315	NM_004293	Hs.239147 guanine deaminase	14.80
	451852	AL120173	Hs.301663 ESTs	14.72
	424687	J05070	Hs.151738 matrix metalloproteinase 9 (gelatinase B	14.89
	447229	BE617135	gb:501441677F1 NIH_MGC_65 Homo sapiens c	14.67
	425818	AB021225	Hs.159581 matrix metalloproteinase 17 (membrane-in	14.65
25	448553	AI638449	Hs.173031 ESTs	14.63
	431089	BE041395	Hs.283676 ESTs, Weakly similar to unknown protein	14.60
	459145	AI803354	gb:RC-BT029-100189-117 BT029 Homo sapien	14.55
	449650	AF055575	Hs.297647 ESTs, Moderately similar to calcium chan	14.54
	400952			14.48
30	445885	AI734009	Hs.127699 EST cluster (not in UniGene)	14.44
	407838	AA905097	Hs.85050 phospholamban	14.42
	431678	AI885464	Hs.282638 ESTs	14.40
	437210	AA311443	Hs.293563 Homo sapiens mRNA; cDNA DKFZp586E2317 (f	14.36
	451900	AB023189	Hs.27207 KIAA0982 protein	14.36
35	445800	AA126419	Hs.301632 ESTs	14.32
	412368	AW945992	Hs.181125 Immunoglobulin lambda locus	14.31
	409055	AW304028	Hs.300578 ESTs	14.23
	408763	W57550	Hs.301526 Homo sapiens cDNA FLJ13181 fis, clone NT	14.22
	446734	AL049278	Hs.16074 Homo sapiens mRNA; cDNA DKFZp5641153 (fr	14.22
40	413551	BE242639	Hs.75425 ubiquitin associated protein	14.22
	421913	AI934365	Hs.109439 osteoglycin (osteoinductive factor, mime	14.22
	452712	AW838616	gb:RCS-LT0054-140200-013-D01 LT0054 Homo	14.22
	451468	AW503398	Hs.210047 ESTs	14.16
	406038	Y14443	Hs.88219 zinc finger protein 200	14.14
45	424909	S78187	Hs.153752 cell division cycle 25B	14.07
	434078	AW880709	Hs.283683 EST	14.07
	415254	AI815831	Hs.184378 ESTs	14.05
	418198	AI745849	Hs.26549 ESTs, Weakly similar to T00066 hypotheti	14.02
	410020	T86315	Hs.728 ribonuclease, RNase A family, 2 (liver,	13.98
50	411352	NM_002890	Hs.758 RAS p21 protein activator (GTPase activa	13.98
	429848	AF145439	Hs.225948 chemokine (C-C motif) receptor 9	13.95
	413729	BE159989	gb:QV1-HT0412-270300-123-d10 HT0412 Homo	13.90
	400125			13.88
	420319	AW406289	Hs.96593 hypothetical protein	13.85
55	448272	AI478094	Hs.170786 ESTs	13.80
	422695	AA315158	gb:EST186958 HCC cell line (matatasis t	13.80
	424565	AW102723	Hs.75285 guanylate cyclase 1, soluble, alpha 3	13.78
	458048	H30340	Hs.173705 Homo sapiens cDNA: FLJ22050 fis, clone H	13.78
	408894	AI935400	Hs.217288 ESTs	13.78
60	454093	AW860158	gb:RC0-CT0379-280100-032-b04 CT0379 Homo	13.75
	410889	X91682	Hs.66744 twist (Drosophila) homolog (acrocephalos	13.74
	457751	AI908238	gb:IL-BT166-180399-010 BT166 Homo sapien	13.72
	455131	AW857913	gb:RC0-CT0323-231189-031-b05 CT0323 Homo	13.69
	408364	AW015238	Hs.128453 ESTs	13.67
65	425907	AA365752	Hs.155965 ESTs	13.62
	402359			13.60
	401044			13.53
	409877	AW502498	Hs.157150 ESTs, Weakly similar to zinc finger prot	13.53
	423690	AA328648	Hs.23804 ESTs	13.49

	430685	AI690234	Hs.191666	ESTs, Weakly similar to reverse transcri	13.47
	414052	AW578849	Hs.283552	ESTs, Weakly similar to unnamed protein	13.46
	447858	AW080339	Hs.211911	ESTs	13.44
	435716	AI573283	Hs.38458	ESTs	13.44
5	439120	H56389	gb:y187c03.r1 Soares_pineal_gland_N3HPG		13.43
	402788				13.40
	451591	AA886446	Hs.146278	ESTs	13.40
	405411				13.38
	426558	AW188574	Hs.24218	ESTs	13.34
10	453506	AA132818	Hs.110407	ESTs, Weakly similar to coded for by C.	13.33
	416445	AL043004	Hs.300878	Human serine/threonine kinase mRNA, part	13.32
	457084	AI074149	Hs.150905	ESTs, Weakly similar to chondroitin 4-su	13.32
	403838				13.32
	427337	Z46223	Hs.176863	Fc fragment of IgG, low affinity IIb, r	13.30
15	434318	AW207552	Hs.116328	ESTs, Weakly similar to cJ134E15.1 [H.sa	13.28
	435193	N41359	Hs.218107	ESTs	13.28
	414758	AW451101	Hs.159489	ESTs, Moderately similar to hexokinase I	13.27
	420826	AF043722	Hs.99491	RAS guanyl releasing protein 2 (calcium	13.26
	420062	AA418850	Hs.44410	ESTs	13.25
20	414020	NM_002984	Hs.75703	small inducible cytokine A4 (homologous	13.25
	403851				13.24
	422647	W07492	Hs.157101	ESTs	13.21
	433598	AI762836	Hs.271433	ESTs, Moderately similar to ALU2_HUMAN A	13.21
	409065	AB033113	Hs.50187	KIAA1287 protein	13.20
25	435063	R21868	Hs.57734	G protein-coupled receptor kinase-intera	13.19
	439367	BE386844	Hs.248748	ESTs	13.17
	451957	AI796320	Hs.10299	Homo sapiens cDNA FLJ13545 fis, clone PL	13.16
	420569	AA278362	Hs.289062	Homo sapiens cDNA FLJ12334 fis, clone MA	13.14
	447883	BE262802	Hs.4909	clckopf (Xenopus laevis) homolog 3	13.07
30	426490	NM_001821	Hs.170087	aryl hydrocarbon receptor	13.06
	414789	AA155859	Hs.79708	ESTs	13.05
	451418	BE387780	Hs.26369	ESTs	13.04
	443494	T99719	Hs.270404	Homo sapiens cDNA: FLJ22389 fis, clone H	13.03
	425878	AW964806	Hs.38085	ESTs, Weakly similar to putative glycine	13.02
35	431912	AI860552	Hs.154903	ESTs, Weakly similar to A56154 Abl subst	13.00
	407122	H20278	Hs.31742	ESTs	13.00
	456491	AL137466	Hs.97277	Homo sapiens mRNA; cDNA DKFZp434H1322 (f	12.99
	448172	N75276	Hs.136904	ESTs	12.98
	452144	AA032197	Hs.102558	ESTs	12.96
40	418953	BE267154	Hs.125752	ESTs	12.96
	418182	NM_004354	Hs.79069	cyclin G2	12.94
	451154	AA015879	Hs.33536	ESTs	12.93
	412257	AW903830	gb:CM4-NN1037-250400-155-h04 NN1037 Homo		12.93
	449784	AW161319	Hs.12915	ESTs	12.92
45	432685	D63480	Hs.278634	KIAA0146 protein	12.92
	454105	NM_001259	Hs.38481	cyclin-dependent kinase 6	12.92
	439093	AA534163	Hs.5476	serine protease inhibitor, Kazal type, 5	12.90
	416098	H41324	Hs.31581	ESTs, Moderately similar to ST1B_HUMAN S	12.88
	424897	D63216	Hs.153684	frizzled-related protein	12.88
50	414604	AU076649	Hs.76556	growth arrest and DNA-damage-inducible 3	12.88
	414664	AA587775	Hs.66295	Homo sapiens HSPC311 mRNA, partial cds	12.84
	452580	BE077084	gb:RC5-BT0603-220200-013-C07 BT0603 Homo		12.84
	413869	NM_000878	Hs.75598	interleukin 2 receptor, beta	12.80
	452359	BE167229	Hs.29206	Homo sapiens clone 24659 mRNA sequence	12.80
55	435886	BE265839	Hs.12126	hepatocellular carcinoma-associated anti	12.78
	445230	U97018	Hs.12451	echinoderm microtubule-associated protei	12.78
	412228	W26788	gb:15d7 Human retina cDNA randomly prime		12.77
	448619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin,	12.76
	447769	AW873704	Hs.48784	ESTs	12.76
60	414478	AI306389	Hs.76240	adenylate kinase 1	12.76
	425393	D83407	Hs.156007	Down syndrome critical region gene 1-lik	12.68
	450704	H85157	Hs.40696	ESTs	12.66
	405856				12.66
	412935	BE267045	Hs.75064	tubulin-specific chaperone c	12.65
65	402802				12.62
	452588	AA889120	Hs.110637	Homeo box A10	12.62
	419978	NM_001454	Hs.93974	forkhead box J1	12.62
	403137				12.60
	430226	BE245562	Hs.2551	adrenergic, beta-2-, receptor, surface	12.57

	448076	AJ133123	Hs.20196	adenylate cyclase 9	12.56
	450462	F07097	Hs.300828	Homo sapiens mRNA full length insert cDN	12.54
	405236				12.52
5	409292	AA071051		gb:zm58e05.s1 Stratagene fibroblast (837	12.47
	421540	AA767689	Hs.10242	ESTs	12.47
	425840	AW978731	Hs.301824	ESTs	12.44
	443181	AJ039201	Hs.54548	ESTs	12.42
	452436	BE077546	Hs.31447	ESTs	12.42
10	455183	AW984111		gb:RC0-HN0007-160300-011-09 HN0007 Homo	12.40
	432887	AJ926047	Hs.182859	ESTs	12.37
	410494	M38564	Hs.64016	protein S (alpha)	12.36
	439024	R96686	Hs.35598	ESTs	12.36
	451246	AW189232	Hs.39140	cutaneous T-cell lymphoma tumor antigen	12.36
15	432892	AL042615	Hs.15995	ESTs	12.35
	418982	AJ348838	Hs.13073	ESTs	12.35
	414516	AJ307802	Hs.279551	ESTs	12.34
	440134	BE410734		gb:601301619F1 NIH_MGC_21 Homo sapiens c	12.29
	443873	AL048542	Hs.16291	ESTs	12.28
	401288				12.28
20	454020	AW962845	Hs.256527	ESTs	12.24
	420077	AW512260	Hs.87767	ESTs	12.24
	443837	AJ984825	Hs.9884	spindle pole body protein	12.24
	407519	X64979		gb:H.sapiens mRNA HTPCRX01 for olfactory	12.23
25	435839	AF249744	Hs.25951	Rho guanine nucleotide exchange factor (12.22
	448552	AW973653	Hs.20104	hypothetical protein FLJ00052	12.20
	405325				12.20
	451009	AA013140	Hs.115707	ESTs	12.18
	423068	Y18264	Hs.120171	ESTs	12.17
30	439556	AJ623752	Hs.163603	ESTs	12.16
	443062	N77999	Hs.8963	Homo sapiens mRNA full length insert cDN	12.15
	445873	AA250970	Hs.251946	Homo sapiens cDNA: FLJ23107 fis, clone L	12.14
	453542	AW836724	Hs.33190	Homo sapiens mRNA expressed only in plac	12.11
	440108	AA864968	Hs.127699	ESTs	12.10
35	417605	AF006809	Hs.82294	regulator of G-protein signalling 3	12.10
	440286	U29589	Hs.7138	cholinergic receptor, muscarinic 3	12.04
	420061	AW024937	Hs.29410	ESTs	12.02
	458727	AJ022813	Hs.92679	Homo sapiens clone CDABP0014 mRNA sequen	11.96
	445407	AJ222658	Hs.221889	ESTs, Weakly similar to la costa [D.mela	11.95
40	418250	U29926	Hs.83918	adenosine monophosphate deaminase (isofo	11.94
	414129	AJ90287	Hs.270798	ESTs	11.93
	409789	D11928	Hs.76845	phosphoserine phosphatase-like	11.82
	438461	AW075485	Hs.288049	phosphoserine aminotransferase	11.82
	443912	R37257	Hs.184780	ESTs	11.82
45	424606	AA343936		gb:EST49786 Gall bladder I Homo sapiens	11.80
	434217	AW014795	Hs.23349	ESTs	11.80
	451533	NM_004657	Hs.26530	serum deprivation response (phosphatidyl	11.80
	422423	AF283777	Hs.116481	CD72 antigen	11.89
	409398	AW386461		gb:PM4-PT0019-121299-004-F02 PT0019 Homo	11.89
50	423853	AB011537	Hs.133466	sit (Drosophila) homolog 1	11.82
	446180	AJ074413	Hs.14220	hypothetical protein FLJ20450	11.80
	414341	D80004	Hs.75909	KIAA0182 protein	11.80
	406538				11.79
	433253	AW450502	Hs.24218	ESTs	11.79
55	447397	BE247676	Hs.18442	E-1 enzyme	11.78
	451684	AF216751	Hs.26813	CDA14	11.76
	416882	R23765	Hs.23575	ESTs	11.74
	425770	NM_014363	Hs.159492	spastic ataxia of Charlevoix-Saguenay (s	11.72
	428828	AL048842	Hs.194019	attractin	11.72
60	433037	NM_014158	Hs.278938	HSPC067 protein	11.72
	447478	BE293466	Hs.20880	ESTs	11.72
	452092	BE245374	Hs.27842	hypothetical protein FLJ11210	11.72
	412922	M60721	Hs.74870	H2.0 (Drosophila)-like homeo box 1	11.72
	401680	NM_005578	Hs.180398	LIM domain-containing preferred transloc	11.69
65	422578	BE548555	Hs.118554	CGI-83 protein	11.68
	450203	AF097994	Hs.301528	L-kynurenine/alpha-aminoadipate aminotra	11.68
	410531	AW752953		gb:QV0-CT0224-261099-035-g02 CT0224 Homo	11.67
	425917	W28517	Hs.117167	Homo sapiens cDNA: FLJ23067 fis, clone L	11.66
	418693	AJ750878	Hs.87409	thrombospondin 1	11.64
	400557				11.62

	416188	BE157260	Hs.79070	v-myc avian myelocytomatosis viral oncog	11.60
	419047	AW952771	Hs.90043	ESTs	11.59
	420441	AI986160	Hs.88448	ESTs	11.59
	400885				11.57
5	409853	AW502327		gb:JH-HF-BR0p-aka-a-07-0-UI.r1 NIH_MGC_5	11.56
	400802				11.56
	434540	NM_018045	Hs.5184	TH1 drosophila homolog	11.55
	431449	M55394	Hs.256278	tumor necrosis factor receptor superfamily	11.55
	425928	S55736	Hs.238652	ESTs, Weakly similar to hypothetical pro	11.54
10	434701	AA480479	Hs.4096	KIAA0742 protein	11.53
	434228	Z42047	Hs.283978	ESTs; KIAA0738 gene product	11.52
	420729	AW964897	Hs.290825	ESTs	11.52
	428328	AA428080	Hs.98489	ESTs	11.50
	433887	AW204232	Hs.278522	ESTs	11.50
15	414812	X72755	Hs.77387	monokine induced by gamma interferon	11.48
	457718	F18572	Hs.22978	ESTs	11.44
	452260	AA453208	Hs.28728	RAB9, member RAS oncogene family	11.42
	459029	AA131376	Hs.285203	fibroblast growth factor 12	11.42
	458267	AI127858	Hs.83393	cystatin E/M	11.39
20	433285	AW975944	Hs.237396	ESTs	11.38
	449186	AW291876	Hs.198986	ESTs	11.37
	447861	AI434593	Hs.164294	ESTs	11.37
	456023	R00028		gb:ye70a08.s1 Soares fetal liver spleen	11.36
	439444	AI277652	Hs.54578	ESTs	11.31
25	401163				11.31
	430886	L36149	Hs.248116	chemokine (C motif) XC receptor 1	11.28
	450784	AW246803	Hs.47289	ESTs	11.28
	452391	AL044829	Hs.29331	camitine palmitoyltransferase I, muscle	11.27
	449625	NM_014253	Hs.23796	odc (odd Oz/ten-m, Drosophila) homolog 1	11.26
30	456827	AA075687	Hs.147176	epidermal growth factor receptor substra	11.24
	439328	W07411	Hs.118212	ESTs, Moderately similar to ALL3_HUMAN A	11.24
	432093	H28383		gb:yl52c03.r1 Soares breast 3NbHBst Homo	11.24
	407335	AA631047	Hs.158761	Homo sapiens cDNA FLJ13054 fls, clone NT	11.23
	442501	AA315267	Hs.23128	ESTs	11.22
35	429746	AI237672	Hs.214142	5,10-methylenetetrahydrofolate reductase	11.21
	422858	R35398		gb:yg64g10.r1 Soares infant brain 1NIB H	11.20
	415156	X84908	Hs.78080	phosphorylase kinase, beta	11.20
	446713	AV660122	Hs.282675	ESTs	11.20
	452221	C21322	Hs.11577	ESTs	11.20
40	418261	W78902	Hs.293297	ESTs	11.17
	433332	AI387347	Hs.127809	ESTs	11.16
	434539	AW748078	Hs.214410	ESTs	11.16
	413471	BE142098		gb:CM4-HT0137-220999-017-d11 HT0137 Homo	11.14
	410037	AB020725	Hs.58009	KIAA0918 protein	11.14
45	405601				11.13
	458332	AI000341	Hs.220491	ESTs	11.12
	427654	AA410183	Hs.137475	ESTs	11.12
	427138	N77624	Hs.173717	phosphatidic acid phosphatase type 2B	11.10
	431475	AI567669	Hs.287316	ESTs	11.10
50	425710	AF030880	Hs.159275	solute carrier family, member 4	11.08
	413748	AW104057	Hs.19183	ESTs	11.07
	409208	Y00093	Hs.51077	integrin, alpha X (antigen CD11C (p150),	11.07
	457278	W92745	Hs.193324	ESTs	11.03
	407021	U52077		gb:Human mariner1 transposase gene, comp	11.02
55	445701	AF055581	Hs.13131	lymphocyte adaptor protein	11.02
	408338	AW867079		gb:MR1-SN0033-120400-002-c10 SN0033 Homo	10.95
	401030	BE382701	Hs.25960	v-myc avian myelocytomatosis viral relat	10.95
	437891	AW006969	Hs.6311	hypothetical protein FLJ20859	10.94
	453874	AW591783	Hs.36131	collagen, type XIV, alpha 1 (undulin)	10.94
60	421562	AA530994	Hs.105803	ghrelin precursor	10.92
	413431	AW246428	Hs.75355	ubiquitin-conjugating enzyme E2N (homolo	10.92
	400132				10.92
	438420	AA443968	Hs.31595	ESTs	10.90
	424880	NM_000328	Hs.153814	retinitis pigmentosa GTPase regulator	10.88
65	433264	D85782	Hs.3229	cysteine dioxygenase, type I	10.88
	429842	AI386213	Hs.173422	KIAA1605 protein	10.87
	412405	AW948126		gb:RCO-MT0013-280300-031-a12 MT0013 Homo	10.85
	400615				10.80
	425018	BE245277	Hs.154186	E4F transcription factor 1	10.80

	458011	BE243628	gb:TCBAP1D1053 Pediatric pre-B cell acut	10.79
	455982	BE176862	gb:RC4-HT0587-170300-012-a04 HT0587 Homo	10.74
	450418	BE218418	Hs.201802 ESTs	10.73
5	412490	AW803584	Hs.268850 ESTs	10.72
	436982	AW377314	Hs.5364 DKFZP564I052 protein	10.70
	437743	AI383497	Hs.131811 ESTs, Weakly similar to ALU1_HUMAN ALU S	10.70
	449967	R40978	Hs.271498 ESTs, Moderately similar to ALU1_HUMAN A	10.70
	449580	AA694070	Hs.268835 ESTs	10.68
10	446035	NM_006558	Hs.13565 Sam68-like phosphotyrosine protein, T-ST	10.68
	426530	U24578	Hs.170250 complement component 4A	10.68
	428600	AW863261	Hs.15036 ESTs, Highly similar to AF181358 1 HSPC0	10.64
	420090	AA220238	Hs.94988 ribonuclease P (38kD)	10.64
	451593	AF151879	Hs.26706 CGI-121 protein	10.62
	438893	AF076031	Hs.28327 ESTs	10.82
15	459324	AW080953	gb:cc28c12.x1 NCL_GGAP_Co18 Homo sapiens	10.61
	439883	AL359652	Hs.171096 Homo sapiens EST from clone DKFZp434A041	10.58
	406513	AA715328	Hs.291205 ESTs	10.57
	407826	AA128423	Hs.40300 calpain 3, (p94)	10.57
20	419550	D50918	Hs.80998 KIAA0128 protein; septin 2	10.56
	428522	R10184	Hs.191987 ESTs, Weakly similar to ALU1_HUMAN ALU S	10.56
	459526	AI142350	Hs.148735 EST	10.55
	411448	AA178955	Hs.271439 ESTs	10.54
	410102	AW248508	Hs.279727 ESTs;	10.52
	406577			10.52
25	408405	AK001332	Hs.44672 hypothetical protein FLJ10470	10.51
	428966	AF059214	Hs.194687 cholesterol 25-hydroxylase	10.50
	400880			10.48
	415875	AA894876	Hs.5687 protein phosphatase 1B (formerly 2C), ma	10.48
30	434715	BE005348	Hs.116410 ESTs	10.46
	406851	AA609784	Hs.180255 major histocompatibility complex, class	10.44
	413409	AI638418	Hs.21745 ESTs	10.44
	418489	U76421	Hs.85302 adenosine deaminase, RNA-specific, B1 (h	10.44
	419465	AW500239	Hs.21187 Homo sapiens cDNA: FLJ23068 fis, clone L	10.44
35	418544	AI909154	gb:QV-BT200-010499-007 BT200 Homo sapien	10.44
	432180	Y18418	Hs.272822 RuvB (E coli homolog)-like 1	10.44
	413822	R08950	Hs.272044 ESTs, Weakly similar to ALU1_HUMAN ALU S	10.42
	437446	AA788946	Hs.16869 ESTs, Moderately similar to CA1C RAT COL	10.41
	415701	NM_003878	Hs.78819 gamma-glutamyl hydrolase (conjugase, fol	10.41
40	443790	NM_003500	Hs.9795 acyl-Coenzyme A oxidase 2, branched chal	10.40
	458873	AW150717	Hs.298176 STAT induced STAT inhibitor 3	10.38
	415082	AA160000	Hs.137396 ESTs	10.37
	429124	AW505086	Hs.196914 minor histocompatibility antigen HA-1	10.36
	417187	AB011151	Hs.81505 KIAA0579 protein	10.34
45	426827	AW067805	Hs.172685 methylenetetrahydrofolate dehydrogenase	10.34
	424280	NM_000030	Hs.271366 alanine-glyoxylate aminotransferase homo	10.33
	446099	T93096	Hs.17126 ESTs	10.32
	423445	NM_014324	Hs.128749 alpha-methylacyl-CoA racemase	10.31
	409995	AW860597	Hs.30164 ESTs	10.30
50	432242	AW022715	Hs.162160 ESTs, Weakly similar to ALU4_HUMAN ALU S	10.30
	406394	AA172108	Hs.110950 Rag C protein	10.30
	406189			10.29
	422283	AW411307	Hs.114311 CDC45 (cell division cycle 45, S.cerevis	10.28
	401598	AA172108	Hs.110950 Rag C protein	10.28
55	456995	T89832	Hs.170278 ESTs	10.28
	418511	NM_006762	Hs.78356 Lysosomal-associated multispanning membr	10.24
	427274	NM_005211	Hs.174142 colony stimulating factor 1 receptor, fo	10.24
	401384			10.23
	456226	D13168	Hs.82002 endothelin receptor type B	10.22
60	426928	AF037062	Hs.172914 retinol dehydrogenase 5 (11-cis and 9-cis	10.21
	423032	AI684746	Hs.119274 ESTs	10.20
	436556	AI364997	Hs.7572 ESTs	10.20
	418400	BE243028	Hs.301989 KIAA0246 protein	10.19
	437401	AA757196	Hs.121190 ESTs	10.19
65	403690			10.17
	423790	BE152393	gb:CM2-HT0323-171199-033-a08 HT0323 Homo	10.16
	434094	AA305589	Hs.238205 hypothetical protein PRO2013	10.16
	434967	AW975009	Hs.292274 ESTs	10.16
	432827	Z68128	Hs.3109 Rho GTPase activating protein 4	10.16
	432660	AI288430	Hs.64004 ESTs	10.14

	452234	AW084176	Hs.223298	ESTs	10.14
	445629	AI245701		gb:qk31105.x1 NCI_CGAP_Kid3 Homo sapiens	10.13
	457238	AA626142	Hs.179991	ESTs, Weakly similar to KPCE_HUMAN PROTE	10.13
	444605	AI174603	Hs.254105	enolase 1, (alpha)	10.12
5	450313	AI038989	Hs.24809	hypothetical protein FLJ10826	10.12
	407482	NM_006056			10.12
	449971	AA807346	Hs.268581	Homo sapiens cDNA FLJ14296 fis, clone PL	10.11
	441201	AW118822	Hs.128757	ESTs	10.10
10	435157	AW014605	Hs.179872	ESTs	10.10
	417303	H60720	Hs.81882	KIAA0101 gene product	10.09
	442582	AI204266	Hs.179303	ESTs	10.05
	437252	AI433833	Hs.164159	ESTs, Weakly similar to ALU1_HUMAN ALU S	10.04
	448663	BE614599	Hs.106823	H.sapiens gene from PAC 42616, similar t	10.04
	434467	BE552368	Hs.231853	Homo sapiens cDNA FLJ13445 fis, clone PL	10.04
15	423698	AA329796	Hs.1098	DKFZp434J1813 protein	10.02
	412707	AW206373	Hs.16443	Homo sapiens cDNA: FLJ21721 fis, clone C	10.00
	414658	X58528	Hs.76781	ATP-binding cassette, sub-family D (ALD)	10.00
	421832	NM_016099	Hs.108725	HSPC040 protein	10.00
20	423554	M80516	Hs.1674	glutamine-fructose-6-phosphate transamin	10.00
	452039	AI922868	Hs.172510	ESTs	10.00
	434673	AW137442	Hs.136965	ESTs	10.00
	427978	AA418280	Hs.180040	Homo sapiens cDNA: FLJ22439 fis, clone H	10.00
	457803	BE501815	Hs.198011	ESTs	9.99
	428279	AA425310	Hs.155766	ESTs	9.98
25	444412	AI147652	Hs.216381	Homo sapiens clone HH409 unknown mRNA	9.98
	417049	N72394	Hs.44862	ESTs	9.96
	427509	M62505	Hs.2161	complement component 5 receptor 1 (C5a I	9.96
	445424	AB028945	Hs.12696	cortactin SH3 domain-binding protein	9.96
30	443678	AW009605	Hs.231923	ESTs	9.96
	447567	AW474513	Hs.224397	ESTs, Weakly similar to B48013 proline-r	9.94
	414709	AA704703	Hs.77031	Sp2 transcription factor	9.94
	434596	T59538		gb:yb65g12.s1 Stratagene ovary (937217)	9.94
	427630	BE276115	Hs.144880	ESTs, Weakly similar to CA13_HUMAN COLLA	9.93
35	416111	AA033813	Hs.79018	chromatin assembly factor 1, subunit A (9.92
	423349	AF010258	Hs.127428	homeo box A9	9.92
	424308	AW975531	Hs.154443	minichromosome maintenance deficient (S.	9.92
	416814	AW192307	Hs.80042	dolichyl-P-Glc:Man9GlcNAc2-PP-dolichyl	9.90
	417986	AA481003	Hs.97128	ESTs	9.90
40	425174	D87450	Hs.154978	KIAA0261 protein	9.90
	438171	AW976507	Hs.293515	ESTs	9.90
	421884	AW972187	Hs.110443	hypothetical protein FLJ22215	9.89
	408597	NM_005291	Hs.46453	G protein-coupled receptor 17	9.88
	413907	AI097570	Hs.71222	ESTs	9.87
45	451286	AW801383	Hs.118578	H.sapiens mRNA for ribosomal protein L18	9.86
	433409	AI278802	Hs.25661	ESTs	9.85
	450360	AW117416	Hs.245484	ESTs	9.85
	433104	AL043002	Hs.128246	ESTs, Moderately similar to unnamed prot	9.84
	449824	AI962552	Hs.226765	ESTs	9.84
50	452744	AI267652	Hs.30504	Homo sapiens mRNA; cDNA DKFZp434E082 (fr	9.82
	431066	AF026273	Hs.249175	interleukin-1 receptor-associated kinase	9.82
	426457	AW894667	Hs.169965	chimerin (chimaerin) 1	9.80
	443371	AI782888	Hs.145489	ESTs	9.80
	437159	AL050072		gb:Homo sapiens mRNA; cDNA DKFZp566E1346	9.75
55	425242	D13635	Hs.155287	KIAA0010 gene product	9.74
	447498	N67619	Hs.43687	ESTs	9.74
	426759	AI590401	Hs.21213	ESTs	9.73
	435129	AI381859	Hs.267086	ESTs	9.72
	437672	AW748265	Hs.5741	flavohemoprotein b5+b5R	9.72
60	438209	AL120859	Hs.6111	KIAA0307 gene product	9.72
	438440	AA807228	Hs.225161	ESTs	9.72
	449720	AA311152	Hs.288708	ESTs; Weakly similar to KIAA0226 [H.sapi	9.72
	414291	AI289619	Hs.13040	ESTs	9.72
	438208	AK001451	Hs.265561	CD2-associated protein	9.70
65	446896	T15767	Hs.22452	Homo sapiens cDNA: FLJ21084 fis, clone C	9.70
	412667	AW977540	Hs.269254	ESTs	9.70
	423301	S67580	Hs.1645	cytochrome P450, subfamily IVA, polypept	9.67
	440757	AW118645	Hs.160004	ESTs	9.67
	441412	AI393657	Hs.159750	ESTs	9.66
	421044	AF061871	Hs.101302	collagen, type XII, alpha 1	9.66

	414728	BE466863	Hs.280099	ESTs	9.68
	418485	R01679	Hs.124981	ESTs	9.66
	433480	X02422	Hs.181125	Immunoglobulin lambda locus	9.65
5	441530	AI248301	Hs.127112	ESTs	9.65
	433533	D53304	Hs.65394	ESTs	9.65
	421470	R27486	Hs.1378	annexin A3	9.64
	438613	C05569	Hs.243122	hypothetical protein FLJ13057 similar to	9.64
	429324	AA488101	Hs.189245	inactivation escape 1	9.62
10	450244	AA007534	Hs.125062	ESTs	9.62
	407660	AW063190	Hs.279101	ESTs	9.61
	406554				9.60
	426404	AA377607	Hs.273138	ESTs	9.58
	447045	AW392394	Hs.278569	KIAA0064 gene product	9.58
15	449894	AK001578	Hs.24129	hypothetical protein FLJ10716	9.58
	448376	AI494332	Hs.198963	ESTs	9.58
	407902	AL117474	Hs.41181	Homo sapiens mRNA; cDNA DKFZp727C191 (fr	9.56
	446572	AV659151	Hs.282961	ESTs	9.56
	459245	BE242623	Hs.31839	manic fringe (Drosophila) homolog	9.55
20	423545	AP000692	Hs.129781	chromosome 21 open reading frame 5	9.54
	414697	BE266134	Hs.76927	translocase of outer mitochondrial membr	9.54
	410846	AW807057		gb:MR4-ST0062-031199-018-b03 ST0062 Homo	9.52
	421181	NM_005574	Hs.184585	LIM domain only 2 (rhombotin-like 1)	9.52
	427308	D26067	Hs.174905	KIAA0033 protein	9.52
25	415995	NM_004573	Hs.994	phospholipase C, beta 2	9.51
	434848	AW295389	Hs.119768	ESTs	9.51
	414342	AA742181	Hs.75912	Homo sapiens cDNA: FLJ22199 fis, clone H	9.50
	416959	D28459	Hs.80612	ubiquitin-conjugating enzyme E2A (RAD6 h	9.50
	443123	AA094538	Hs.6588	ESTs	9.50
30	439312	AA833902	Hs.270745	ESTs	9.48
	449375	R07114	Hs.271224	ESTs	9.48
	436357	AJ132085		gb:Homo sapiens mRNA for axonemal dynein	9.44
	458723	AW137726	Hs.244352	ESTs, Moderately similar to laminin alph	9.44
	457526	AW450584	Hs.192131	ESTs, Weakly similar to RIBB [H.sapiens]	9.43
	404741				9.43
35	422409	NM_005428	Hs.116237	vav 1 oncogene	9.43
	403708				9.42
	408806	AW847814	Hs.289005	Homo sapiens cDNA: FLJ21532 fis, clone C	9.42
	417380	T06809		gb:EST04698 Fetal brain, Stratagene (cat	9.42
40	422501	AA354890	Hs.144967	ESTs	9.42
	426197	AA004410	Hs.167835	acyl-Coenzyme A oxidase 1, palmitoyl	9.42
	452624	AJ076606	Hs.30054	coagulation factor V (proaccelerin, labi	9.42
	412110	AW893569		gb:RC0-NN0021-040400-021-c10 NN0021 Homo	9.41
	414158	AA361623	Hs.288775	Homo sapiens cDNA FLJ13900 fis, clone TH	9.41
45	408101	AW968504	Hs.123073	CDC2-related protein kinase 7	9.40
	414171	AA380328	Hs.865	RAP1A, member of RAS oncogene family	9.40
	415947	U04045	Hs.78934	mutS (E. coli) homolog 2 (colon cancer,	9.40
	426959	BE262745		gb:601153869F1 NIH_MGC_19 Homo sapiens c	9.39
	417519	AI689987	Hs.177669	ESTs, Weakly similar to RMS1_HUMAN REGUL	9.39
50	457181	BE514362	Hs.296422	FK506-binding protein 3 (25kD)	9.39
	402835				9.38
	404632				9.38
	446568	H95741	Hs.17914	Homo sapiens cDNA: FLJ22801 fis, clone K	9.37
	455369	AW903533		gb:CM1-NN1031-060400-178-d05 NN1031 Homo	9.37
55	444001	AI095087	Hs.152299	ESTs, Moderately similar to ALU5_HUMAN A	9.36
	458191	AI420611	Hs.127832	ESTs	9.36
	431374	BE258532	Hs.251871	CTP synthase	9.34
	429327	AA283981	Hs.199248	prostaglandin E receptor 4 (subtype EP4)	9.33
	407061	X97748		gb:H.sapiens PTX3 gene promotor region.	9.33
60	416967	BE616731	Hs.80645	interferon regulatory factor 1	9.33
	423013	AW875443	Hs.22209	secreted modular calcium-binding protein	9.33
	439461	AA693960	Hs.103158	ESTs	9.33
	418830	BE513731	Hs.88959	Human DNA sequence from clone 867N21 on	9.32
	422763	AA033699	Hs.83938	ESTs, Moderately similar to MASP-2 [H.sa	9.32
65	442739	NM_007274	Hs.8679	cytosolic acyl coenzyme A thioester hydr	9.32
	452859	AI300555	Hs.288158	Homo sapiens cDNA: FLJ23591 fis, clone L	9.32
	403237				9.32
	415000	AW025529	Hs.239812	ESTs, Weakly similar to CALM_HUMAN CALMO	9.31
	417951	AW976410	Hs.289069	Homo sapiens cDNA: FLJ21016 fis, clone C	9.30
	419068	Z98492	Hs.6975	PRO1073 protein	9.30

	448443	AW167128	Hs.231834	ESTs	9.30
	405125				9.30
	409768	AW499568		gb:U1-HF-BR0p-aj-h-03-0-U1.r1 NIH_MGC_5	9.28
5	453708	AI191811	Hs.54628	ESTs	9.28
	442271	AF000652	Hs.8180	syndecan binding protein (syntenin)	9.27
	410055	AJ250839	Hs.58241	gene for serine/threonine protein kinase	9.26
	448892	AW013907	Hs.224276	ESTs, Moderately similar to predicted us	9.26
	417381	AF164142	Hs.82042	solute carrier family 23 (nucleobase tra	9.25
	422497	D28642	Hs.1528	KIAA0053 gene product	9.25
10	414140	AA281279	Hs.23317	ESTs	9.24
	435880	AF274571	Hs.129142	ESTs; Weakly similar to DEOXYRIBONUCLEAS	9.24
	458530	BE395035	Hs.199889	ESTs, Weakly similar to KIAA0874 protein	9.24
	402585				9.24
	420819	AA280700		gb:zs95h11.s1 NCL_CGAP_GCB1 Homo sapiens	9.23
15	444755	AA431791	Hs.183001	ESTs	9.22
	411630	U42349	Hs.71119	Putative prostate cancer tumor suppressor	9.22
	421246	AW582962	Hs.300961	ESTs, Highly similar to AF151805 1 CGI-4	9.20
	421824	BE514514	Hs.109606	coronin, actin-binding protein, 1A	9.19
	414888	AL039185	Hs.77558	thyroid hormone receptor interactor 7	9.18
20	434267	AI206589	Hs.116243	ESTs	9.17
	409213	U81412	Hs.51133	PTK6 protein tyrosine kinase 6	9.17
	428242	H55709	Hs.2250	leukemia inhibitory factor (cholinergic	9.16
	451736	AW080356	Hs.293684	ESTs, Weakly similar to alternatively sp	9.15
	413627	BE182082	Hs.246973	ESTs	9.14
25	416134	AA528402	Hs.74861	activated RNA polymerase II transcriptio	9.14
	449251	AW151860	Hs.31444	ESTs	9.14
	452813	U54727	Hs.191445	ESTs	9.14
	443622	AI911527	Hs.11805	ESTs	9.14
	413260	BE075281		gb:PM1-BT0585-290200-005-d07 BT0585 Homo	9.12
30	413450	Z99716	Hs.75372	N-acetyl-galactosaminidase, alpha-	9.12
	446442	BE221533	Hs.257858	ESTs	9.12
	438540	AA810021	Hs.136906	ESTs	9.12
	426251	M24283	Hs.168383	intercellular adhesion molecule 1 (CD54)	9.11
	410280	AA402307	Hs.73818	ubiquinol-cytochrome c reductase hinge p	9.10
35	437398	AA913738	Hs.126715	ESTs	9.10
	421559	NM_014720	Hs.105751	Sta20-related serine/threonine kinase	9.10
	439599	AF086534	Hs.187561	ESTs, Moderately similar to ALU1_HUMAN A	9.10
	430799	C19035	Hs.164259	ESTs	9.09
	424544	M88700	Hs.150403	dopa decarboxylase (aromatic L-amino aci	9.08
40	453942	AW180920	Hs.19928	ESTs	9.08
	425844	T68073	Hs.159628	serine (or cysteine) proteinase inhibito	9.08
	434658	AI624436	Hs.194488	ESTs	9.07
	453999	BE328153	Hs.240087	ESTs	9.06
	436490	R71543	Hs.18713	ESTs	9.05
45	409192	AA065131	Hs.233439	ESTs, Weakly similar to ALU7_HUMAN ALU S	9.05
	446223	BE300091	Hs.119699	hypothetical protein FLJ12969	9.04
	447247	AW369351	Hs.287955	Homo sapiens cDNA FLJ13090 fis, clone NT	9.04
	450094	AI174947	Hs.295789	Homo sapiens mRNA; cDNA DKFZp564D1164 (f	9.04
	432012	AW301344	Hs.195969	ESTs	9.04
50	422520	AJ076730	Hs.117977	kinesin 2 (60-70kD)	9.02
	418650	BE386750	Hs.86978	prolyl endopeptidase	9.02
	423008	M81590	Hs.123018	5-hydroxytryptamine (serotonin) receptor	9.02
	436476	AA326108	Hs.53631	ESTs	9.02
	448206	BE622585	Hs.3731	ESTs	9.02
55	431574	AW572659	Hs.261373	adenosine A2b receptor pseudogene	9.01
	443453	R99878	Hs.269882	ESTs	9.01
	435472	AW972330	Hs.283022	triggering receptor expressed on myeloid	9.01
	420337	AW285840	Hs.14555	Homo sapiens cDNA: FLJ21513 fis, clone C	9.00
	449810	AB008681	Hs.23994	activin A receptor, type IIB	9.00
60	406780	AA902386	Hs.286	ribosomal protein L4	8.99
	429169	AW341130	Hs.197757	ESTs, Moderately similar to FGFE_HUMAN F	8.99
	421326	AF051428	Hs.103504	estrogen receptor 2 (ER beta)	8.97
	425491	AA883316	Hs.255221	ESTs	8.96
	425516	BE000707	Hs.29567	ESTs	8.96
65	439773	AI051313	Hs.143315	ESTs	8.96
	443247	BE614387	Hs.47378	ESTs	8.96
	456623	AI084125	Hs.108106	transcription factor	8.95
	438707	L08239	Hs.5326	porcupine	8.95
	402240				8.95

	444152	AI125694	Hs.149305	Homo sapiens cDNA FLJ14264 fis, clone PL	8.95
	409842	AW501756		gb:U1-HF-BR0p-ajm-o-09-0-ULr1 NIH_MGC_5	8.94
	416277	W78765	Hs.73580	ESTs	8.94
5	456697	AI908006	Hs.111334	ferritin, light polypeptide	8.94
	410762	AF226053	Hs.66170	HSKM-B protein	8.92
	412942	AL120344	Hs.75074	mitogen-activated protein kinase-activat	8.92
	442320	AI287817	Hs.129638	ESTs	8.92
	449673	AA002084	Hs.18920	ESTs	8.91
	411486	N85785	Hs.181165	eukaryotic translation elongation factor	8.90
10	437816	BE566249	Hs.20999	Homo sapiens cDNA: FLJ23142 fis, clone L	8.90
	442732	AA257161	Hs.8658	hypothetical protein DKFZp434E0321	8.89
	419741	NM_007019	Hs.93002	ubiquitin carrier protein E2-C	8.89
	411499	AW849292		gb:IL3-CT0215-020300-090-E06 CT0215 Homo	8.89
	431154	AW971228	Hs.290259	ESTs	8.89
15	414922	D00723	Hs.77631	glycine cleavage system protein H (amino	8.88
	418036	Z37976	Hs.83337	latent transforming growth factor beta b	8.87
	406422				8.87
	422926	NM_016102	Hs.121748	ring finger protein 16	8.87
	435220	D50030	Hs.104	HGF activator	8.86
20	418203	X54942	Hs.83758	CDC28 protein kinase 2	8.86
	418613	AA744529	Hs.86575	mitogen-activated protein kinase kinase	8.85
	439250	H66568	Hs.271711	ESTs	8.85
	432359	AA076049	Hs.274415	Homo sapiens cDNA FLJ10229 fis, clone HE	8.84
25	450000	AI952797	Hs.10888	Homo sapiens cDNA: FLJ21559 fis, clone C	8.83
	425657	T89839	Hs.119471	ESTs	8.83
	425694	U51333	Hs.159237	hexokinase 3 (white cell)	8.82
	419972	AL041465	Hs.294038	ESTs, Moderately similar to ALU2_HUMAN A	8.82
	436396	AI683487	Hs.299112	Homo sapiens cDNA FLJ11441 fis, clone HE	8.82
	413413	D82520	Hs.301834	Homo sapiens cDNA FLJ10952 fis, clone PL	8.82
30	428807	AA435997	Hs.104930	ESTs	8.82
	415839	R40811	Hs.137565	ESTs	8.81
	418553	N34145	Hs.250614	ESTs	8.80
	420309	AW043637	Hs.21766	ESTs	8.80
35	421863	AI952677	Hs.108972	Homo sapiens mRNA; cDNA DKFZp434P228 (tr	8.80
	447965	AW292577	Hs.94445	ESTs	8.80
	459172	BE063380		gb:PMO-BT0275-291089-002-g10 BT0275 Homo	8.80
	403259				8.78
	411534	AW850473		gb:IL3-CT0219-280100-061-B11 CT0219 Homo	8.78
40	456161	BE264645	Hs.282093	Homo sapiens cDNA: FLJ21918 fis, clone H	8.77
	413654	AA331881	Hs.75454	peroxiredoxin 3	8.76
	401744				8.76
	425348	AL137477	Hs.155912	cadherin-like 24	8.76
	423396	AI382555	Hs.127850	bromodomain-containing 1	8.75
45	450649	NM_001429	Hs.297722	Human DNA sequence from clone RP1-85F18	8.75
	408331	NM_007240	Hs.44229	dual specificity phosphatase 12	8.74
	423872	AB020316	Hs.134015	uronyl 2-sulfotransferase	8.74
	424906	AI566088	Hs.153716	Homo sapiens mRNA for Hmob33 protein, 3'	8.74
	427596	AA449506	Hs.179765	Homo sapiens mRNA; cDNA DKFZp586H1921 (f	8.73
	432488	AA551010	Hs.216640	ESTs	8.72
50	448980	AL137527	Hs.22703	Homo sapiens mRNA; cDNA DKFZp434P1018 (f	8.72
	429455	AI472111	Hs.292507	ESTs	8.71
	429855	AW385597	Hs.138902	ESTs, Weakly similar to B34087 hypotheti	8.71
	441746	H59955	Hs.127829	ESTs	8.70
55	411945	AL033527	Hs.92137	v-myc avian myelocytomatosis viral oncog	8.70
	413492	D87470	Hs.75400	KIAA0280 protein	8.70
	435708	W31254	Hs.7045	GL004 protein	8.70
	433741	AA608019	Hs.159343	ESTs	8.70
	426340	Z97989	Hs.169370	FYN oncogene related to SRC, FGR, YES	8.69
60	422779	AA317036	Hs.41989	ESTs	8.67
	449785	AI225235	Hs.288300	Homo sapiens cDNA: FLJ23231 fis, clone C	8.67
	420144	AA811813	Hs.119421	ESTs	8.66
	420235	AA256756	Hs.31178	ESTs	8.66
	432606	NM_002104	Hs.3068	granzyme K (serine protease, granzyme 3;	8.66
65	425762	BE244076	Hs.159578	Homo sapiens mRNA for FLJ00020 protein,	8.65
	427448	BE246449	Hs.2157	Wiskott-Aldrich syndrome (eczema-thrombo	8.64
	418033	W68180	Hs.259855	Homo sapiens cDNA FLJ12507 fis, clone NT	8.64
	429084	AJ001443	Hs.195814	splicing factor 3b, subunit 3, 130kD	8.64
	417094	NM_006895	Hs.81182	histamine N-methyltransferase	8.64
	457277	NM_004736	Hs.227656	xenotropic and polytropic retrovirus rec	8.63

	422631	BE218919	Hs.118793	hypothetical protein FLJ10688	8.63
	410879	AW795186	Hs.215857	ring finger protein 14	8.63
	431585	BE242803	Hs.282823	hypothetical protein FLJ10326	8.62
	401851				8.62
5	401866				8.62
	407783	AW986872	Hs.172028	a disintegrin and metalloproteinase doma	8.62
	408242	AA251594	Hs.43913	PIBF1 gene product	8.62
	422250	AW408530	Hs.113823	CtpX (caseinolytic protease X, E. coli)	8.62
	430259	BE550182	Hs.127828	Ra/GEF-like protein 3, mouse homolog	8.62
10	452598	AI831594	Hs.68647	ESTs, Weakly similar to ALU7_HUMAN ALU S	8.62
	418541	AW749617		gb:RC3-BT0502-130100-012-g07 BT0502 Homo	8.60
	428839	AI767756	Hs.82302	ESTs	8.60
	429328	AA829402	Hs.47839	ESTs	8.60
	451491	AI972094	Hs.286221	Homo sapiens cDNA FLJ13741 fis, clone PL	8.60
15	452561	AI692181	Hs.49169	KIAA1634 protein	8.60
	420027	AF009746	Hs.94395	ATP-binding cassette, sub-family D (ALD)	8.60
	435205	X54136	Hs.181125	immunoglobulin lambda locus	8.60
	430900	U91939	Hs.248123	G protein-coupled receptor 25	8.60
	405074				8.59
20	437991	AI479773	Hs.181679	ESTs	8.59
	436346	BE328882	Hs.193098	ESTs, Moderately similar to U119_HUMAN U	8.58
	411079	AA091228		gb:chr2152.seq.F Human fetal heart, Lam	8.57
	418452	BE378749	Hs.85201	C-type (calcium dependent, carbohydrate-	8.56
	429109	AL008637	Hs.198352	neutrophil cytosolic factor 4 (40kD)	8.56
25	448019	AW947184	Hs.185641	ESTs	8.56
	449865	AW204272	Hs.198371	ESTs	8.55
	431180	H55883		gb:yc94h03.r1 Soares fetal liver spleen	8.54
	445988	BE007663	Hs.13503	inactivation escape 2	8.54
	405876				8.54
30	407235	D20569	Hs.169407	SAC2 (suppressor of actin mutations 2, y	8.54
	414807	AI738616	Hs.77348	hydroxyprostaglandin dehydrogenase 15-(N	8.54
	425671	AF183612	Hs.159142	lunatic fringe (Drosophila) homolog	8.54
	452413	AW082633	Hs.212715	ESTs	8.54
	421620	AA446183	Hs.91885	ESTs	8.53
35	444539	AI855765	Hs.146907	ESTs	8.52
	415102	M31899	Hs.77929	excision repair cross-complementing rode	8.51
	405552				8.51
	418068	AW971155	Hs.293902	ESTs, Weakly similar to prollyl 4-hydroxy	8.50
	420133	AA426117	Hs.14373	ESTs	8.50
40	438887	R68857	Hs.265499	ESTs	8.50
	446468	AI765890	Hs.16341	ESTs, Moderately similar to III ALU SUB	8.50
	446585	AV659397	Hs.262948	ESTs	8.50
	441896	AW891873		gb:CM3-NT0090-040500-173-b02 NT0090 Homo	8.50
	437718	AI927288	Hs.196779	ESTs	8.48
45	420656	AA279098	Hs.187636	ESTs	8.48
	429303	AW137635	Hs.44238	ESTs	8.48
	450624	AL043983	Hs.125063	Homo sapiens cDNA FLJ13825 fis, clone TH	8.48
	452573	AI907857	Hs.287622	Homo sapiens cDNA FLJ14082 fis, clone HE	8.48
	456341	AA229128	Hs.122647	N-myristoyltransferase 2	8.48
50	423024	AA593731	Hs.75613	CD36 antigen (collagen type I receptor,	8.47
	446985	AL039704	Hs.156827	ESTs, Weakly similar to ALU1_HUMAN ALU S	8.46
	431778	AL080276	Hs.268562	regulator of G-protein signalling 17	8.46
	400268				8.46
	421828	AW891965	Hs.289109	dimethylarginine dimethylaminohydrolase	8.45
55	417022	NM_014737	Hs.80905	Ras association (RalGDS/AF-6) domain fam	8.44
	421029	AW057782	Hs.293053	ESTs	8.44
	425171	AW732240	Hs.300615	ESTs	8.44
	459070	AI814302		gb:wj71c12.x1 NCL_CGAP_Lu19 Homo sapiens	8.42
	406006				8.42
60	412643	AW971239	Hs.293982	ESTs	8.42
	424775	AB014540	Hs.153026	SWAP-70 protein	8.42
	446848	AW136083	Hs.195268	ESTs, Weakly similar to S59501 Interfero	8.42
	448043	AI458853	Hs.201881	ESTs	8.41
	407183	AA358015		gb:EST66864 Fetal lung III Homo sapiens	8.40
65	412324	AW978439	Hs.69504	ESTs	8.40
	419594	AA013051	Hs.91417	topoisomerase (DNA) II binding protein	8.40
	430968	AW972830		gb:EST394925 MAGE resequences, MAGL Homo	8.40
	431689	AA305688	Hs.287695	UDP-Gal:betaGlcNAc beta 1,3-galactosyltr	8.40
	438582	AI521310	Hs.283365	ESTs, Weakly similar to ALU5_HUMAN ALU S	8.40

	447685	AL122043	Hs.19221	hypothetical protein DKFZp566G1424	8.40
	459119	AW844498	Hs.289052	Homo sapiens LENG8 mRNA, variant C, part	8.38
	400817				8.37
5	425285	BE245297		gb:TCBAP1E2482 Pediatric pre-B cell acute	8.37
	409385	AA071287		gb:zm61g01.r1 Stratagene fibroblast (937	8.36
	439121	BE047779	Hs.44701	ESTs	8.36
	419968	X04430	Hs.83913	Interleukin 6 (interferon, beta 2)	8.36
	408327	AW182309	Hs.249963	ESTs, Highly similar to dJ1170K4.4 [H.s]	8.35
	403978				8.34
10	448064	AA379038		gb:EST91809 Synovial sarcoma Homo sapien	8.33
	442914	AW188551	Hs.99519	Homo sapiens cDNA FLJ14007 fis, clone Y7	8.33
	428032	AW997704	Hs.11493	Homo sapiens cDNA FLJ13536 fis, clone PL	8.32
	434194	AF119847	Hs.283940	Homo sapiens PRO1550 mRNA, partial cds	8.32
	458677	AW937670		ESTs	8.32
15	420925	NM_015698	Hs.100391	T54 protein	8.30
	418475	T70298		gb:yd26g02.s1 Scores fetal liver spleen	8.30
	416852	AF283776	Hs.80285	Homo sapiens mRNA; cDNA DKFZp586C1723 (f	8.30
	430676	AF084866		gb:Homo sapiens envelope protein RIC-3 (8.30
	428455	AI732694	Hs.98520	ESTs	8.29
20	435343	AW194962	Hs.199028	ESTs	8.29
	450783	BE266695		gb:801190242F1 NIH_MGC_7 Homo sapiens cD	8.29
	404948				8.28
	422942	AF054839	Hs.122540	tetraspan 2	8.28
	453716	AA037675	Hs.152675	ESTs	8.28
25	437098	AA744488	Hs.132842	ESTs, Moderately similar to ALU1_HUMAN A	8.28
	443807	AJ076484	Hs.9963	TYRO protein tyrosine kinase binding pro	8.27
	401930	AF106069	Hs.23168	ubiquitin specific protease 15	8.26
	446554	AA151730	Hs.301789	ESTs, Weakly similar to similar to C.ala	8.26
	426280	AB007918	Hs.169182	KIAA0449 protein	8.25
30	418904	AA974411	Hs.18672	ESTs	8.25
	413888	AW958264	Hs.103832	ESTs, Weakly similar to TRHY_HUMAN TRICH	8.24
	424738	AI963740	Hs.46826	ESTs	8.24
	427359	AW020782	Hs.79881	Homo sapiens cDNA: FLJ23008 fis, clone L	8.24
	424534	D87682	Hs.150275	KIAA0241 protein	8.24
35	424429	U63830	Hs.146847	TRAF family member-associated NFKB activ	8.24
	442604	BE263710	Hs.279904	ESTs	8.22
	442992	AI914699	Hs.13297	ESTs	8.22
	427210	BE396283	Hs.173987	eukaryotic translation initiation factor	8.22
	457229	BE222450	Hs.266390	ESTs	8.21
40	423730	AA330214		gb:EST33935 Embryo, 12 week II Homo sapi	8.21
	411828	AA888624	Hs.19121	adaptor-related protein complex 2, alpha	8.20
	416051	AA835868	Hs.25253	Homo sapiens cDNA: FLJ20935 fis, clone A	8.20
	417231	R40739	Hs.21326	ESTs	8.20
	422049	W25760	Hs.77631	glycine cleavage system protein H (amino	8.20
45	427528	AJ077143	Hs.179565	minichromosome maintenance deficient (S.	8.20
	458776	AV654978	Hs.19904	cystathionase (cystathionine gamma-lyase	8.19
	417687	AI828598	Hs.250691	ESTs	8.18
	423218	NM_015896	Hs.167380	BLU protein	8.18
	425397	JO4088	Hs.156346	topoisomerase (DNA) II alpha (170kD)	8.18
50	406994	M21305	Hs.247948	Human alpha satellite and satellite 3 ju	8.18
	402401	U42349	Hs.71119	Putative prostate cancer tumor suppressor	8.18
	423397	NM_001838	Hs.1652	chemokine (C-C motif) receptor 7	8.18
	427857	AL133017	Hs.2210	thyroid hormone receptor interactor 3	8.17
	401519				8.17
55	447188	H65423	Hs.17631	Homo sapiens cDNA FLJ20118 fis, clone CO	8.16
	424704	AI263293	Hs.152096	cytochrome P450, subfamily IIJ (arachido	8.16
	435854	AJ278120	Hs.4998	DKFZP564D168 protein	8.14
	448556	AW885606	Hs.5064	ESTs	8.14
	449217	AA278538	Hs.23262	ribonuclease, RNase A family, k6	8.14
60	453124	AI139058	Hs.23298	ESTs	8.14
	442812	AI018406	Hs.131284	ESTs	8.14
	421129	BE439899	Hs.89271	ESTs	8.14

TABLE 9A shows the accession numbers for those primekeys lacking a unigeneID in Table 9. For each probeset we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

10	Pkey: CAT number: Accession:	Unique Eos probeset identifier number Gene cluster number Genbank accession numbers	
15	Pkey	CAT number	Accession
20	408057	1035720_-1	AW139565
	408069	103655_1	H81785 Z42291 R20973 AA046920
	408182	104479_1	AA047854 AA057506 AA053841
	408338	1052148_1	AW867079 AW867086 AW182772
	408828	108463_1	BE540279 AW410659 AA057857 R77693 BE278674
	409126	110159_1	AA063426 AW862323 AW408063 AA063503 AA772927 AW753492 BE175371 AA311147
	409292	111586_1	AA071051 AA070584 AA069838 AA102136 AA074430
	409314	111841_1	AA070266 AA084967 AA126998
25	409385	112523_1	AA071267 T65940 T64515 AA071334
	409398	1126716_1	AW386461 AW876408 AW386672 AW386599 AW876258 AW386619 AW386289 AW876136 AW876203 AW876213 AW876301 AW876295 AW876349 AW876365 AW876160 AW876369 AW876352 AW876271
	409671	114731_1	AA076769 AA076781 A1087988
	409768	1154035_1	AW499566 AW502378 AW499522 AW502046 AW502671 AW501917 AW501868 AW501721 AW502813
30	409841	1156088_1	AW502139 AW502432 AW502235 AW501683 AW502847
	409842	1156119_1	AW501756 AW502096 AW502465 AW501715
	409853	1156226_1	AW502327 AW502488 AW501829 AW502625 AW502687
	410531	1207200_1	AW752853 H88044 BE156082
	410688	1216101_1	AW796342 AW796356 BE161430
35	410846	1223902_1	AW807057 AW807054 AW807189 AW807193 AW807369 AW807429 AW807364 AW807365 AW807078 AW807256 AW807180 AW807331
	410896	1226053_1	AW809637 AW809687 AW810554 AW809707 AW809885 AW810000 AW810088 AW809742 AW809816 AW809749 AW809639 AW809722 AW809836 AW809774 AW810023 AW810013 AW809813 AW809660 AW809728 AW809768 AW809951 AW809657 AW809954
40	411079	123128_1	AA091228 H71860 H71073
	411424	1245497_1	AW845985 AW845991 AW845982
	411499	1248105_1	AW849292 AW849431 AW849422 AW849428 AW849420 AW849424 AW849427
	411507	1248607_1	AW850140 AW850185 AW850192
	411534	1248827_1	AW850473 AW850471 AW850431 AW850523
45	411972	1268491_1	BE074959 AW880160
	412110	1277844_1	AW893569 AW893571 AW893588 AW893593
	412226	1284289_1	W26786 AW998612 AW902272
	412257	1285376_1	AW903830 BE071918
50	412405	1293012_1	AW948126 AW948139 AW948196 AW948145 AW948162 AW948134 AW948127 AW948124 AW948153 AW948157 AW948125 AW948131 AW948158 AW948164 AW948151
	413260	1356003_1	BE075281 BE075218 BE075123 BE075119 BE075046
	413471	1371778_1	BE142098 BE142092
	413729	1385114_1	BE159999 BE160056 BE160107 BE160139
	414182	142409_1	AA136301 A1381776 AA136321
55	414989	1511339_1	T81668 C19040 C17569
	415354	1534763_1	F06495 R24336 R13046
	416011	1566439_1	H14487 R50911 Z43216
	416475	1596398_1	T70288 H58072 R02750
	417380	1672481_1	T06809 N75735
60	418392	1843934_-1	W28573
	419541	185724_1	AW749617 R64714 AA244138 AA244137 BE094019
	419544	185760_2	A1909154 AA526337 AA244193 A1909153
	420819	196721_1	AA280700 AW875494 AA687385
	421245	200620_1	AA285363 AA285333 AA285359 AA285326 AA285350
65	422673	219674_1	N59027 AA314694 N59937 R08100

	422695	219998_1	AA315158 AW981288 N76087 AW802759 A1858495 W04474
	422858	222209_1	R35398 BE252178 AA318153
	422940	223106_1	BE077458 AA337277 AA319285
5	423730	231462_1	AA330214 AW982519 T54709
	423790	232031_1	BE152393 AA330984 BE073904
	424385	238731_1	AA339666 AW952809 AA349119
	424606	241409_1	AA343938 AA344060 AW983081
	425265	249175_1	BE245297 AA353976 AW505023
	426959	273830_-1	BE262745
10	430676	32168_1	AF084866 AF084870 AF084884 AF084887 AF084869 AF084865 AF084868 AW818206 AW812038 BE144813 BE144812 AW812041 AW812040 AW812067 BE061583 BE061604 T05808 A1352469 AA580921 BE141783 BE141782 BE061601 AW814393 AW885029
	430968	326269_1	AW972830 AA527847 AA489820 AA570362
	431180	328908_1	H55883 AW971249 AA493900 H55788
15	432093	341283_1	H28383 AW972670 H28359 AA525808
	434596	38937_1	T59538 T59589 T59598 T59542 AF147374
	436357	41842_1	AJ132085 Z83805
	437159	43393_1	AL050072 AW900148
	437495	43765_1	BE177778 BE177779 AL390180 AA359908
20	439097	46858_1	H66948 AF085954 H66949
	439120	46879_1	H56389 AF085977 H56173
	440134	48675_1	BE410734 BE560117 BE270054 BE296330 BE287957 A1003007 BE545259
	441896	52842_1	AW891873 AW891897 BE564764
	445629	645767_1	A1245701 BE272724
25	447229	71288_1	BE817135 AW504051 AW504293
	448064	74761_1	AA379036 AA150589 A1696854 BE621316
	450783	84655_1	BE266695 BE265474 N53200 BE267333
	451045	85673_1	AA215872 A1696628 AA013335 H86334 AA017006
	452549	921802_1	A1907039 A1907081
30	452560	922216_1	BE077084 A1139963 AW863127 AW806209 AW806204 AW806205 AW806206 AW806211 AW806212 AW806207 AW806208 AW806210 A1907497
	452712	928309_1	AW838616 AW838660 BE144343 A1914520 AW888910 BE184854 BE184784
	453758	980026_1	U83527 AL120938 U83522
	454093	1007366_1	AW860158 AW862385 AW860159 AW862386 AW862341 AW821869 AW821893 AW062660 AW062656
35	454563	1224342_1	AW807530 AW807540 AW807537 AW846086 BE141634 AW846089 AW807499 AW807533 AW838499
	454791	1234759_1	BE071874 BE071882 AW820782 AW821007
	454977	1247099_1	AW848032 AW848630 AW848478 AW848623 AW848484 AW848169 AW848830 AW848149 AW848119 AW848893 AW848903 AW848407
	455131	1254674_1	AW857913 AW857916 AW857914 AW861627 AW861626 AW861624
40	455183	1259023_1	AW894111 AW863918 AW863856
	455254	1266449_1	AW877015 AW877133 AW876978 AW877071 AW876988 AW877069 AW877063 AW877013
	455369	1285173_16	AW903533 AW903516 AW903562 BE085202 BE085215 BE085214 BE085209 BE085172 BE085175 BE085193 BE085211 BE085199
	455982	1396849_1	BE176862 BE176876 BE176947 BE176878
45	456011	1410860_1	BE243628 BE246081 BE247016 BE241984 BE241534 BE246091 BE245679 BE243620 BE245998 BE242329 BE241417 BE241457 BE242522 BE241989 BE241464
	456023	1416335_1	R00028 BE247630
	457586	360505_1	AW062439 AW751554 AA579463
	457595	364225_-1	AA584854
50	457751	399422_1	A1908236 AA663731
	459070	883688_1	A1814302 A1814428
	459081	889426_1	W07808 A1822068
	459145	918957_1	A1903354 A1903489 A1903488
	459172	921149_1	BE063380 BE063346 A1906097
55	459234	945240_-1	A1940425

TABLE 9B shows the genomic positioning for those primekeys lacking unigene ID's and accession numbers in Table 9. For each predicted exon, we have listed the genomic sequence source used for prediction. Nucleotide locations of each predicted exon are also listed.

5	Pkey:	Unique number corresponding to an Eos probeset		
	Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.		
	Strand:	Indicates DNA strand from which exons were predicted.		
10	Nt_position:	Indicates nucleotide positions of predicted exons.		
	Pkey	Ref	Strand	Nt_position
15	400452	8113550	Minus	90308-90505
	400557	9801261	Plus	208453-208528,209833-209813
	400615	9908994	Plus	118036-118166,118681-118607
	400802	8567887	Minus	174571-174856
	400817	8568984	Plus	170793-170948
20	400880	9931121	Plus	28235-29336,36363-36580
	400885	9958187	Minus	58242-58733
	400926	7651921	Minus	52033-52158,53956-54120,54957-55052,55420-55480,56452-56666,57221-57718
	400952	7658481	Plus	192667-192826,194387-194876
	400991	8096825	Plus	159197-159320
25	401044	8117619	Plus	73501-73874
	401124	8570296	Minus	124181-124391
	401163	6981820	Plus	5302-5545
	401201	9743387	Minus	138534-138629,139234-139294,140121-140335,142033-142479
	401286	9801342	Minus	147036-147318
30	401384	6850939	Minus	58360-58545
	401468	6433826	Plus	13056-13482
	401515	7630851	Plus	29929-30126
	401519	6849315	Plus	157315-157950
	401672	9838136	Plus	128526-128704,130755-130860
35	401744	2578349	Plus	14585-14751
	401851	7770425	Minus	146443-146664,147794-147971,148351-148480,148980-149111,149801-149949
	401866	8018106	Plus	73126-73623
	402240	7690131	Plus	104382-104527,106136-106372
40	402359	9211204	Minus	40403-41961
	402585	9908890	Minus	174893-175050,183210-183435
	402788	9796102	Plus	98273-101430
	402802	3287156	Minus	53242-53432
	402812	6010110	Plus	25026-25091,25844-25920
	402828	8918414	Plus	69071-69642
45	402835	9187337	Plus	26981-27101
	402838	9369121	Minus	32589-32735,35478-35666
	402842	9369121	Minus	76355-76479
	402895	9567547	Plus	85537-85671,86379-86469
50	402964	9581599	Minus	46824-46784
	403137	9211494	Minus	92349-92572,92958-93084,93579-93712,93949-94072,94591-94748,95214-95337
	403237	7637807	Plus	7271-7527
	403259	7770585	Plus	4693-4857
	403683	7331517	Plus	217175-217448
55	403690	7387384	Minus	78627-79583
	403708	5705981	Minus	134394-134812
	403838	4176355	Plus	19197-19502
	403851	7708872	Plus	22733-23007
	403876	7657840	Plus	24755-24969
60	404407	7329316	Minus	48154-48499
	404426	7407959	Plus	77842-77954
	404632	9796668	Plus	45098-45229
	404741	8574139	Plus	143025-143467
	404758	7706327	Plus	82849-83627
	404946	7382189	Plus	134445-134750
65	405074	7770440	Plus	44340-44559,44790-45059
	405125	8247873	Plus	137113-137814
	405172	9966752	Plus	153027-153262

	405238	7249076	Minus	151699-151915
	405325	6094661	Minus	25818-26380
	405411	3451356	Minus	17503-17778,18021-18290
	405495	8050852	Minus	72182-72373
5	405552	1552506	Plus	45199-45647
	405601	5815493	Minus	147835-147935,149220-149299
	405685	4508129	Minus	37956-38097
	405777	7263187	Minus	104773-105051
	405856	7653009	Plus	101777-102043
10	405878	6758747	Plus	39694-40031
	405932	7767812	Minus	123525-123713
	405934	6758795	Plus	159913-160605
	406006	8247801	Minus	42640-42776
	406134	9163473	Plus	153291-153452
15	406189	7289992	Minus	22007-22234
	406422	9256411	Plus	163003-163311
	406516	7711422	Minus	128375-128449,128560-128784
	406538	7711478	Plus	35196-35367,38229-38476,40080-40216,43522-43840
	406554	7711566	Plus	106956-107121
20	406577	7711730	Plus	11377-11509

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TABLE 11: shows genes, including expression sequence tags that are up-regulated in prostate tumor tissue compared to normal prostate tissue as analyzed using Affymetrix/Eos Hu01 GeneChip array. Shown are the ratios of "average" normal prostate to "average" prostate cancer tissues.

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	Pkey:	Unique Eos probeset identifier number			
	ExAccn:	Exemplar Accession number, Genbank accession number			
	UnigenelD:	Unigene number			
	Unigene Title:	Unigene gene title			
	R1:	Background subtracted normal prostate : prostate tumor tissue			
	Pkey	ExAccn	UnigenelD	Unigene Title	R1
10	101336	L49169	Hs.75678	FBJ murine osteosarcoma viral oncogene homolog B	0.012
	130642	M63438	Hs.156110	Immunoglobulin kappa variable 1D-8	0.015
	133512	X01677	Hs.195188	glyceraldehyde-3-phosphate dehydrogenase	0.017
	133436	H44631	Hs.737	immediate early protein	0.017
	129292	X13810	Hs.1101	POU domain; class 2; transcription factor 2	0.019
15	100610	HQ2566-HT4782		Microtubule-Associated Protein Tau, Alt. Splice 3, Exon 8	0.02
	133448	M34516	Hs.170118	immunoglobulin lambda-like polypeptide 3	0.021
	125193	W67577	Hs.84298	CD74 antigen (invariant polypeptide of major histocompatibility complex; class II antigen-associated)	0.022
	133456	T49257	Hs.183704	ubiquitin C	0.022
	134546	AA459310	Hs.8518	Homo sapiens mRNA; cDNA DKFZp586L1722 (from clone DKFZp586L1722)	0.023
20	102131	U15085	Hs.1162	major histocompatibility complex; class II; DM beta	0.023
	101375	M13560	Hs.84298	CD74 antigen (invariant polypeptide of major histocompatibility complex; class II antigen-associated)	0.023
	100674	HG3033-HT3194		Spliceosomal Protein Sap 62	0.023
	134365	R32377	Hs.82240	syntaxin 3A	0.024
	132335	D60387	Hs.189885	ESTs	0.027
25	110303	H37901	Hs.32708	ESTs	0.027
	131678	N59162	Hs.30542	ESTs	0.028
	116599	D80046	Hs.250879	ESTs	0.028
	133769	M17733	Hs.75968	thymosin; beta 4; X chromosome	0.029
	107904	AA026548	Hs.61389	ESTs	0.029
30	129427	T80746	Hs.111334	ferritin; light polypeptide	0.03
	105987	AA406631	Hs.110299	mitogen-activated protein kinase kinase 7	0.03
	131466	F03233	Hs.27189	ESTs	0.03
	102859	X00274	Hs.76807	Human HLA-DR alpha-chain mRNA	0.032
	134626	S82198	Hs.8709	caldesmon (serum calcium decreasing factor; elastase IV)	0.032
35	134170	M63138	Hs.79572	cathepsin D (lysosomal aspartyl protease)	0.033
	131713	X57809	Hs.181125	immunoglobulin lambda gene cluster	0.033
	100748	HG3517-HT3711		Alpha-1-Antitrypsin, 5' End	0.034
	118769	N74496		ESTs	0.034
	111734	R25375	Hs.126916	ESTs	0.034
40	109221	AA192755	Hs.85840	ESTs; Weakly similar to stac [H.sapiens]	0.036
	133846	AA480073	Hs.76719	U6 snRNA-associated Sm-like protein	0.036
	135281	AA401575	Hs.97757	ESTs	0.036
	119073	R32894	Hs.45514	v-ets avian erythroblastosis virus E26 oncogene related	0.037
	100760	HG3576-HT3779		Major Histocompatibility Complex, Class II Beta W52	0.037
45	101426	M18483	Hs.25	ATP synthase; H+ transp.; mitochondri F1 complex; beta polypept	0.038
	129568	AA428025	Hs.114360	transforming growth factor beta-stimulated protein TSC-22	0.038
	130900	Z38468	Hs.21036	ESTs; Moderately similar to F25965_3 [H.sapiens]	0.038
	133879	M13829	Hs.77183	v-rat murine sarcoma 3511 viral oncogene homolog 1	0.039
	100627	HG2702-HT2798		Serine/Threonine Kinase (Gb:Z25424)	0.039
50	129424	M55593	Hs.111301	matrix metalloproteinase 2 (gelatinase A; 72kD gelatinase; 72kD type IV collagenase)	0.039
	128652	AA621245	Hs.103147	ESTs; Weakly similar to similar to SP:YR40_BACSU [C.elegans]	0.039
	129979	T72635	Hs.13956	ESTs	0.039
	133468	X03068	Hs.73931	major histocompatibility complex; class II; DQ beta 1	0.04
	102636	U67092		Human ataxia-telangiectasia locus protein (ATM) gene, exons 1a, 1b, 2, 3 and 4, partial cds	0.04
55	129536	M33493	Hs.184504	trypsin; alpha	0.04
	133599	M64788	Hs.75151	RAP1; GTPase activating protein 1	0.04
60					0.041

5	102104	U12139		Human alpha1(XI) collagen (COL11A1) gene, 5' region and exon 1	0.041
	131340	AA478305	Hs.25817	Homo sapiens chromosome 19; cosmid R27216	0.041
	130446	X78510	Hs.155693	protein tyrosine phosphatase; non-receptor type 21	0.042
	101352	L77701	Hs.16297	COX17 (yeast) homolog; cytochrome c oxidase assembly protein	0.042
	122593	AA453310	Hs.128749	alpha-methylacyl-CoA racemase	0.042
10	130181	R39552	Hs.151608	Homo sapiens clone 23622 mRNA sequence	0.042
	134071	Z14093	Hs.78950	branched chain keto acid dehydrogenase E1; alpha polypeptide (maple syrup urine disease)	0.042
	108129	AA053252	Hs.185848	ESTs; Weakly similar to II ALU SUBFAMILY J WARNING ENTRY II [H.sapiens]	0.043
	130511	L32137	Hs.1584	cartilage oligomeric matrix protein (pseudoachondroplasia; epiphyseal dysplasia 1; multiple)	0.043
	133336	AA291456	Hs.711190	ESTs	0.043
15	132982	L02326	Hs.198118	immunoglobulin lambda-like polypeptide 2	0.044
	131880	AA047034	Hs.33818	RecQ protein-like 5	0.044
	130540	U35234	Hs.159534	protein tyrosine phosphatase; receptor type; S	0.044
	133457	AA258595	Hs.73931	major histocompatibility complex; class II; DQ beta 1	0.044
	101191	L20688	Hs.83656	Rho GDP dissociation inhibitor (GDI) beta	0.044
20	101860	M85810	Hs.37165	collagen; type IX; alpha 2	0.044
	102799	U88998		Human endogenous retroviral H protease/integrase-derived ORF1 mRNA, complete cds, and putative envelope prot mRNA, partial cds	0.044
	107200	D20350	Hs.5628	ESTs	0.044
	101166	L14927	Hs.2099	lipocalin 1 (protein migrating faster than albumin; tear prealbumin)	0.044
	134289	M54915	Hs.81170	pln-1 oncogene	0.044
25	135329	AA438028	Hs.98858	ESTs	0.044
	124850	T03786	Hs.151531	protein phosphatase 3 (formerly 2B); catalytic subunit; beta isoform (calcineurin A beta)	0.044
	102919	X12447	Hs.183760	aldolase A; fructose-bisphosphate	0.044
	100574	HG2279-HT2375		Triosephosphate isomerase	0.045
	131286	AA450092	Hs.25300	Homo sapiens clones 24718 and 24825 mRNA sequence	0.045
30	102675	U72512		Human B-cell receptor associated protein (hBAP) alternatively spliced mRNA, partial 3'UTR	0.045
	131332	R50487	Hs.25717	ESTs	0.045
	101634	M57731	Hs.75765	GRO2 oncogene	0.046
	113118	T47906	Hs.220512	ESTs	0.046
	124884	R77276	Hs.120911	ESTs	0.046
35	130523	W76097	Hs.214507	ESTs	0.046
	110244	H26742	Hs.25357	ESTs; Weakly similar to ALR [H.sapiens]	0.046
	131932	AA454980	Hs.25601	chromodomain helicase DNA binding protein 3	0.046
	132509	H09751	Hs.5038	neuropathy target esterase	0.046
	133372	AA291139	Hs.72242	ESTs	0.046
40	100817	HG4011-HT4804		Dystrophin-Associated Glycoprotein, 50 Kda, Alt. Splice 2	0.047
	106746	AA476436	Hs.7991	ESTs	0.047
	135401	L14813	Hs.169271	carboxyl ester lipase-like (bile salt-stimulated lipase-like)	0.047
	130479	R44163	Hs.12457	Homo sapiens clone 23770 mRNA sequence	0.047
	102589	U62015	Hs.8867	cysteine-rich; angiogenic inducer; 61	0.047
45	121521	AA412165	Hs.97358	EST	0.048
	135340	AA425137	Hs.99093	Homo sapiens chromosome 19; cosmid R28379	0.048
	132336	AA342422	Hs.45073	ESTs	0.048
	115368	AA282133	Hs.88980	ESTs; Weakly similar to similar to collagen [C.elegans]	0.048
	101278	L38487	Hs.110849	estrogen-related receptor alpha	0.048
50	103284	X80200	Hs.8375	TNF receptor-associated factor 4	0.048
	100564	HG2239-HT2324		Potassium Channel Protein (Gb-Z11585)	0.048
	133132	Z40883	Hs.65588	ESTs; Weakly similar to dJ393P12.2 [H.sapiens]	0.048
	121811	AA424535	Hs.98416	ESTs	0.048
	129613	AA279481	Hs.238831	ESTs; Weakly similar to collagen alpha 1(XVIII) chain [M.musculus]	0.049
55	132468	S79854	Hs.49322	deiodinase; liothyronine; type III	0.049
	120111	W95841	Hs.136031	ESTs	0.049
	103668	Z83741	Hs.248174	H2A histone family; member M	0.049
	130386	F10874	Hs.234249	mitogen-activated protein kinase 8 interacting protein 1	0.049
	104275	C02170	Hs.39387	ESTs; Weakly smlr to weak smrlity to ribosomal prot L14 [C.elegans]	0.049
60	106305	AA436146	Hs.12828	ESTs	0.05
	116431	AA609878	Hs.55289	ESTs; Weakly smlr to 110 KD CELL MEMBRANE GLYCOPROTEIN [H.sapiens]	0.813
	120339	AA206465	Hs.256470	EST	0.05
	114427	AA017063		ESTs; Highly similar to Miz-1 protein [H.sapiens]	0.05
	118821	N79070	Hs.94789	ESTs	0.05
65	118979	N93788	Hs.43666	protein tyrosine phosphatase type IVA; member 3	0.05
	107495	W78776	Hs.90375	ESTs	0.051
	120240	Z41732	Hs.66049	ESTs	0.051

5	114331	Z41309	Hs.12400	ESTs	0.051
	130947	R40037	Hs.21508	ESTs	0.052
	129242	W81679	Hs.5174	ribosomal protein S17	0.052
	131413	AA482390	Hs.26510	ESTs; Modly smir to vacuolar prot sorting homolog v-ps33b [R.norvegicus]	0.052
	112304	R54798	Hs.26239	ESTs	0.052
10	101416	M17254	Hs.45514	v-ets avian erythroblastosis virus E26 oncogene related	0.052
	131201	AA426304	Hs.24174	ESTs	0.052
	101054	K02405	Hs.73933	Human MHC class II HLA-DQ-beta mRNA (DR7 DQw2); complete cds	0.052
	101306	L41143	Hs.232069	T-cell leukemia translocation altered gene	0.053
	129311	T55087		yb45c08.r1 Stratagene fetal spleen (#937205) Homo sapiens cDNA	
15	129942	U95301	Hs.144442	clone IMAGE:74126 5', mRNA sequence.	0.053
	119210	R83340	Hs.92995	phospholipase A2; group X	0.053
	110106	K01160		ESTs	0.053
	114086	Z38266	Hs.12770	Accession not listed in Genbank	0.053
	110171	H19984	Hs.31709	Homo sapiens PAC clone DJ0777023 from 7p14-p15	0.053
20	101004	J04101	Hs.248109	ESTs	0.053
	129715	N58479	Hs.12126	v-ets avian erythroblastosis virus E26 oncogene homolog 1	0.053
	101581	M34998	Hs.198253	ESTs; Weakly similar to LR8 [H.sapiens]	0.053
	113285	T66830	Hs.182712	major histocompatibility complex, class II; DQ alpha 1	0.053
	127537	AA569531	Hs.162859	ESTs	0.053
25	100813	HG3995-HT4265		ESTs	0.054
	101841	M93107	Hs.76893	Cpg-Enriched Dna, Clone S19	0.054
	135053	R77159	Hs.93678	3-hydroxybutyrate dehydrogenase (heart; mitochondrial)	0.054
	101419	M17886	Hs.177592	ESTs	0.054
	119724	W69468	Hs.47622	ribosomal protein; large; P1	0.054
30	102673	U72509		ESTs	0.055
	129877	AA248589	Hs.13094	Human alternatively spliced B8 (B7) mRNA, partial sequence	0.055
	114788	AA156737	Hs.103904	ESTs; Weakly similar to ORF YGR101w [S.cerevisiae]	0.055
	123812	AA620607	Hs.111591	EST	0.055
	117669	N39237	Hs.44977	ESTs	0.055
35	123782	AA810111	Hs.162695	EST	0.055
	102395	U41767	Hs.92208	a disintegrin and metalloproteinase domain 15 (metargidin)	0.055
	133795	M12529	Hs.169401	apolipoprotein E	0.055
	123193	AA489228	Hs.136956	ESTs	0.056
	132595	AA253369	Hs.155742	glyoxylate reductase/hydroxypyruvate reductase	0.056
40	104161	AA458471	Hs.7724	KIAA0963 protein	0.056
	115330	AA281145	Hs.88827	ESTs	0.056
	112693	T08000	Hs.194684	bassoon (presynaptic cytomatrix protein)	0.056
	133475	L29217	Hs.73987	CDC-like kinase 3	0.056
	128699	K03207	Hs.103972	proline-rich protein BstNI subfamily 4	0.056
45	102940	X13956	Hs.24998	Hu 12S RNA induced by poly(rI); poly(rC) and Newcastle disease virus	0.056
	131299	AA431464	Hs.25426	ESTs; Weakly similar to unknown [H.sapiens]	0.057
	102485	U51240	Hs.79356	Lysosomal-associated multispinning membrane protein-5	0.057
	129594	R70379	Hs.115396	Human germline IgD chain gene; C-region; C-delta-1 domain	0.057
	118593	N69020	Hs.207689	EST	0.057
50	126702	U54602	Hs.2785	keratin 17	0.057
	124386	N27368	Hs.212414	sema domain; immunoglobulin domain (Ig); short basic domain;	0.057
	130538	M20786	Hs.159509	secreted; (semaphorin) 3E	0.057
	114299	Z40782	Hs.22920	alpha-2-plasmin inhibitor	0.057
	115604	AA400378	Hs.49391	similar to S68401 (cattle) glucose induced gene	0.057
55	106052	AA416947	Hs.6382	ESTs	0.057
	131730	U05681	Hs.31210	ESTs; Highly similar to KIAA0612 protein [H.sapiens]	0.057
	131285	AA479498	Hs.25274	B-cell CLL/lymphoma 3	0.057
	129705	X78706	Hs.12068	ESTs; Modly smir to putative seven pass transmembrane prot [H.sapiens]	0.058
	123175	AA489010	Hs.178400	carbamoyl transferase	0.058
60	103592	Z30644	Hs.123059	ESTs	0.058
	118198	N59478	Hs.48396	chloride channel Kb	0.058
	104888	AA053348	Hs.144626	ESTs; Moderately similar to tumor necrosis factor-alpha	0.058
	104250	AF000575	Hs.105928	-induced protein B12 [H.sapiens]	0.058
				growth differentiation factor 11	0.058
65	113301	T87452	Hs.13104	leukocyte immunoglobulin-like receptor; subfamily B (with TM	0.058
	110441	H50302	Hs.19845	and ITIM domains); member 3	0.058
	125297	Z39215	Hs.159409	EST	0.058
	135258	AA292423	Hs.97272	ESTs; Highly smir to prot phosphatase 2A BR gamma subunit [H.sapiens]	0.058
	130633	T92363	Hs.178703	ESTs	0.058
	112006	R42607	Hs.22241	ESTs; Weakly similar to dJ281H8.2 [H.sapiens]	0.058
				ESTs	0.058
				hypothetical protein	0.058

5	130805	U12194	Hs.170238	sodium channel; voltage-gated; type I; beta polypeptide	0.058
	134907	D80002	Hs.178292	KIAA0180 protein	0.058
	132619	AA404565	Hs.53447	ESTs; Moderately similar to kinesin light chain 1 [M.musculus]	0.058
	135115	N35489	Hs.94653	neurochondrin	0.058
	100531	HG1872-HT1907		Major Histocompatibility Complex, Dg	0.058
10	124530	N62256	Hs.102727	EST	0.058
	118960	W87533	Hs.32699	ESTs; Moderately similar to LIV-1 protein [H.sapiens]	0.058
	132793	AA478999	Hs.56966	KIAA0906 protein	0.058
	101076	L04270	Hs.1116	lymphotoxin beta receptor (TNFR superfamily; member 3	0.058
	130655	N92934	Hs.17409	cysteine-rich protein 1 (intestinal)	0.058
15	134458	AA192614	Hs.83577	cysteine and glycine-rich protein 3 (cardiac LIM protein)	0.058
	105904	AA401452	Hs.32060	ESTs	0.059
	132878	AA026793	Hs.58679	ESTs; Weakly similar to 4F2/CD98 light chain [M.musculus]	0.059
	121828	AA425166	Hs.98497	ESTs	0.059
	133418	U76366	Hs.172727	Treacher Collins-Franceschetti syndrome 1	0.059
20	129317	N46244	Hs.110373	ESTs	0.059
	130153	D85815	Hs.15114	ras homolog gene family; member D	0.059
	124403	N31745	Hs.102493	ESTs	0.059
	127683	AA668123	Hs.134170	ESTs	0.059
	129814	W20070	Hs.168625	KIAA0979 protein	0.059
25	131770	D59682	Hs.31833	ESTs	0.06
	117557	N33920	Hs.44532	diubiquitin	0.06
	103522	Y10514		H.sapiens mRNA for CD152 protein	0.06
	120029	W91960	Hs.250640	sequence-specific single-stranded-DNA-binding protein	0.06
	120135	U15480	Hs.41691	activating transcription factor B	0.06
30	123617	AA609183	Hs.181131	ESTs	0.06
	112136	R46100	Hs.9739	ESTs	0.061
	133725	V00563	Hs.179543	immunoglobulin mu	0.061
	102069	U09196	Hs.82520	Hu 1.1 kb mRNA upregulated in retinoic acid treated HL-60 neutrophilic cells	0.061
	106555	AA455000	Hs.16725	ESTs	0.061
35	123269	AA491226	Hs.105280	ESTs; Weakly similar to dJ963K23.2 [H.sapiens]	0.061
	109088	AA166837	Hs.72620	DKFZP434I114 protein	0.061
	129399	AA263028	Hs.111076	malate dehydrogenase 2; NAD (mitochondrial)	0.061
	129375	W79850	Hs.11081	ESTs; Weakly similar to HPBR11-7 protein [H.sapiens]	0.061
	135271	AA397763	Hs.97562	ESTs	0.061
40	132858	W90398	Hs.6147	KIAA1075 protein	0.061
	129364	AA477106	Hs.110757	DNA segment on chromosome 21 (unique) 2056 expressed sequence	0.061
	123427	AA598548	Hs.112471	ESTs	0.061
	105236	AA218179	Hs.19105	translocase of inner mitochondrial membrane 17 (yeast) homolog B	0.061
	101012	J04444	Hs.697	cytochrome c-1	0.062
45	134791	L18983	Hs.89655	protein tyrosine phosphatase; receptor type; N	0.062
	133700	K01396	Hs.75621	protease inhibitor 1 (anti-elastase); alpha-1-antitrypsin	0.062
	123897	AA621065	Hs.112943	ESTs	0.062
	129363	H05704	Hs.110748	H sapiens HCR (a-helix coiled-coil rod homologue) mRNA; complete cds	0.062
	105719	AA291644	Hs.36783	ESTs	0.062
50	124226	H62396	Hs.190266	ESTs	0.062
	117437	N27645		yw5e3.s1 Weizmann Olfactory Epithelium H sapiens cDNA clone	0.062
	132741	AA394133	Hs.55898	IMAGE255676 3' smir to contains L1.13 L1 repetitive element +, mRNA seq	0.062
	134437	M26041	Hs.198253	ESTs; Highly similar to OASIS protein [M.musculus]	0.062
	107684	AA010594	Hs.5326	major histocompatibility complex; class II; DQ alpha 1	0.062
55	120844	AA348417	Hs.96917	ESTs; Moderately similar to p1m-1 protein [H.sapiens]	0.062
	101574	M34182	Hs.159029	ESTs	0.062
	131219	C00476	Hs.24395	protein kinase; cAMP-dependent; catalytic; gamma	0.062
	103495	Y09022	Hs.153591	small inducible cytokine subfamily B (Cys-X-Cys); member 14 (BRAC)	0.062
	129607	AA404594	Hs.11607	Not56 (D. melanogaster)-like protein	0.062
60	106467	AA450040	Hs.154162	ESTs	0.062
	128841	T16358	Hs.106443	ADP-ribosylation factor-like 2	0.062
	100515	HG1723-HT1729		ESTs	0.062
	118332	T54095		Macrophage Scavenger Receptor, Alt. Splice 2	0.062
	134516	AA171939	Hs.23413	ESTs; Weakly similar to II ALU SUBFAMILY J WARNING ENTRY II [H.sapiens]	0.062
65	135012	X73808	Hs.93029	ESTs	0.062
	103576	Z26256		sparc/osteonectin; cwcv and kazal-like domains proteoglycan (testican)	0.063
	115514	AA297739	Hs.55609	H.sapiens isoform 1 gene for L-type calcium channel, exon 1	0.063
	103996	AA321355		ESTs; Weakly similar to ISOLEUCYL-TRNA SYNTHETASE;	0.063
	110505	H55992	Hs.20495	CYTOPLASMIC [H.sapiens]	0.063
	133912	X62744	Hs.77522	EST2393 Bone marrow Homo sapiens cDNA 5' end, mRNA sequence	0.063
	129581	M33600	Hs.180255	DKFZP434F011 protein	0.063
				major histocompatibility complex; class II; DM alpha	0.063
				major histocompatibility complex; class II; DR beta 1	0.063

5	130139	R38280	Hs.150922	BCS1 (yeast homolog)-like	0.064
	105817	AA397825	Hs.5307	synaptopodin	0.064
	134858	AA410617	Hs.178009	ESTs	0.064
	100306	D50495	Hs.80598	transcription elongation factor A (SII); 2	0.064
	100277	D42053	Hs.75890	site-1 protease (subtilisin-like; sterol-regulated; cleaves sterol regulatory element binding proteins)	0.064
10	133116	D61259	Hs.6529	ESTs	0.064
	134909	AA521488	Hs.90998	KIAA0128 protein	0.064
	130319	X74794	Hs.154443	mitochondrion maintenance deficient (S. cerevisiae) 4	0.064
	132057	AA102489	Hs.173484	ESTs	0.064
	108334	AA070473		zm7c8.s1 Stratagene neuroepithelium (#937231) Homo sapiens cDNA clone IMAGE:5399 3', mRNA sequence	0.064
15	129763	F10815	Hs.12373	KIAA0422 protein	0.064
	135112	T67484	Hs.94617	ESTs; Weakly similar to predicted using Genefinder [C.elegans]	0.064
	122269	AA436856	Hs.98910	ESTs	0.064
	133082	AA457129	Hs.6455	RuvB (E. coli homolog)-like 2	0.064
	113213	T58607		ya94a02.s1 Stratagene placenta (#937225) Homo sapiens cDNA clone IMAGE:69290 3', mRNA sequence.	0.065
20	106228	AA429290	Hs.17719	ESTs	0.065
	130182	Y12661	Hs.171014	VGF nerve growth factor inducible	0.065
	104894	AA054087	Hs.18858	phospholipase A2; group IVC (cytosolic; calcium-independent)	0.065
	103508	Y10141		H.sapiens DAT1 gene, partial, VNTR	0.065
	128474	U40671	Hs.100298	ligase III; DNA; ATP-dependent	0.065
25	134012	AA417821	Hs.237924	ESTs; Highly similar to CGI-69 protein [H.sapiens]	0.065
	134536	AA457735	Hs.850	IMP (inosine monophosphate) dehydrogenase 1	0.065
	111714	R23146	Hs.23468	ESTs	0.065
	110521	H57060	Hs.108268	ESTs	0.065
	103282	X80198	Hs.77628	steroidogenic acute regulatory protein related	0.065
30	113921	W80730	Hs.28355	ESTs	0.065
	129331	N93465	Hs.110453	ESTs; Highly similar to CGI-38 protein [H.sapiens]	0.065
	111318	N74597	Hs.180535	ESTs; Weakly similar to mitogen inducible gene mig-2 [H.sapiens]	0.065
	135138	AA036794	Hs.95186	ESTs; Weakly similar to T20B12.3 [C.elegans]	0.065
	107289	T10792	Hs.172098	ESTs	0.065
35	121405	AA406083	Hs.98007	ESTs	0.065
	124965	T16275	Hs.106359	ESTs	0.065
	106595	AA456933	Hs.174481	ESTs	0.065
	100106	AF015910		Homo sapiens unknown protein mRNA, partial cds	0.066
	134715	AA282757	Hs.89040	prepronociceptin	0.066
40	135367	AA480109	Hs.9963	TYRO protein tyrosine kinase binding protein	0.066
	111533	R08548	Hs.251651	EST	0.066
	128509	R53109	Hs.247362	dimethylarginine dimethylaminohydrolase 2	0.066
	101030	J05037	Hs.78751	serine dehydratase	0.066
	102753	U80226		Human gamma-aminobutyric acid transaminase mRNA, partial cds	0.067
45	126991	R31652	Hs.821	biglycan	0.067
	109583	F02322	Hs.26135	ESTs	0.067
	119241	T12559	Hs.221382	ESTs	0.067
	130569	AA156597	Hs.256441	EST; Moderately similar to CGI-136 protein [H.sapiens]	0.067
	112928	T10316	Hs.4302	ESTs	0.067
50	120495	AA256073	Hs.190626	ESTs	0.067
	130931	AA278412	Hs.21346	ESTs; Weakly similar to F42C5.7 gene product [C.elegans]	0.067
	129982	M87789	Hs.140	immunoglobulin gamma 3 (Gm marker)	0.067
	133832	H03387	Hs.241305	estrogen-responsive B box protein	0.067
	110697	H93721	Hs.20798	ESTs	0.067
55	121183	AA400138	Hs.97703	ESTs	0.067
	130953	U12707	Hs.2157	Wiskott-Aldrich syndrome (eczema-thrombocytopenia)	0.067
	102218	U24183	Hs.75160	phosphofructokinase; muscle	0.067
	114181	Z39079	Hs.8021	KIAA1058 protein	0.067
	116581	D51287	Hs.82148	ribosomal protein S12	0.067
60	132498	T87708	Hs.50098	ESTs	0.068
	103788	AA096014	Hs.9527	ESTs; Highly similar to HSPC013 [H.sapiens]	0.068
	102459	U48936		Human amiloride-sensitive epithelial sodium channel gamma subunit mRNA, 5' end, partial cds	0.068
	100373	D79999	Hs.77225	ADP-ribosyltransferase (NAD+; poly (ADP-ribose) polymerase)-like 1	0.068
	132717	AA203321	Hs.151696	DKFZP727G051 protein	0.068
65	128863	D87462	Hs.106674	BRCA1 associated protein-1 (ubiquitin carboxy-terminal hydrolase)	0.068
	115183	AA262029	Hs.88218	ESTs	0.068
	124558	N68048	Hs.141605	ESTs	0.069
	117225	N20382	Hs.42848	ESTs	0.069
	110665	H83380	Hs.32757	ESTs	0.069

5	132805	U70683	Hs.182965	Kruppel-like factor 4 (gut)	0.069
	105778	AA348910	Hs.153289	DOM-3 (C. elegans) homolog Z	0.069
	134770	R72079	Hs.89575	CD79B antigen (immunoglobulin-associated beta)	0.069
	123097	AA485869	Hs.105671	ESTs	0.069
	100750	HG3523-HT4899		Proto-Oncogene C-Myc, Alt. Splice 3, Orf 114	0.069
10	125091	T91518		ye20f05.s1 Stratagene lung (#937210) H sapiens cDNA clone IMAGE:	
				3' similar to contains Alu repetitive element; contains MER12 repetitive element;	
				mRNA sequence.	0.069
				Zinc Finger Protein (Gbj.M88357)	0.069
				ESTs	0.069
15	100756	HG3565-HT3768		complement component 2	0.07
	113483	T87768	Hs.16439	interleukin 15 receptor; alpha	0.07
	101119	L08708	Hs.2253	collagen-binding protein 2 (collagen 2)	0.07
	102286	U31628	Hs.12503	plasminogen activator inhibitor; type I	0.07
	135349	D83174	Hs.9930	ESTs; Weakly similar to T25G3.1 [C.elegans]	0.07
20	100991	J03764	Hs.82085	ESTs	0.07
	133675	AA443720	Hs.7551	CD14 antigen	0.07
	105422	AA251014	Hs.12210	ESTs	0.07
	102932	X13334	Hs.75627	ESTs; Weakly similar to ACROSIN PRECURSOR [H.sapiens]	0.07
	119147	R58878	Hs.85739	ESTs	0.07
25	104900	AA055048	Hs.180481	eukaryotic translation initiation factor 4E binding protein 1	0.07
	133185	AA481404	Hs.6686	ESTs	0.07
	115496	AA290674	Hs.71819	ESTs; Weakly similar to F55A12.9 [C.elegans]	0.071
	121005	AA398332	Hs.97613	mannosidase; alpha; class 2B; member 1	0.071
	124869	R69088	Hs.28728	ESTs; Wdly smlr to II ALU SUBFAMILY J WARNING ENTRY II [H.sapiens]	0.071
30	129154	N23673	Hs.108969	ESTs	0.071
	112181	R48295		collagen; type II; alpha 1 (primary osteoarthritis; spondyloepiphyseal	
	125251	W87486	Hs.141464	dysplasia; congenital)	0.071
	134298	J00118	Hs.81343	ESTs	0.071
				ESTs	0.071
35	119745	W70264	Hs.58093	ESTs	0.071
	131306	AA232686	Hs.25489	ESTs	0.071
	107776	AA018820	Hs.221147	ESTs	0.071
	134271	AA199630	Hs.184456	ESTs; Wdly smlr to II ALU SUBFAMILY SX WARNING ENTRY II [H.sapiens]	0.071
	101798	M85220		Accession not listed in Genbank	0.071
40	135402	S76942	Hs.99922	dopamine receptor D4	0.071
	118742	N74052	Hs.50424	EST	0.071
	131867	N64856	Hs.3353	Homo sapiens clone 24940 mRNA sequence	0.071
	102923	X12517	Hs.1063	small nuclear ribonucleoprotein polypeptide C	0.072
	100775	HG371-HT26388		Mucin 1, Epithelial, Alt. Splice 9	0.072
45	111020	N54361	Hs.185726	ESTs	0.072
	134224	X60822	Hs.163593	ribosomal protein L18a	0.072
	124059	F13673	Hs.99769	ESTs	0.072
	133972	AA160743	Hs.78019	Homo sapiens clone 24432 mRNA sequence	0.072
	129681	AA436009	Hs.178186	ESTs; Weakly similar to WASP-family protein [H.sapiens]	0.072
50	103065	X58399	Hs.81221	Human L2-9 transcript of unrearranged immunoglobulin V(H)5 pseudogene	0.072
	124968	T19271	Hs.155560	calnexin	0.072
	112270	R53021	Hs.203358	ESTs	0.072
	116704	F10183	Hs.66140	EST	0.072
	129890	M13699	Hs.111461	ceruloplasmin (ferroxidase)	0.072
55	127345	AA972008	Hs.166253	ESTs; Highly similar to KIAA0476 protein [H.sapiens]	0.072
	112436	R63090	Hs.28391	ESTs	0.072
	114531	AA053033	Hs.203330	ESTs	0.072
	135122	H99080	Hs.94814	ESTs	0.072
	103934	AA281338	Hs.134200	Homo sapiens mRNA; cDNA DKFZp564C186 (from clone DKFZp564C186)	0.072
60	109363	AA215369	Hs.185764	ESTs; Weakly similar to hypothetical protein [H.sapiens]	0.072
	112647	R83329	Hs.33403	ESTs	0.073
	127083	Z44079	Hs.91608	otoferlin	0.073
	133027	AA402624	Hs.63236	synuclein; gamma (breast cancer-specific protein 1)	0.073
	122086	AA432121	Hs.250986	EST	0.073
65	110405	H47542	Hs.33962	ESTs	0.073
	128697	AB002344	Hs.103915	KIAA0346 protein	0.073
	112221	R50380	Hs.25670	ESTs	0.073
	100478	HG1067-HT1067		Mucin (Gbj.M22406)	0.073
	115598	AA400129	Hs.65735	ESTs	0.073
65	132491	AA227137	Hs.4984	KIAA0828 protein	0.073
	101655	M60299		Human alpha-1 collagen type II gene, exons 1, 2 and 3	0.073
	106018	AA411887	Hs.34737	ESTs	0.073
	129683	W05348	Hs.158198	DKFZP434B103 protein	0.073
	134137	F10045	Hs.79347	KIAA0211 gene product	0.073
	114008	W89128	Hs.19872	ESTs	0.073

5	107653	AA010210	Hs.47041	ESTs	0.073
	104798	AA029462	Hs.17235	ESTs	0.073
	134082	L16991	Hs.79008	deoxythymidylate kinase	0.073
	119180	R80413	Hs.92520	ESTs	0.073
	107741	AA016982	Hs.64341	ESTs	0.073
10	133683	AA335223	Hs.75558	pepsinogen 5; group I (pepsinogen A)	0.073
	111694	R22035	Hs.23331	ESTs	0.073
	120764	AA338729	Hs.133086	ESTs	0.073
	119389	T88826	Hs.90973	ESTs	0.074
	100829	HG688-HT688		Major Histocompatibility Complex, Class II, Dr Beta 2 (Gb:X65561)	0.074
15	119388	T88798		plasminogen activator inhibitor; type I	0.074
	133019	AF008674	Hs.184434	axin	0.074
	105185	AA191495	Hs.189937	ESTs	0.074
	133413	S72043	Hs.73133	metallothionein 3 (growth inhibitory factor (neurotrophic))	0.074
	101017	J04599	Hs.821	biglycan	0.074
20	132865	K02765	Hs.251972	complement component 3	0.074
	110882	N38001	Hs.17348	ESTs; Wkly smlr to II ALU SUBFAMILY SQ WARNING ENTRY II [H.sapiens]	0.074
	129197	T90303	Hs.109308	ESTs; Wkly smlr to leucine-rich glioma-inactivated prot precursor [H.sapiens]	0.074
	101184	L19871	Hs.480	activating transcription factor 3	0.075
	134910	AA431320	Hs.9100	ESTs	0.075
25	119411	T96821	Hs.203658	EST	0.075
	102000	U01824	Hs.380	solute carrier family 1 (glial high affinity glutamate transporter); member 2	0.075
	114691	AA121883	Hs.103779	ESTs; Weakly similar to envelope protein [H.sapiens]	0.075
	134179	U53204	Hs.79706	plectin 1; intermediate filament binding protein; 500kD	0.075
	134503	U34860	Hs.84183	diphtheria toxin resistance protein required for diphthamide biosynthesis (Saccharomyces)-like 1	0.075
30	129719	N68398	Hs.167768	ESTs; Moderately similar to Pro-a2(XI) [H.sapiens]	0.075
	113916	W80464	Hs.31928	ESTs; Wkly smlr to alternatively spliced product using exon 13A [H.sapiens]	0.075
	113897	W73928	Hs.4947	ESTs	0.075
	129697	R00841	Hs.172069	DKFZP434C212 protein	0.075
	112078	R44155	Hs.112218	ESTs	0.075
35	121880	AA429886	Hs.110407	ESTs; Weakly similar to coded for by C. elegans cDNA yk173c12.5 [C.elegans]	0.075
	100898	HG4638-HT5050		Spliceosomal Protein Sap 49	0.075
	121626	AA416974	Hs.98174	ESTs	0.075
	133670	AA243416	Hs.75470	hypothetical protein; expressed in osteoblast	0.075
	131879	AA017161	Hs.33782	ESTs	0.075
40	100254	D38037	Hs.77643	FK506-binding protein 1B (12.6 kD)	0.075
	133194	AA291728	Hs.67201	ESTs	0.075
	106081	AA418394	Hs.25354	ESTs	0.075
	115544	AA351433	Hs.66187	Homo sapiens clone 23700 mRNA sequence	0.076
	119955	W87480	Hs.58989	ESTs	0.076
45	104407	H61361	Hs.102171	immunoglobulin superfamily containing leucine-rich repeat	0.076
	135019	X58431	Hs.98428	Human Hox2.2 gene for a homeobox protein	0.076
	114815	AA161488	Hs.103931	DKFZP434B0335 protein	0.076
	119471	W31352	Hs.55445	ESTs	0.076
	117788	N48292	Hs.46849	ESTs	0.076
50	119406	T95064	Hs.183771	EST	0.076
	130777	R61742	Hs.256554	ESTs	0.076
	130494	L13197	Hs.75874	pregnancy-associated plasma protein A	0.076
	104107	AA424111	Hs.12598	T-cell lymphoma invasion and metastasis 2	0.076
	121483	AA411981	Hs.25274	ESTs; Modly smlr to putative seven pass transmembrane prot [H.sapiens]	0.076
55	104451	M13299	Hs.102119	blue cone pigment	0.076
	118027	N52770	Hs.75968	thymosin; beta 4; X chromosome	0.076
	109419	AA227560	Hs.86987	receptor-interacting serine-threonine kinase 3	0.076
	115783	AA424487	Hs.72289	ESTs; Weakly similar to LJV-1 protein [H.sapiens]	0.076
	110585	H62223	Hs.133526	ESTs; Wkly smlr to III ALU SUBFAMILY SB1 WARNING ENTRY III [H.sapiens]	0.076
60	123165	AA488863	Hs.105216	ESTs; Weakly smlr to II ALU SUBFAMILY J WARNING ENTRY II [H.sapiens]	0.077
	103966	AA303168	Hs.127270	ESTs	0.077
	109549	F01528	Hs.21192	Homo sapiens clone 25155 mRNA sequence	0.077
	106730	AA465520	Hs.22313	ESTs	0.077
	120310	AA193676	Hs.118926	DKFZP586K0919 protein	0.077
65	104078	AA402801	Hs.222010	ESTs	0.077
	117624	N35978	Hs.82364	ESTs	0.077
	112421	R62441	Hs.23127	ESTs	0.077
	106958	AA497026	Hs.22059	ESTs	0.077
	128984	W92811	Hs.183927	ESTs; Weakly similar to II ALU SUBFAMILY J WARNING ENTRY II [H.sapiens]	0.077
	122044	AA431458	Hs.98738	EST	0.077
	123280	AA491285	Hs.175144	ESTs	0.077
	115710	AA412535	Hs.55235	sphingomyelin phosphodiesterase 2; neutra	0.077

			I membrane (neutral sphingomyelinase)	0.077
			KIAA0255 gene product	0.077
			Homo sapiens clone 643 unknown mRNA; complete sequence	0.078
			ESTs	0.078
			Interferon; gamma-inducible protein 30	0.078
			ESTs	0.078
			KIAA0298 gene product	0.078
			ESTs	0.078
			ESTs; Moderately similar to KIAA0544 protein [H.sapiens]	0.078
			glycine receptor; beta	0.078
			ESTs	0.078
			even-skipped homeo box 1 (homolog of Drosophila)	0.078
			ESTs; Weakly similar to sphingosine kinase [M.musculus]	0.078
			ESTs	0.078
			ESTs	0.078
			EST	0.078
			EST; Weakly similar to hypothetical protein [H.sapiens]	0.078
			ESTs	0.078
			ESTs	0.078
			ESTs	0.078
			ESTs; Highly similar to HYPOTHETICAL PROTEIN KIAA0195 [H.sapiens]	0.078
			protein with polyglutamine repeat	0.078
			ESTs	0.078
			Human clone 23548 mRNA sequence	0.078
			lymphotoxin beta (TNF superfamily; member 3)	0.078
			ESTs; Weakly similar to predicted using Genefinder [C.elegans]	0.079
			ESTs; Weakly similar to chondromodulin-I precursor [H.sapiens]	0.079
			Proline-Rich Protein Prb4, Allele	0.079
			netrin 2 (chicken)-like	0.079
			Human DNA from chromosome 19-specific cosmid R30923; genomic sequence	0.079
			Human liver GABA transport protein mRNA; 3' end	0.079
			ESTs	0.079
			KIAA0521 protein	0.079
			ESTs	0.079
			KIAA0081 protein	0.079
			extracellular matrix protein 2; female organ and adipocyte specific	0.079
			ESTs	0.079
			za56d02_r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone	0.079
			IMAGE:296547 5', mRNA sequence.	0.079
			ESTs	0.079
			thyroid hormone responsive SPOT14 (rat) homolog	0.079
			ESTs	0.079
			displatin resistance associated	0.079
			tanascin R (restrictin; janusin)	0.079
			ribosomal protein L3-like	0.079
			solute carrier family 21 (prostaglandin transporter); member 2	0.079
			ESTs	0.079
			homeo box C6	0.08
			ESTs; Weakly similar to II ALU SUBFAMILY J WARNING ENTRY II [H.sapiens]	0.08
			thrombospondin 4	0.08
			KIAA1021 protein	0.08
			ESTs	0.08
			ESTs; Weakly similar to DY3.6 [C.elegans]	0.08
			EST; Highly similar to CMP-N-acetylneuraminic acid hydroxylase [H.sapiens]	0.08
			zo8f12.s1 Stratagene neuroepithelium NT2RAM1 937234 Homo sapiens	0.08
			cDNA clone IMAGE:567119 3', mRNA sequence	0.08
			KIAA1066 protein; JSAP1 homolog (mouse); JIP3 homolog (mouse)	0.08
			ESTs	0.08
			Interleukin 8	0.08
			dolichyl-phosphate mannosyltransferase polypeptide 2; regulatory subunit	0.08
			ESTs	0.08
			ESTs; Weakly similar to Miller-Dieker lissencephaly gene [H.sapiens]	0.08
			ESTs; Weakly similar to O-linked GlcNAc transferase [H.sapiens]	0.08
			EST	0.08
			EST	0.08
			EST	0.08
			chaperonin containing TCP1; subunit 5 (epsilon)	0.081
			STIP1 homology and U-Box containing protein 1	0.081
			filamin C; gamma (actin-binding protein-280)	0.081

	103958	AA282411	Hs.233348	ESTs	0.081
	112706	R89828	Hs.138493	ESTs	0.081
	126126	M85370		EST01884 Fetal brain, Stratagene (cat#936206) Homo sapiens cDNA clone HFBC110, mRNA sequence.	0.081
5	130094	H43286	Hs.167017	gamma-aminobutyric acid (GABA) B receptor; 1	0.081
	100800	HG3945-HT4215		Phospholipid Transfer Protein	0.081
	108675	AA115240	Hs.61816	ESTs	0.081
	129420	AA234259	Hs.89816	ESTs	0.081
	129666	M77349	Hs.118787	transforming growth factor; beta-induced; 68kD	0.081
10	101645	M59807	Hs.943	natural killer cell transcript 4	0.081
	130538	T17045	Hs.159492	spastic ataxia of Charlevoix-Saguenay (sacsin)	0.081
	107732	AA016181	Hs.59752	ESTs	0.081
	123071	AA482593	Hs.104285	ESTs	0.081
	113537	T90457	Hs.191293	ESTs	0.081
15	101250	L34060	Hs.79133	cadherin 8	0.081
	122521	AA449433	Hs.149227	ESTs; Weakly similar to PROLINE-RICH PROTEIN MP-3 [M.musculus]	0.081
	133914	N32811	Hs.77542	ESTs	0.081
	102038	U05659	Hs.477	hydroxysteroid (17-beta) dehydrogenase 3	0.081
	110338	H40338	Hs.174094	ESTs; Weakly similar to !! ALU SUBFAMILY J WARNING ENTRY !! [H.sapiens]	0.081
20	118637	N70274	Hs.49822	ESTs	0.081
	117966	N51589	Hs.94012	ESTs	0.082
	104424	H87671	Hs.182320	ESTs; Weakly similar to Mouse 19.5 mRNA; complete cds [M.musculus]	0.082
	100361	D78361	Hs.125078	Human mRNA for ornithine decarboxylase antizyme; ORF 1 and ORF 2	0.082
25	112974	T17291	Hs.101174	microtubule-associated protein tau	0.082
	132832	D63482	Hs.57734	KIAA0148 gene product	0.082
	132039	Z39489	Hs.3781	Homo sapiens BAC clone RG118D07 from 7q31	0.082
	113272	T85383	Hs.12807	ESTs	0.082
	104924	AA058532	Hs.28774	ESTs	0.082
	111061	N58054	Hs.36859	ESTs	0.082
30	129269	R45977	Hs.163593	ribosomal protein L18a	0.082
	102453	U48437	Hs.74565	amyloid beta (A4) precursor-like protein 1	0.082
	126204	AJ080388	Hs.134296	ESTs	0.082
	116615	D80666	Hs.45203	ESTs	0.082
35	128856	AA219552	Hs.204144	ESTs; Modly smlr to tumor necrosis factor-alpha-induced prot B12 [H.sapiens]	0.082
	112776	R95850	Hs.34494	ESTs	0.082
	105494	AA258273	Hs.28288	Homo sapiens mRNA; cDNA DKFZp434P174 (from clone DKFZp434P174)	0.082
	117000	H84718	Hs.112236	ESTs; Weakly similar to repressor protein [H.sapiens]	0.082
	112656	R85260	Hs.133151	transient receptor potential channel 7	0.082
40	128963	J03890	Hs.1074	surfactant; pulmonary-associated protein C	0.083
	116957	H79292	Hs.39960	ESTs	0.083
	101057	K03430		Human complement C1q B-chain gene, exon A+1	0.083
	121948	AA429452	Hs.98582	ESTs	0.083
	130822	M80647	Hs.2001	thromboxane A synthase 1 (platelet; cytochrome P450; subfamily V)	0.083
45	122743	AA458674	Hs.99478	EST	0.083
	114569	AA063316		zm2d1.s1 Stratagene corneal stroma (#937222) Homo sapiens cDNA clone IMAGE512947 3' similar to TRLE198281 E198281 THIOREDOXIN	0.083
				REDUCTASE ;contains Alu repetitive element;; mRNA sequence	0.083
	132270	U70671	Hs.43509	ataxin 2 related protein	0.083
50	108128	AA052951	Hs.47413	ESTs	0.083
	102880	X04325	Hs.2679	gap junction protein; beta 1; 32kD (connexin 32; Charcot-Marie-Tooth neuropathy; X-linked)	0.083
	115365	AA282089	Hs.88599	ESTs	0.083
	114529	AA052980	Hs.206704	ESTs	0.083
55	135017	AA249588	Hs.9315	ESTs; Weakly similar to NEURONAL OLFACTOMEDIN-RELATED ER LOCALIZED PROTEIN [H.sapiens]	0.083
	123776	AA610071	Hs.112813	ESTs	0.083
	114454	AA021091	Hs.226208	ESTs	0.083
	101248	L33799	Hs.202097	procollagen C-endopeptidase enhancer	0.083
60	107368	U78310	Hs.13501	pescadillo (zebrafish) homolog 1; containing BRCT domain	0.083
	132779	T89601	Hs.95497	ESTs; Weakly similar to GLUCOSE TRANSPORTER TYPE 5; SMALL INTESTINE [H.sapiens]	0.083
	129709	AA112209	Hs.1209	acyl-Coenzyme A dehydrogenase; long chain	0.083
65	115244	AA278767	Hs.914	Human mRNA for SB classII histocompatibility antigen alpha-chain	0.083
	123253	AA490878	Hs.111334	ferritin; light polypeptide	0.083
	128469	T23724	Hs.258877	EST	0.083
	132220	AA431847	Hs.42409	ESTs; Highly similar to CGI-146 protein [H.sapiens]	0.083
	111664	R17839	Hs.22344	ESTs	0.083
	102354	U38268		Human cytochrome b pseudogene, partial cds	0.084
	112828	R88774	Hs.194338	ESTs	0.084

5	110410	H47868	Hs.34024	ESTs	0.084
	102620	U66052		Human clone W2-6 mRNA from chromosome X	0.084
	102550	U58087	Hs.14541	cullin 1	0.084
	108417	AA075716		zm89a5.s1 Stratagene ovarian cancer (#937219) H sapiens cDNA clone IMAGE:54512 3' similar to gb:X14723 CLUSTERIN PRECURSOR (HUMAN); mRNA sequence	0.084
10	113299	T67285	Hs.13089	ESTs	0.084
	117869	N49947	Hs.46990	ESTs	0.084
	113734	T98484	Hs.18377	EST	0.084
	133325	C00424	Hs.7101	periodontal ligament fibroblast protein	0.084
15	123368	AA505022	Hs.124838	ESTs	0.084
	101615	M55153	Hs.8265	transglutaminase 2 (C polypeptide; protein-glutamine -gamma-glutamyltransferase)	0.084
	119352	T65972	Hs.193365	ESTs; Moderately similar to alternatively spliced product using exon 13A [H.sapiens]	0.084
	123828	AA620686	Hs.112884	EST	0.084
20	103811	Z38133	Hs.113973	myosin; heavy polypeptide 8; skeletal muscle; perinatal	0.084
	131289	AA485697	Hs.25334	ESTs; Weakly similar to ION CHANNEL HOMOLOG R1C PRECURSOR [M.musculus]	0.084
	128678	T15896	Hs.103535	ESTs	0.084
	130814	AA256695	Hs.19813	ESTs	0.084
25	133391	X57579	Hs.727	inhibin; beta A (activin A; activin AB alpha polypeptide)	0.084
	128322	AA437153	Hs.110407	ESTs; Weakly similar to coded for by C. elegans cDNA yk173c12.5 [C.elegans]	0.084
	109284	AA196995	Hs.86092	ESTs	0.085
	118689	F09222	Hs.66099	ESTs	0.085
30	100545	HG2147-HT2217		Mucin 3, Intestinal (Gb:M55405)	0.085
	102634	U66711	Hs.77667	lymphocyte antigen 6 complex; locus E	0.085
	111735	R25389	Hs.23856	ESTs; Weakly similar to FAST kinase [H.sapiens]	0.085
	105181	AA190878	Hs.10974	ESTs; Moderately similar to unknown [R.norvegicus]	0.085
35	122681	AA455350	Hs.99401	EST	0.085
	114543	AA056121	Hs.158419	ESTs	0.085
	133597	AA425908	Hs.75139	partner of RAC1 (arlaplin 2)	0.085
	121064	AA398647	Hs.97406	ESTs	0.085
40	122231	AA436369	Hs.197728	ESTs; Weakly similar to ZINC FINGER PROTEIN 135 [H.sapiens]	0.085
	100309	D50550	Hs.95659	lethal giant larvae (Drosophila) homolog 1	0.085
	101727	M73481	Hs.73883	gastrin-releasing peptide receptor	0.085
	131226	AA165400	Hs.24478	ESTs	0.085
45	133580	AA095041	Hs.181073	ESTs	0.085
	102792	U87984	Hs.227578	GTP binding protein 1	0.085
	104976	AA086480	Hs.183869	ESTs; Weakly similar to II ALU SUBFAMILY J WARNING ENTRY II [H.sapiens]	0.085
	120865	AA350631	Hs.86963	EST	0.085
50	106080	AA418046	Hs.35124	ESTs	0.085
	128571	AA416819	Hs.101861	ESTs	0.085
	101838	M82934	Hs.75511	connective tissue growth factor	0.085
	128514	H84261	Hs.100843	ESTs; Weakly similar to similar to GTP-binding protein [C.elegans]	0.085
55	123099	AA485931	Hs.79	aminoacylase 1	0.085
	134067	Y08200	Hs.78920	Rab geranylgeranyltransferase; alpha subunit	0.085
	116967	H80336	Hs.40124	EST	0.085
	110053	H12586	Hs.89563	nuclear cap binding protein 1; 80kD	0.085
60	114395	AA007313	Hs.110155	ESTs	0.085
	107465	W44681	Hs.251385	murine retrovirus integration site 1 homolog	0.085
	101983	S85655	Hs.75323	prohibitin	0.085
	112544	R70948	Hs.29153	ESTs	0.086
65	111423	R01165	Hs.188507	ESTs	0.086
	127918	AA806043	Hs.115398	Human germline IgD chain gene; C-region; C-delta-1 domain	0.086
	107300	T40348	Hs.80488	ESTs	0.086
	134947	R51184		y71a08.r1 Soares breast 2NbHBst Homo sapiens cDNA clone IMAGE:154168 5' similar to gb:U11284 DUAL SPECIFICITY MITOGEN-ACTIVATED PROTEIN KINASE KINASE 1 (HUMAN); mRNA sequence.	0.086
70	124579	N68345	Hs.127179	ESTs; Weakly similar to TERATOCARCINOMA-DERIVED GROWTH FACTOR 1 [H.sapiens]	0.086
	130471	Z68280	Hs.183706	adducin 1 (alpha)	0.086
	116596	D60755	Hs.92955	ESTs	0.086
	105069	AA136345	Hs.23617	ESTs; Weakly similar to ZFOC1 gene product [H.sapiens]	0.086
75	102491	U51010		Human nicotinamide N-methyltransferase gene, exon 1 and 5' flanking region	0.086
	130069	AA055898	Hs.146428	collagen; type V; alpha 1	0.086
	130234	AA280413	Hs.157441	spleen focus forming virus (SFFV) proviral integration oncogene sp1	0.086
	120540	AA262892	Hs.96417	ESTs	0.086
80	122508	AA449221	Hs.20432	ESTs	0.086

5	128054	AI205718	Hs.125418	ESTs	0.086
	133020	AA053248	Hs.185182	ESTs; Highly similar to 40S RIBOSOMAL PROTEIN S10 [H.sapiens]	0.086
	130056	AA017356	Hs.171900	arradillo repeat gene deletes in velocardiofacial syndrome	0.086
	130504	U48665	Hs.158323	CCAAT/enhancer binding protein (C/EBP); epsilon	0.086
	133978	W73859	Hs.78061	transcription factor 21	0.086
10	105265	AA227941	Hs.26088	ESTs	0.086
	133035	T15965	Hs.6333	ESTs	0.086
	100768	HG3636-HT3846		Myosin, Heavy Polypeptide 9, Non-Muscle	0.086
	129338	T56800	Hs.47274	Homo sapiens mRNA; cDNA DKFZp584B176 (from clone DKFZp584B176)	0.086
	132789	W23781	Hs.56876	ESTs	0.086
15	116099	AA456309	Hs.58831	regulator of Fas-induced apoptosis	0.086
	100721	HG3355-HT3532		Peroxisome Proliferator Activated Receptor (Gbz30972)	0.087
	112569	R73150	Hs.75270	GTP-binding protein homologous to Saccharomyces cerevisiae SEC4	0.087
	130645	AA020942	Hs.17200	STAM-like protein containing SH3 and ITAM domains 2	0.087
	100751	HG3527-HT3721		Luteinizing Hormone, Beta Subunit	0.087
20	134550	M27161	Hs.85258	CD8 antigen; alpha polypeptide (p32)	0.087
	130885	AA338646	Hs.20812	adenomatous polyposis coli like	0.087
	101446	M21302	Hs.56306	small proline-rich protein 2A	0.087
	116287	AA487856	Hs.155829	KIAA0676 protein	0.087
	134034	X89267	Hs.78601	uroporphyrinogen decarboxylase	0.087
25	130860	U68061	Hs.241395	protease; serine; 1 (trypsin 1)	0.087
	109901	H04992	Hs.30499	ESTs	0.087
	107537	Z20777	Hs.9857	ESTs; Weakly similar to peroxisomal short-chain alcohol dehydrogenase [H.sapiens]	0.087
	133232	AA498030	Hs.6845	ESTs	0.087
	108559	AA085161		zn12c5.s1 Striatogene hNT neuron (#837233) H sapiens cDNA clone IMAGE:54728 3' similar to TR:G1151228 G1151228 LPG1P. ; mRNA seq	0.087
30	121288	AA401735	Hs.87340	EST	0.087
	108844	AA132916	Hs.177961	Human Chromosome 16 BAC clone CIT987SK-A-388D4	0.087
	129874	AA408488	Hs.181551	ESTs	0.087
	105139	AA164543	Hs.110082	ESTs	0.088
	124789	R43803	Hs.78110	ESTs; Weakly similar to F17A9.2 [C.elegans]	0.088
35	115923	AA441929	Hs.38205	ESTs	0.088
	123640	AA609282	Hs.112681	ESTs	0.088
	131607	AA351409	Hs.172740	microtubule-associated protein; RP/EB family; member 3	0.088
	130064	T67053	Hs.181125	immunoglobulin lambda gene cluster	0.088
	108752	AA127070	Hs.71055	ESTs	0.088
40	124249	H68077	Hs.108211	ESTs	0.088
	100109	AJ000480	Hs.143513	phosphoprotein regulated by mitogenic pathways	0.088
	104642	AA004662	Hs.184245	KIAA0929 protein Mx2 interacting nuclear target (MINT) homolog	0.088
	131752	AA453311	Hs.31566	ESTs	0.088
	114727	AA132545	Hs.190202	ESTs	0.088
45	120965	AA398089	Hs.179715	ESTs	0.088
	100396	D84361	Hs.151123	Human mRNA for p52 and p64 isoforms of N-Shc; complete cds	0.088
	106218	AA428451	Hs.91148	DKFZP586E0820 protein	0.088
	111562	R09567	Hs.187569	ESTs	0.088
	121219	AA400606	Hs.144344	EST	0.088
50	101187	L20316	Hs.208	glucagon receptor	0.088
	101513	M28210	Hs.27744	RAB3A; member RAS oncogene family	0.088
	116454	AA621071	Hs.42034	ESTs; Moderately similar to T-complex protein 10A [H.sapiens]	0.088
	116171	AA463434	Hs.42658	ESTs	0.089
	117500	N31909	Hs.44278	ESTs	0.089
55	119978	W88623	Hs.59190	EST	0.089
	132005	D58231	Hs.173091	DKFZP434K151 protein	0.089
	109914	H05529	Hs.184704	leucine-rich; glioma inactivated 1	0.089
	130370	M55265	Hs.155140	casein kinase 2; alpha 1 polypeptide	0.089
	104262	AF009801	Hs.105941	bagpipe homeobox (Drosophila) homolog 1	0.089
60	129708	AA417181	Hs.120858	ESTs	0.089
	106398	AA447545	Hs.18268	adenylate kinase 5	0.089
	120884	AA365358	Hs.97041	ESTs	0.089
	130404	X72012	Hs.76753	endoglin (Oster-Rendu-Weber syndrome 1)	0.089
	114072	Z38184	Hs.123633	ESTs	0.089
65	131470	X54938	Hs.2722	Inositol 1,4,5-trisphosphate 3-kinase A	0.089
	124573	N67935	Hs.194703	adaptor-related protein complex 4; mu 1 subunit	0.089
	114717	AA131240	Hs.252014	EST	0.089
	133808	M12759	Hs.76325	Human Ig J chain gene	0.09
	130470	AA398552	Hs.15711	KIAA0639 protein	0.09
	133182	Z80787	Hs.240135	H4 histone family; member J	0.09
	116038	AA452572	Hs.43866	ESTs	0.09

5	132404	AA393903	Hs.4768	ESTs	0.09
	122695	AA456048	Hs.99403	ESTs; Moderately similar to undulin 2 [H.sapiens]	0.09
	125975	AA495891	Hs.152280	ESTs; Highly similar to PACAP type-3/VIP type-2 receptor [H.sapiens]	0.09
	110783	N23669	Hs.26407	ESTs	0.09
	129860	AA410343	Hs.129826	tetraspan transmembrane 4 super family	0.09
10	120740	AA302650	Hs.96654	EST	0.09
	119564	W38206		Accession not listed in Genbank	0.09
	134474	AA054746	Hs.8379	ESTs	0.09
	119014	N95435	Hs.55144	ESTs	0.09
	109791	F10669	Hs.13228	DRE-antagonist modulator; calsenilin	0.09
15	117605	N35073	Hs.44433	ESTs	0.09
	121589	AA416627	Hs.191598	ESTs	0.09
	104326	D81655	Hs.143067	ESTs	0.09
	129861	N69507	Hs.129849	DKFZP564M182 protein	0.09
	102795	U88667	Hs.198396	ATP-binding cassette; sub-family A (ABC1); member 4	0.09
20	119628	W49499	Hs.184456	ESTs; Widely similar to II ALU SUBFAMILY SX WARNING ENTRY II [H.sapiens]	0.09
	110516	H56894	Hs.37368	EST	0.09
	105382	AA236853	Hs.111801	Homo sapiens mRNA; cDNA DKFZp564H2023 (from clone DKFZp564H2023)	0.09
	123754	AA609984	Hs.102021	ESTs	0.09
	108008	AA039430	Hs.61820	ESTs	0.09
25	121057	AA398619	Hs.142375	ESTs; Moderately similar to putative envelope protein [H.sapiens]	0.091
	123675	AA608474	Hs.112713	EST	0.091
	135194	C20975	Hs.9813	ESTs; Highly similar to angiopoietin-related protein [H.sapiens]	0.091
	127070	AA641812	Hs.190037	ESTs	0.091
	134051	S67070	Hs.78846	heat shock 27kD protein 2	0.091
30	133382	AA112532	Hs.7247	ESTs	0.091
	103615	Z46967	Hs.115460	calicin	0.091
	118457	N68593	Hs.49230	EST	0.091
	118504	N67334	Hs.50158	ESTs	0.091
	112915	T10176	Hs.4254	ESTs	0.091
35	132088	AA470121	Hs.243960	HLA-B associated transcript-3	0.091
	101504	M27288	Hs.248156	oncostatin M	0.091
	112550	R71391	Hs.29074	ESTs	0.091
	128551	H09058	Hs.237323	N-acetylglucosamine-phosphate mutase; DKFZP434B187 protein	0.091
	112979	T03541	Hs.115960	ESTs	0.091
40	127079	A1364691	Hs.128628	ESTs; Moderately similar to CL3BC [R.norvegicus]	0.091
	101993	U01062	Hs.77515	inositol 1,4,5-trisphosphate receptor; type 3	0.091
	113020	T23830	Hs.7303	ESTs; Weakly similar to PROHIBITIN [H.sapiens]	0.091
	120465	AA251505	Hs.130861	ESTs	0.091
	130152	U32645	Hs.151139	E74-like factor 4 (ets domain transcription factor)	0.091
45	104941	AA065169	Hs.17805	ESTs	0.091
	110090	H16076	Hs.6915	ESTs	0.091
	135375	AA480888	Hs.89741	ESTs; Weakly similar to BRAIN PROTEIN H5 [H.sapiens]	0.091
	123769	AA620418	Hs.112861	ESTs	0.092
	118968	N93438	Hs.78907	ESTs; Highly similar to HSPC002 [H.sapiens]	0.092
50	116969	H80633	Hs.143038	ESTs	0.092
	125147	W38150		Accession not listed in Genbank	0.092
	100836	HG4113-HT4383		Olfactory Receptor Or17-201	0.092
	114726	AA132509	Hs.103827	EST	0.092
	107311	T57738	Hs.174112	ESTs	0.092
55	112863	T03148	Hs.4810	EST	0.092
	128280	AA521407	Hs.110096	ESTs	0.092
	103384	X92762	Hs.78021	talazzin (cardiomyopathy; dilated 3A (X-linked); endocardial fibroelastosis 2; Barth syndrome)	0.092
	112508	R68213	Hs.28847	ESTs	0.092
	111863	R37495	Hs.23578	ESTs	0.092
60	131184	AA452705	Hs.23954	ESTs; Weakly similar to KIAA0584 protein [H.sapiens]	0.092
	107420	W26567	Hs.4775	ESTs	0.092
	111768	R27806	Hs.24185	ESTs	0.092
	112290	R53940	Hs.26016	ESTs	0.092
	130581	AA481982	Hs.16258	ESTs; Weakly similar to RAS-RELATED PROTEIN RAB-5A [H.sapiens]	0.092
65	120744	AA302772	Hs.228649	EST	0.093
	112226	R50761	Hs.25739	ESTs	0.093
	116154	AA460951	Hs.57100	ESTs	0.093
	102640	U67674	Hs.194783	solute carrier family 10 (sodium/bile acid cotransporter family); member 2	0.093
	129797	X53595	Hs.1252	apolipoprotein H (beta-2-glycoprotein I)	0.093
	102705	U77180	Hs.50002	small inducible cytokine subfamily A (Cys-Cys); member 19	0.093
	132408	AA035547	Hs.47822	KIAA0380 gene product; RhoA-specific guanine nucleotide exchange factor	0.093
	108441	AA079079		zm97c9.s1 Stratagene colon HT29 (#937221) Homo sapiens cDNA clone	0.093

			IMAGE:545872 3' similar to contains element MER22 MER22 repetitive element ;, mRNA sequence	0.093	
	108145	AA054133	Hs.63085	ESTs	0.093
	108486	AA449990	Hs.76057	lysophospholipase II	0.093
5	101697	M64358		Human rhom-3 gene, exon	0.093
	121294	AA401958	Hs.240170	ESTs; Moderately similar to alternatively spliced product using exon 13A [H.sapiens]	0.093
	117824	N49065	Hs.125201	ESTs; Weakly similar to B7 [M.musculus]	0.093
	115771	AA422049	Hs.40780	ESTs	0.093
10	102303	U33053	Hs.2499	protein kinase C-like 1	0.093
	131405	U79255	Hs.28468	amyloid beta (A4) precursor protein-binding; family A; member 2 (X11-like)	0.093
	112909	T10069	Hs.101094	ESTs	0.093
	124173	H41281	Hs.107619	ESTs	0.093
	112488	R66896	Hs.28788	ESTs	0.093
15	130554	X59303	Hs.159637	valyl-tRNA synthetase 2	0.093
	108413	AA447964	Hs.6311	ESTs	0.093
	111711	R22891	Hs.7093	ESTs	0.094
	117595	N34933	Hs.44664	EST	0.094
	113813	W45174	Hs.31382	ESTs	0.094
20	107769	AA018449	Hs.125220	Homo sapiens DNA from chromosome 19-cosmids R30102-R29350-R27740 containing MEF2B; genomic sequence	0.094
	114968	AA250743	Hs.92198	ESTs; Highly similar to calcium-regulated heat stable protein CRHSP-24 [H.sapiens]	0.094
	130297	H94949	Hs.171955	trophinin-assisting protein (tastin)	0.094
25	109589	F02429	Hs.6581	ESTs	0.094
	112592	R77631	Hs.29128	ESTs	0.094
	102314	U34038	Hs.154299	coagulation factor II (thrombin) receptor-like 1	0.094
	116128	AA459915	Hs.112193	mutS (E. coli) homolog 5	0.094
30	106809	AA479704	Hs.220324	Human DNA sequence from clone 283E3 on chromosome 1p36.21-36.33. Contains the alternatively spliced gene for Matrix Metalloproteinase in the Female Reproductive tract MIFR1; -2; MMP21/22A; -B and -C; a novel gene; the alternatively spliced CDC2L2 gene for	0.094
	130607	AA043894	Hs.16603	ESTs	0.094
	120592	AA281929	Hs.143974	ESTs	0.094
35	117230	N20535	Hs.43265	melastatin 1	0.094
	105948	AA404597	Hs.7133	ESTs	0.094
	101333	L47738	Hs.80313	p53 inducible protein	0.094
	101909	S69265		Homo sapiens mRNA for PLE21 protein; complete cds	0.094
	106959	AA497031	Hs.8857	ESTs; Highly similar to CTG7a [H.sapiens]	0.094
40	127034	AA352389		ESTs; Wkly smir to glucose-6-phosphatase catalytic subunit [R.norvegicus]	0.095
	134430	H52105	Hs.8309	KIAA0747 protein	0.095
	120342	AA207105	Hs.45068	Homo sapiens mRNA; cDNA DKFZp434I143 (from clone DKFZp434I143)	0.095
	104450	L77564	Hs.103978	serine/threonine kinase 22B (spermiogenesis associated)	0.095
	130902	AA424530	Hs.21061	ESTs	0.095
45	102708	U77594	Hs.37682	retinoic acid receptor responder (tazarotene induced) 2	0.095
	107373	U85773	Hs.154695	phosphomannomutase 2	0.095
	123569	AA608952	Hs.185292	ESTs; Weakly similar to RNA helicase HDB/DICE1 [H.sapiens]	0.095
	102687	U73379	Hs.93002	ubiquitin carrier protein E2-C	0.095
	128888	AA034951	Hs.106893	ESTs	0.095
50	100283	D43642	Hs.2430	transcription factor-like 1	0.095
	102747	U78303	Hs.82482	protein predicted by clone 23882	0.095
	107798	AA018346	Hs.60918	EST	0.095
	123565	AA608907	Hs.112614	EST	0.095
	116010	AA449450	Hs.56421	ESTs; Weakly similar to Similarity to H.Influenza ribonuclease PH [C.elegans]	0.095
55	117155	H97538	Hs.42391	EST	0.095
	133094	AA115572	Hs.64746	chloride intracellular channel 3	0.095
	113174	T54659	Hs.9779	ESTs	0.095
	102018	U03270	Hs.122511	centrin; EF-hand protein; 1	0.095
	130128	AB002318	Hs.150443	KIAA0320 protein	0.095
60	134813	X14767	Hs.89768	gamma-aminobutyric acid (GABA) A receptor; beta 1	0.095
	132055	N69440	Hs.38132	ESTs	0.095
	122229	AA436198	Hs.103902	ESTs	0.096
	127574	AA907314	Hs.188905	ESTs	0.096
	134432	AA053022	Hs.8312	ESTs	0.096
65	128052	AA878398	Hs.190491	ESTs	0.096
	101637	M58285	Hs.132834	hematopoietic protein 1	0.096
	103386	X92972	Hs.80324	protein phosphatase 6; catalytic subunit	0.096
	133079	AA477561	Hs.6449	ESTs	0.096
	120328	AA196979	Hs.104129	ESTs; Weakly similar to protease [H.sapiens]	0.096

5	107640	AA008815	Hs.257808	ESTs	0.098
	123389	AA521178	Hs.221231	ESTs	0.098
	103222	X74795	Hs.77171	minichromosome maintenance deficient (S. cerevisiae) 5 (cell division cycle 46)	0.098
	111704	R22450	Hs.23398	ESTs; Highly similar to ZINC FINGER PROTEIN 140 [H.sapiens]	0.098
	126856	AA306523		EST177475 Jurkat T-cells VI Homo sapiens cDNA 5' end, mRNA sequence.	0.733
	127071	AA250808		ESTs	0.098
	114550	AA058755	Hs.151714	ESTs	0.098
	125955	AJ356943	Hs.143761	ESTs	0.098
10	134363	M37033	Hs.82212	CD53 antigen	0.098
	128550	W76492	Hs.170142	ESTs	0.098
	122598	AA453465	Hs.89329	ESTs	0.098
	118898	N90703	Hs.4236	KIAA0478 gene product	0.098
	117681	N39092	Hs.44940	ESTs	0.098
15	120996	AA398281	Hs.143684	ESTs	0.098
	123388	AA521172	Hs.134417	ESTs	0.098
	106700	AA463929	Hs.28701	ESTs	0.098
	112962	T16814	Hs.6828	ESTs	0.098
	121282	AA401372	Hs.97723	ESTs	0.098
20	134551	R44839	Hs.8526	H-beta-1,3-N-acetylglucosaminyltransferase	0.098
	112060	R43754	Hs.21164	ESTs	0.098
	134678	AA039935	Hs.182595	dynein; axonemal; light polypeptide 4	0.098
	100855	HG4234-HT4504		Methylenetetrahydrofolate Reductase	0.097
	132414	N91193	Hs.48145	ESTs	0.097
25	112900	T08758	Hs.3813	ESTs	0.097
	115989	AA447777	Hs.93135	ESTs	0.097
	103561	Z21488	Hs.143434	contactin 1	0.097
	131087	AA009738	Hs.22824	ESTs; Weakly similar to p160 myb-binding protein [M.musculus]	0.097
	120293	AA190859	Hs.191428	ESTs	0.097
30	111830	R36081	Hs.25085	EST	0.097
	113854	T95770	Hs.17688	ESTs	0.097
	132675	AA179338	Hs.5476	serine proteinase inhibitor	0.097
	120182	Z40125	Hs.91968	ESTs	0.097
	132879	U16282	Hs.5881	ELL gene (11-19 lysine-rich leukemia gene)	0.097
35	134211	AA056681	Hs.80021	ESTs; Weakly similar to 62D9.p [D.melanogaster]	0.097
	115448	AA284845	Hs.165051	ESTs	0.097
	118118	N56901	Hs.47995	ESTs	0.097
	107598	AA004528	Hs.169444	ESTs	0.097
	128933	H01824	Hs.760	GATA-binding protein 2	0.097
40	114892	AA235988	Hs.86024	ESTs	0.097
	101822	S75168	Hs.274	megakaryocyte-associated tyrosine kinase	0.097
	105444	AA252374	Hs.19333	ESTs; Weakly similar to ATP(GTP)-binding protein [H.sapiens]	0.097
	128155	AA826843	Hs.143302	ESTs	0.097
	116276	AA485870	Hs.44914	ESTs	0.097
45	111984	R41227	Hs.21860	ESTs	0.097
	135100	AA398926	Hs.251108	Homo sapiens mRNA; chromosome 1 specific transcript KIAA0493	0.097
	124872	R69251	Hs.101508	EST	0.097
	103084	X59932	Hs.77783	c-src tyrosine kinase	0.097
	124138	H23199	Hs.107010	ESTs	0.098
50	130048	R31745	Hs.211612	SEC24 (S. cerevisiae) related gene family; member A	0.098
	100208	D26129	Hs.78224	ribonuclease; RNase A family; 1 (pancreatic)	0.098
	123537	AA608775	Hs.112589	ESTs	0.098
	118999	N95019	Hs.55092	ESTs	0.098
	118847	W80384	Hs.9853	ESTs	0.098
55	112819	R98618	Hs.35984	ESTs	0.098
	131080	J05008	Hs.2271	endothelin 1	0.098
	127353	AA190853	Hs.155360	ESTs	0.098
	132068	X66365	Hs.38481	cyclin-dependent kinase 6	0.098
	105744	AA283438	Hs.12909	ESTs	0.098
60	133680	M92357	Hs.101382	tumor necrosis factor; alpha-induced protein 2	0.098
	122899	AA489960	Hs.178420	ESTs; Highly similar to WASP interacting protein [H.sapiens]	0.098
	128700	U59286	Hs.103982	small inducible cytokine subfamily B (Cys-X-Cys); member 11	0.098
	104393	H46486	Hs.226499	nesca protein	0.098
	123320	AA498792	Hs.139572	EST	0.098
65	129169	N31641	Hs.109058	ribosomal protein S6 kinase; 90kD; polypeptide 5	0.098
	135093	U51333	Hs.159237	hexokinase 3 (white cell)	0.098
	113269	T85159	Hs.85044	ESTs	0.098
	124263	H86783	Hs.184138	ESTs; Moderately similar to zinc finger protein RIN ZF [R.norvegicus]	0.098
	114376	GMCSF		Accession not listed in Genbank	0.099
	100881	HG4458-HT4727		Immunoglobulin Heavy Chain, Vdjc Regions (Gb1.23563)	0.099

	116572	D45654	Hs.65582	DKFZP586C1324 protein	0.099
	123956	AA621747	Hs.112847	EST	0.099
	100818	HG4018-HT4288		Opioid-Binding Cell Adhesion Molecule	0.099
	132754	W47419	Hs.56007	Human DNA from chromosome 19-specific cosmid F25965; genomic sequence	0.099
5	112741	R93080	Hs.35035	ESTs	0.099
	112748	R93289	Hs.168482	ESTs	0.099
	130858	S57235	Hs.246381	CD68 antigen	0.099
	124870	R69233	Hs.101504	ESTs	0.099
	125304	Z39833	Hs.124940	GTP-binding protein	0.099
10	121297	AA401995	Hs.97860	ESTs	0.099
	128602	AA046103	Hs.102367	ESTs	0.099
	124062	H00440	Hs.144524	ESTs; Weakly similar to signal transducer and activator of transcription 2 [M.musculus]	0.099
	100547	HG2149-HT2219		Mucin (Gb:M57417)	0.099
15	105652	AA282505	Hs.19015	ESTs	0.099
	133390	AA459945	Hs.72660	KIAA0585 protein	0.099
	133503	M33185	Hs.743	Fc fragment of IgE; high affinity I; receptor for; gamma polypeptide	0.099
	109461	AA232667	Hs.58210	ESTs	0.099
	102068	U09117	Hs.80776	phospholipase C; delta 1	0.099
20	113464	T86931	Hs.16295	ESTs	0.099
	104240	AB002368	Hs.70500	KIAA0370 protein	0.099
	121113	AA399109	Hs.161813	ESTs	0.1
	122896	AA469952	Hs.97899	ESTs; Weakly similar to dal2; len:343; CAI: 0.17; ALC_YEAST P25335	0.1
25	102405	U43148	Hs.159526	ALLANTOICASE [S.cerevisiae]	0.1
	103599	Z33905	Hs.81218	patched (Drosophila) homolog	0.1
	121079	AA398719	Hs.14169	receptor-associated protein of the synapse; 43kD	0.1
	115820	AA427487	Hs.39619	ESTs; Weakly similar to CREB-binding protein [H.sapiens]	0.1
	125106	T95766	Hs.189760	ESTs; Weakly similar to RETICULOCALBIN 1 PRECURSOR [H.sapiens]	0.781
30	131373	N68116	Hs.26148	ESTs	0.1
	120224	Z41239	Hs.108960	Down syndrome critical region gene 3	0.1
	133090	AA448228	Hs.6468	ESTs	0.1
	132300	AA133244	Hs.44234	ESTs	0.1
	113129	T49384	Hs.8988	EST	0.1
35	110638	H73197	Hs.17241	ESTs	0.1
	131364	R53255	Hs.26010	ESTs	0.1
	105370	AA236476	Hs.22791	ESTs; Weakly similar to transmembrane protein with EGF-like and two follistatin-like domains 1 [H.sapiens]	0.238
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TABLE 11A shows the accession numbers for those primekeys lacking unigeneID's for Table 11. For each probeset we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

Pkey: CAT number: Accession:	Unique Eos probeset Identifier number Gene cluster number Genbank accession numbers
Pkey CAT number Accession	
100610 19864_1	AW161357 AI878062 AI928938 AW161097 AW161167 BE314465 AA351715 F07086 AA178034 F08510 F00653 AI938671 AA476718 AW772454 AI807703 R44253 AA878667 AI985186 AI650254 H38942 R84829 AA018724 AA001000 H85934 AA019126 H85809 AA017000 AA339355 AW950556 D51397 AA213981 BE548002 AI056359 AA001560 AW952113 AA317769 AI857477 AI857475 AW249771 AW162661 H38943 AA018628 R85885 AI984613 AI934785 AI796172 AW157488 AI929191 R85523 D51221 D53851 H85810 AI749674 F21582 AA323145 AA019127 AA687444 T08745 AI699293 H29532 AA214029 AA223656 NM_016834 X14474 R19697 H09695 R17455 R13812 R19056 AI681231 AI590200 R37671 AA851828 AI990023 AI935669 AW005821 AA324581 H17335 R37659 R42802 R46242 R60936 R59731 H28993 AA479907 R44570 AI890696 AA308884 AA507078 R41274 AI365507 T16348 AI560453 F03259 F04722 T16312 AA016081 AW073061 BE314824 W28930 R44098 R51045
100674 21517_2	AW403342 AW248986 BE561709 AA357312 BE311834 BE389496 BE294887 AW732696 BE047888 AI702383 BE019155 AI702367 BE408966 BE280458 BE313759 BE513482 BE535404 BE280258 AC005263 NM_007165 L21890 AW732711 AI564920 AW249094 BE265365 AW607186 AW607346 BE005217 H27211 U46230 BE260066 BE207043 BE546782 AW248659
108559 41469_9	AA085228 AA085161
100721 19818_1	L40904 NM_005037 X90563 AB005526 H21598 AA088517
100748 41861_1	X06096 X05826
100750 15759_1	BE157260 BE157265 R48118 H43827 Z17877 AW379070 AW291778 M20605 J03253 M14206 V00568 AI860465 AW296022 M13930 AL047400 J00120 BE018476 AW675223 T26980 F06694 R22709 R24720 H22753 AI903100 AI903094 AW937823 X00364 D10493 K01904 K01906 K00535 L00058 AA410662 AW384760 AA304930 AI680985 X00198 H58025 AW998901 AV653447 N31654 AW610357 AW610369 AW682480 BE223010 AW384172 AW384219 AW384171 AW384218 AA298522 BE140421 AW945162 AW751711 AA514409 AW747912 AI214214 W87741 AA972406 AA554513 BE302087 AI249030 AA477850 AV653129 AI281360 AI274110 W87881 AA841386 X66258 AI051600 AA877139 AA527483 AA857219 AI250782 AA625531 AA807892 AI278811 AI224033 H24033 AA593398 AW129709 R45453 N22772 AA235530 T29737 AI016409 AI688907 AA568370 AW722760 AI539329 AA550843 AW674698 AI538452 AI538453 AI337957 AA477744 AA484600 AI140319 AW948294 AI339781 AI828738 AA923634 AA344094 AI278350 AA975567 AA908416 AA857170 AW023520 R43413 R48004 F02858 AI989439 R11207 AA737307 D10493 AW950652 AI093842 AW74024 AW703369 R11264 M13930 M13930 M13930 M13930 M13930 J00120 M13930 M13930 X00364 J00120 R19507 AA639812
100751 24700_1	N32759 N29730 N30831 N32604 N31955 AI206390 H87574 R23494 AI186215 N30036 AI741512 J00117 NM_000737 AI453626 AA330974 AI188729 AI188604 AI188864 N30276 AI188947 AI188830 AI188303 AI200457 AI219166 AI192459 AI183280 AI189275 AI188639 AI186353 AI189616 AI184224 AI130720 AI188454 AI188391 AI148857 AI182447 AI209155 AI190013 AI206355 AI188721 AI189429 AI189384 AI188330 AI431595 AI189595 AI188781 AI148867 AI200022 AI221552 AI220923 AI188728 AA233034 AI189807 AI189641 AI219044 AI148774 AI200658 W71889 AI207360 AI188824 AI200559 AI200270 AA644163 AI199943 AI151301 AI189555 AI262724 AI148590 AI148695 AI126906 AI149163 K03183 K03189 AI189842 AI221014 N30608 AI188465 AI220885 AI188498 AI138228 AI189968 AI221019 AI138197 AI149428 AI148904 AI188218 AI188348 AI160579 AI189460 AI149039 AI160936 AI219055 AI184784 AI221580 AI161082 AI160814 AI123896 AI417614 AI126101 AI188872 AI149571 AI168533 AI149072 AI149467 AI131286 N30684 AI160705 AI160692 AI149559 AI273580 AI189442 AI138448 AI149591 N27302 AA400910 AI138431 AI138435 AI128407 N30216 AI128298 AI219589 AI188492 AI149447 AI168482 H95374 AI219009 N31616 AI276216 N32233 AI291937 N30741 AI188689 N27111 R23214 AI221605 AI184348 AI200375 H94451 N26397 AI871881 AA232905 N30833 AI220760 H94446 N30822 H87484 R68815 N30290 AI128424 H12587 T47334 H87631 H87156 AI219133 AI868741 AA330859 H86993 AA330413 H93658 N30817 T90191 H93668 AI200054 H95207 T47316 H95381 T49170 R00880 T49171 N27381 H94107 R63352 T85053 AW451899 H95142 N30313 H94015 H86987 T28278 N29701 C18834 AA331267 AA330939 AI554483 N27073 N29831 R68113 N30758 R26086 N32108 H95135 AA330414 AA330978 AI219422 AI189453 AI199951 X00264 NM_000894 AA371909 AA063496 T29543 AA371971 AA372028 AA371978 AA371348 AI051683 AI188418 AI220659 AI189068 AI219266 AI186552 AI188716 AI149156
100760 1934_7	AW794628 M27126 M27014
100775 18179_3	J05581 M81170 T27692 M34088 M34089 AW880335 AW578047 AW610437 AW610386 AW610422 AW610473 AW578078 AW604897 AW860163 AW579067 AW862410 AI816584 AW177757 AW602769 AI909780 AW860331 AI909787 AI909811

		AI909813 AW845083 AI905920 AW387919 BE140766 AI909279 AW369405 AA429321 AA429320 AA367451 AA847972 AW001137 AI567905 T84561 AI631295 AA151351 H02932 AI884519 AA367457 AW369421 AI678846 AW391803 AI610869 AW192838 AI922289 AI952140 AI910233 AI479474 AW001395 AA488073 AI985760 AW130017 AI658369 AA827845 AW081805 AA158865 AI624443 AA344985 AA569793 R72486 AI589329 AI903204 AI269893 AA641284 AI279932 AA149270 AI697120 AA729146 AI589353 AA480067 AI923310 AA530908 AI275395 AA425062 AA580280 AA889527 AA158866 AW131341 AA573028 AA877326 T29335 AW951288 H04235 AA089243 AA994658 AI658618 AA887919 AI292927 AW001116 AW263844 AI270578 AA970828 AW572126 AA775299 AW369449 AW368398 AW369452 AI933677 AI870710 AI092911 AI582484 AI497674 AA937028 AA885865 L38597 AA908325 AW369432 AW026623 AA627778 AI264942 AA932409 AI187328 AI672970 AI866098 AW440471 AW138860 AI866858 AI802528 AI926172 AW243914 AI933690 AA996114 AA536189 AW009937 AI918060 AI270379 AI973169 AW175838 AW369413 100800 24735_1 NM_006227 L26232 R50649 AU077024 AL008726 AA411079 R35151 BE278163 BE278139 AI459777 R88036 Z43210 F07326 AF052157 R17844 BE615478 T82160 R71985 H21863 AA299158 AW368248 R48123 R50628 R70441 H27245 H72015 R72345 R39392 AI909738 BE612778 BE613234 D52116 D52136 D52132 D52067 D51922 D51995 D51905 N34249 N25459 AA484438 AA297350 AA297468 R81736 H02737 AW582505 R27523 AI834241 AW130867 W72668 W76426 AI358363 R50262 AW473860 H52335 H43953 H21864 T39505 AI887517 AW156925 AW369850 H02628 AW007705 15 AI561008 F22392 R71279 AA954533 R50725 W24462 R71931 AA484437 AW591731 R25667 R52695 R50810 AI560805 AI089266 H88388 H41353 H28590 AW001880 AI141623 AA250773 AI284778 AW511412 AW083975 AA130377 AW026047 R50551 R81494 AI357668 AI078272 F32666 F36981 AW304865 H43906 AA931088 R48010 AI540217 AI017339 AI291812 20 AI741954 AA58490 AI088378 AA288764 H61168 AA358382 AA288725 AA298515 AA484148 AA443538 R43046 AA084314 T40641 T47608 T48940 AI082477 AW470145 N92284 AI758958 AA298512 AA284586 AI597777 AA480277 AI932559 AI869081 AA476615 AA503851 AI656024 AW168522 AI682051 AI689106 AI274592 AI520917 BE258918 BE615881 BE280282 R53386 BE278255 BE278398 T47607 AA477662 H88385 100817 19648_1 L34355 L46810 NM_000023 U08895 AA424260 AI097272 AA424162 N79764 F19290 F25278 AI479385 AA460662 AA432059 AW016935 F25770 F32549 F36677 F33016 F35992 F38010 AW172497 AA835076 F28727 AA211643 AA453282 25 100818 19604_3 U79251 AA843851 R38201 R66461 R44908 AA683289 H17477 R37364 R52832 AW288336 AA351391 NM_002545 L34774 AA286886 AW967001 T28889 R13451 T77331 AL119196 AL118830 H08459 AW892812 AW905838 H17585 R52878 100881 458_127 BE561958 BE561728 BE397612 BE514391 BE269037 BE514207 BE562381 BE514256 BE514403 BE514250 BE397832 BE269598 BE559865 BE396881 BE560031 BE514199 BE560037 BE560454 30 100885 12707_3 X07881 NM_006249 X07637 AA376715 AA376877 X07715 X07704 S80916 100898 8542_1 BE387614 R51501 AA199714 AW674779 F08178 BE269071 AA376313 H08264 AA380420 H18785 AL042151 BE277758 BE267438 NM_005850 L35013 BE540833 BE390802 BE391494 BE277459 BE385592 BE390612 BE384263 BE387779 BE388647 BE537373 BE547158 AW409585 AW374033 AW602185 AA355725 AW577548 AW935015 AW935160 W40232 35 AW938647 AW374332 AA434040 BE293488 AL138361 BE560260 AI745075 AA317980 AW949382 AI834311 AI653582 AI831042 AI361878 AA618606 AA729052 AI424959 AA199715 AW769374 AI828422 AW044307 AI862816 AI203533 AW084461 AW514855 AA831883 AA290672 AA831286 AA578510 AW089965 AW150746 AA292743 H22232 AI468275 AW439312 AA282744 AW471443 AI473989 AA593336 AA464070 AI678937 AW069451 AA970763 AA610480 AA593328 AA464009 AA768985 AI298928 AA436600 AA464718 AA699361 D61482 D55935 AI389591 AA470695 AI809135 AA840827 40 AI568446 R51502 W45487 AI655316 AA463934 AW168609 AW518663 BE045525 Z41251 AI868091 AA808160 AI026697 AI886259 AI612932 AA215437 AI956014 BE541087 BE255652 BE265878 BE394102 W27502 U48936 L35952 X87160 NM_001039 AL036606 AL036420 U35630 AW298574 W80551 M85370 AA976427 U66052 45 AI457548 U72509 U72512 T98357 R31335 F18090 L32961 NM_000663 U80228 S75578 AA425061 AA29317 AI815143 AA910669 AI286022 AI286019 U88896 U88898 AA916056 T03285 AI341594 AI359534 AI834031 U88897 BE397750 AA232171 BE562800 BE384894 BE242228 BE206819 BE261742 AA296468 AW959763 BE276164 BE264109 BE392626 BE256735 AA301453 N55872 H01676 AA292746 AA427485 AA498400 AA352389 50 Y10518 Y10514 Z83935 Y10508 AK000055 Y10519 AI142012 AI681175 BE222219 AA890586 BE504347 BE328064 N63044 N51226 AI151248 AI521996 AI924777 AW375954 AI860275 W00549 AI742673 AW612288 AI763082 AA632510 AI097347 AI088070 AI214349 AA890297 AI494156 AI698598 AA631658 AA504593 AA860733 AI266781 AW663214 AW771231 AA639610 AI769806 AI769748 AW014326 AI288611 AA250806 AA458220 55 AA429212 W00881 T88798 R92430 AI084125 AI083773 AI479687 AI939609 AI968662 AF129507 NM_013282 AW971840 AW298508 AA744240 AA811217 AA827671 AA811055 AA806567 AA488977 AA808902 AI637637 AA927056 AI870139 AW340482 AA488755 AA129794 AA306523 AA354253 BE256277 AC053467 AW962084 60 AA321355 AW964592 R23284 H73983 R23382 N47914 C01377 H04688 AW806248 R34447 AA847136 AI684489 AI523112 AW044269 AI379138 N29366 AA761543 N79248 AA960845 AA768316 AI147826 AI718599 AI880620 R67467 AI216016 AI738663 H04648 113213 23798_1 NM_001395 Y08302 AI434619 AI470328 AI261807 AW024965 AI806537 AI830549 AI640337 AI219065 AW271700 AW028488 AI133339 AI859205 R51175 U87167 BE379324 BE392008 AA340819 AA343110 T57275 D59164 AW299312 AI434422 AI936390 AW024975 R40262 65 AW269126 R09430 T56590 AI367247 AI253132 BE464248 T58658 AW207785 T58607 R51194 AI732276 R53587 AI820697 134947 844579_1 AK000526 BE550084 W30689 AW271859 AA411456 AI341551 AA242980 AA240327 H87046 D20360 AI184053 AA146956 129311 16078_1 AI721023 AI718944 AA146955 F18215 AA903890 AI700355 AI075430 AA411584 AA878210 AI476760 AW945637 AA630586
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		AA431522 AA301989 AI909058 D12149 N41960 BE222214 AA609922 AA828176 AA393359 AA398693 AW024956 BE467805 AW288623 AW264085 AI024454 AI024719 AI431927 T55087 AI611014 T54820 AA131253 AI436344 AA017176 AI359979 AA047836 AA017063 AA016303 AA001545 AA063315 AA063316 AF015910 AA305746 D90187 T63943 AW951154 T29182 AI734941 D13264 AI299239 Z18812 AW299859 W24476 AA933064 AA489759 AW888554 AW807282 AA319988 M28590 M55405 AW752552 AA326895 M10036 NM_000365 N84665 H69414 N84657 AA380453 AA329743 AA357387 AA189770 AA376532 AA353653 AA158953 AA083176 BE537313 AA181433 D53373 R57376 AA206698 R14807 H18899 H11191 H93892 R25593 T61134 N83285 AA083081 AA831788 H13137 AA497014 AA079330 AA182861 H13138 W47161 R62913 AA687089 AA211112 AA429237 ALQ35923 AA100070 AW392898 AI568433 AA866006 AA214002 AW392865 N79454 AA197181 AI680371 AA176501 AA737987 AI089225 F34874 AW571437 AI620620 AA573489 AA423816 AA164917 AA458455 T47072 AI569087 AI261656 AA730919 AI633441 AW185182 AI351622 AW243465 AI872649 AI359227 AA987941 AI693770 T47073 AW779948 AW510580 AI635626 AW627601 AA864326 AA953578 AI341418 BE222853 AI241963 AI094863 AA928380 AA493373 AW043762 AI377783 AW958987 BE619760 AA385240 BE277975 BE280095 AW631443 AA581048 BE618715 BE299610 C14874 BE559858 BE378455 BE618290 BE544585 AI525575 BE548897 BE267110 AA804738 BE269821 AA918133 BE277647 AA599947 BE280735 BE390239 N74150 T12504 AI208197 AW955527 AA113897 N40081 H73835 H70393 AI434041 W22950 AI192661 BE264461 W26486 AA626424 AA186694 T69209 AA857976 AI540287 AA410589 AA864287 AW850564 AA013320 T49283 AI541438 AW804703 AA335534 AA335659 BE562269 BE618802 BE277850 BE546413 BE280994 AA204813 BE561694 BE543524 BE253847 AW001452 W19116 BE542508 AA205894 BE254875 BE270033 AI525906 BE251782 AA975700 BE272138 AW807671 N87686 M10036 BE515060 BE298607 AI745178 U47824 H03183
5	114427 9724_2 114569 110077_1 100106 16621_5 100515 342_1	
10	100531 46038_1 100545 22955_1 100574 17320_2	
15		
20		
25	100627 tigr_HT2798 100756 tigr_HT3768 100768 tigr_HT3848 100813 tigr_HT4265 100836 tigr_HT4383 100855 tigr_HT4504	Z25424 M88357 L29141 M69180 M81105 L33999 U04688 U09806
30	102104 entrez_U12139 125091 genbank_T91518 100929 tigr_HT688 125147 _entrez_W38150 102354 entrez_U38268 102491 entrez_U51010 102636 entrez_U67092 118769 genbank_N74496 101048 entrez_K01160 101057 entrez_K03430	U12139 T91518 X65561 W38150 U38268 U51010 U67092 N74496 K01160 K03430
40	108334 genbank_AA070473 108417 483241_1 108441 genbank_AA079079 108786 genbank_AA128999 101655 entrez_M80299 101697 entrez_M84358 117437 genbank_N27645 101798 entrez_M85220 101909 entrez_S69265 103508 entrez_Y10141 103575 entrez_Z26256 118332 genbank_T54095 112161 genbank_R48295 118584 NOT_FOUND_entrez_W38206 114376 NOT_FOUND_entrez_GMCSF 100478 tigr_HT1067 100547 tigr_HT2219 100564 tigr_HT2324	AA070473 AA070853 AA075749 AA075716 AA079079 AA128999 M60299 M84358 N27645 M85220 S69265 Y10141 Z26256 T54095 R48295 W38206 GMCSF M22406 M57417 Z11585
55		

TABLE 12: shows genes, including expression sequence tags, that are down-regulated in prostate tumor tissue compared to normal prostate tissue as analyzed using Affymetrix/Eos Hu01 GeneChip array. Shown are the ratios of "average" normal prostate to "average" prostate cancer tissues.

10	Pkey: ExAccn: UnigeneID: Unigene Title: R1:	Unique Eos probeset identifier number Exemplar Accession number, Genbank accession number Unigene number Unigene gene title Background subtracted normal prostate : prostate tumor tissue
15	Pkey ExAccn UnigeneID Unigene Title	R1
20	100522 HG1763-HT1780 Prolactin-Induced Protein 130803 M81650 Hs.1968 semenogelin I 118068 N53943 Hs.13743 ESTs 114251 Z39898 Hs.21948 ESTs 112134 R46025 Hs.7413 ESTs 101436 M20642 Hs.158295 Human alkali myosin light chain 3 mRNA; complete cds 104028 AA361094 Hs.221128 ESTs 108944 AA149204 Hs.175783 ESTs; Highly similar to growth arrest inducible gene product [H.sapiens] 103838 AA174173 Hs.12622 ESTs 120469 AA251741 Hs.25882 DKFZP586M1824 protein 110279 H29231 Hs.27384 ESTs 127472 AA761378 Hs.192013 ESTs	17.4 16.785 13.225 12.7 8.735 8.175 8.15 7.535 7.212 7.175 6.701 6.642 6.411 6.395
30	114011 W80385 Hs.15082 ESTs 101249 L33881 Hs.1904 protein kinase C; iota 123265 AA491209 Hs.105265 ESTs; Weakly similar to reverse transcriptase [M.musculus] 119322 T49655 Hs.241569 ESTs; Modly smir to II ALU SUBFAMILY SQ WARNING ENTRY II [H.sapiens] 101673 M81908 Hs.6241 phosphoinositide-3-kinase; regulatory subunit; polypeptide 1 (p85 alpha) 115586 AA399218 Hs.92423 ESTs	6.15 6 6 5.95 5.925 5.7 5.7 5.625 5.5 5.486
35	120590 AA281780 Hs.111441 ESTs; Weakly similar to similar to Kruppel-like zinc finger protein [C.elegans] 109748 F10192 Hs.248323 Tubulin; alpha; brain-specific 134727 X80507 Hs.8939 yes-associated protein 65 kDa 129171 AA234048 Hs.7753 calumenin 120390 AA233122 Hs.111460 ESTs; Highly similar to multifunctional calcium/calmodulin-dependent protein kinase II delta2 isoform [H.sapiens]	5.4 5.279 5.268 5.151 5.134 5.075 5.075 5.055 5.033 4.675 4.626 4.6 4.559 4.451 4.45 4.45 4.301 4.2 4.175 4.1 4.05 4.048 4.041 4.028
40	131699 R68657 Hs.90421 ESTs; Modly smir to II ALU SUBFAMILY SX WARNING ENTRY II [H.sapiens] 104490 N71503 Hs.43087 ESTs; Weakly similar to dysferlin [H.sapiens] 102124 U14528 Hs.29981 solute carrier family 26 (sulfate transporter); member 2 109280 AA198635 Hs.86081 ESTs 109707 F09739 Hs.185701 Homo sapiens mRNA full length insert cDNA clone EUROIIMAGE 21920 108087 AA045709 Hs.40545 ESTs 135006 M21665 Hs.929 myosin; heavy polypeptide 7; cardiac muscle; beta 119182 R80664 Hs.77067 ESTs 129806 R62444 Hs.173373 KIAA0831 protein 101435 M20543 Hs.1288 actin; alpha 1; skeletal muscle 125954 R93943 yf72c12.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:275735 5'	5.4 5.279 5.268 5.151 5.134 5.075 5.075 5.055 5.033 4.675 4.626 4.6 4.559 4.451 4.45 4.45 4.301 4.2 4.175 4.1 4.05 4.048 4.041 4.028
45	113989 W87544 Hs.221184 ESTs 104432 J03460 Hs.99949 prolactin-induced protein 112326 R56068 Hs.4268 ESTs 119063 R16833 Hs.53106 ESTs; Weakly similar to II ALU SUBFAMILY J WARNING ENTRY II [H.sapiens] 130376 R40873 Hs.155174 KIAA0432 gene product 122484 AA448286 Hs.98074 ESTs; Highly similar to atrophin-1 interacting protein 4 [H.sapiens] 104142 AA447006 Hs.11123 ESTs; Moderately similar to II ALU SUBFAMILY SQ WARNING 129413 N32787 Hs.11123 ESTs; Moderately similar to hypothetical protein 2 [H.sapiens] 103678 Z84483 Human DNA sequence from PAC 46H23, BRCA2 gene region chromosome 13q12-13q10.5 114266 Z40188 Hs.26409 ESTs 115206 AA262491 Hs.186572 ESTs 123723 AA609749 Hs.112759 ESTs; Highly similar to unknown protein [R.norvegicus] 129130 H97893 Hs.172788 ESTs; Weakly similar to KIAA0512 protein [H.sapiens]	5.4 5.279 5.268 5.151 5.134 5.075 5.075 5.055 5.033 4.675 4.626 4.6 4.559 4.451 4.45 4.45 4.301 4.2 4.175 4.1 4.05 4.048 4.041 4.028
50	129806 R62444 Hs.173373 KIAA0831 protein 101435 M20543 Hs.1288 actin; alpha 1; skeletal muscle 125954 R93943 yf72c12.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:275735 5'	5.4 5.279 5.268 5.151 5.134 5.075 5.075 5.055 5.033 4.675 4.626 4.6 4.559 4.451 4.45 4.45 4.301 4.2 4.175 4.1 4.05 4.048 4.041 4.028
55	113989 W87544 Hs.221184 ESTs 104432 J03460 Hs.99949 prolactin-induced protein 112326 R56068 Hs.4268 ESTs 119063 R16833 Hs.53106 ESTs; Weakly similar to II ALU SUBFAMILY J WARNING ENTRY II [H.sapiens] 130376 R40873 Hs.155174 KIAA0432 gene product 122484 AA448286 Hs.98074 ESTs; Highly similar to atrophin-1 interacting protein 4 [H.sapiens] 104142 AA447006 Hs.11123 ESTs; Moderately similar to II ALU SUBFAMILY SQ WARNING 129413 N32787 Hs.11123 ESTs; Moderately similar to hypothetical protein 2 [H.sapiens] 103678 Z84483 Human DNA sequence from PAC 46H23, BRCA2 gene region chromosome 13q12-13q10.5 114266 Z40188 Hs.26409 ESTs 115206 AA262491 Hs.186572 ESTs 123723 AA609749 Hs.112759 ESTs; Highly similar to unknown protein [R.norvegicus] 129130 H97893 Hs.172788 ESTs; Weakly similar to KIAA0512 protein [H.sapiens]	5.4 5.279 5.268 5.151 5.134 5.075 5.075 5.055 5.033 4.675 4.626 4.6 4.559 4.451 4.45 4.45 4.301 4.2 4.175 4.1 4.05 4.048 4.041 4.028
60	129806 R62444 Hs.173373 KIAA0831 protein 101435 M20543 Hs.1288 actin; alpha 1; skeletal muscle 125954 R93943 yf72c12.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:275735 5'	5.4 5.279 5.268 5.151 5.134 5.075 5.075 5.055 5.033 4.675 4.626 4.6 4.559 4.451 4.45 4.45 4.301 4.2 4.175 4.1 4.05 4.048 4.041 4.028
65	113989 W87544 Hs.221184 ESTs 104432 J03460 Hs.99949 prolactin-induced protein 112326 R56068 Hs.4268 ESTs 119063 R16833 Hs.53106 ESTs; Weakly similar to II ALU SUBFAMILY J WARNING ENTRY II [H.sapiens] 130376 R40873 Hs.155174 KIAA0432 gene product 122484 AA448286 Hs.98074 ESTs; Highly similar to atrophin-1 interacting protein 4 [H.sapiens] 104142 AA447006 Hs.11123 ESTs; Moderately similar to II ALU SUBFAMILY SQ WARNING 129413 N32787 Hs.11123 ESTs; Moderately similar to hypothetical protein 2 [H.sapiens] 103678 Z84483 Human DNA sequence from PAC 46H23, BRCA2 gene region chromosome 13q12-13q10.5 114266 Z40188 Hs.26409 ESTs 115206 AA262491 Hs.186572 ESTs 123723 AA609749 Hs.112759 ESTs; Highly similar to unknown protein [R.norvegicus] 129130 H97893 Hs.172788 ESTs; Weakly similar to KIAA0512 protein [H.sapiens]	5.4 5.279 5.268 5.151 5.134 5.075 5.075 5.055 5.033 4.675 4.626 4.6 4.559 4.451 4.45 4.45 4.301 4.2 4.175 4.1 4.05 4.048 4.041 4.028

	120217	Z41078	Hs.66035	ESTs	4.028
	108538	AA084524		zn19d8.s1 Stratagene neuroepithelium NT2RAMI 937234 Homo sapiens cDNA	4.023
	134460	AA400030	Hs.8360	ESTs; Weakly similar to II ALU CLASS B WARNING ENTRY II [H.sapiens]	3.925
5	120418	AA238010	Hs.26813	Homo sapiens mRNA; cDNA DKFZp586F1323 (from clone DKFZp586F1323)	3.91
	132783	N74897	Hs.5683	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 15	3.889
	125052	T80174	Hs.222779	ESTs; Moderately similar to similar to NEDD-4 [H.sapiens]	3.85
	108600	AA099585	Hs.41175	ESTs	3.833
	103099	X61100	Hs.8248	NADH dehydrogenase (ubiquinone) Fe-S protein 1 (75kD) (NADH-coenzyme	3.818
10	134948	H06773	Hs.93850	protein kinase; AMP-activated; gamma 2 non-catalytic subunit	3.792
	120511	AA258144	Hs.221578	ESTs	3.779
	111861	R37460	Hs.25231	ESTs	3.768
	113966	W86600	Hs.9842	ESTs	3.75
	131849	AA481254	Hs.30120	ESTs	3.708
	129775	R94659	Hs.12420	ESTs	3.707
15	110191	H20568	Hs.27182	phospholipase A2-activating protein	3.7
	112878	R87160	Hs.33665	ESTs	3.7
	127115	AA375791	Hs.131894	ESTs	3.674
	132892	W92797	Hs.59378	DKFZP434G162 protein	3.653
	115023	AA252079	Hs.63931	dachshund (Drosophila) homolog	3.625
20	114932	AA242751	Hs.16218	KIAA0903 protein	3.62
	106865	AA487228	Hs.19479	ESTs	3.614
	134480	AA024664	Hs.83916	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex; 5 (13kD; B13)	3.613
	124780	R42493	Hs.220839	ESTs	3.6
	130631	AA025399	Hs.169737	ESTs	3.592
25	134154	AA211320	Hs.79404	neuron-specific protein	3.568
	104160	AA455706	Hs.99722	ESTs; Weakly similar to 78 KD GLUCOSE REGULATED PROTEIN PRECURSOR	3.559
	105524	AA258158	Hs.22153	ESTs; Weakly similar to KIAA0352 [H.sapiens]	3.542
30	110168	H19673	Hs.176586	ESTs	3.525
	109480	AA233299	Hs.72158	ESTs	3.522
	109585	F02367	Hs.27252	ESTs	3.5
	115134	AA257107	Hs.184331	ESTs	3.5
	116083	AA455653	Hs.44581	ESTs; Weakly similar to HEAT SHOCK 70 KD PROTEIN 6 [H.sapiens]	3.459
	120524	AA261852	Hs.182905	ESTs	3.45
35	116932	H74330	Hs.150000	ESTs	3.425
	130748	AA256976	Hs.18800	ESTs; Weakly similar to KIAA0579 protein [H.sapiens]	3.42
	107513	X05451	Hs.158285	Human alkali myosin light chain 3 mRNA; complete cds	3.417
	118641	N70298	Hs.48828	ESTs	3.407
	128584	AI028384	Hs.127331	ESTs	3.399
40	105134	AA159953	Hs.22895	ESTs; Weakly similar to arylsulfatase B precursor [H.sapiens]	3.325
	123502	AA600116	Hs.112528	ESTs	3.318
	132389	N50866	Hs.47135	ESTs	3.317
	105691	AA287097	Hs.75356	transcription factor 4	3.315
	131505	H85897	Hs.27755	ESTs	3.309
45	120776	AA342104	Hs.96777	EST	3.3
	105579	AA278824	Hs.19218	ESTs	3.295
	128180	AA948876	Hs.148378	ESTs	3.292
	100819	HG4020-HT4290		Transglutaminase	3.289
50	130217	D29956	Hs.152818	ubiquitin specific protease 8	3.273
	130068	AA608903	Hs.106220	KIAA0336 gene product	3.269
	134719	L07515	Hs.89232	chromobox homolog 5 (Drosophila HP1 alpha)	3.266
	110277	H29209	Hs.151231	ESTs; Highly similar to FYVE finger-containing phosphoinositide kinase [M.musculus]	3.26
	127354	AA418880	Hs.185797	ESTs	3.212
	129173	R60523	Hs.109087	ESTs	3.197
55	127484	AA970504	Hs.148103	ESTs	3.179
	124923	R84500	Hs.108048	ESTs	3.175
	122465	AA448164	Hs.99153	ESTs; Highly similar to CGI-73 protein [H.sapiens]	3.151
	122027	AA431302	Hs.98721	EST; Weakly similar to N-copine [H.sapiens]	3.151
60	103329	X85134	Hs.72984	retinoblastoma-binding protein 5	3.15
	129937	M95767	Hs.135578	chitinase; dN-acetyl-	3.15
	134197	AA057341	Hs.87889	helicase-mol	3.15
	107764	AA018219	Hs.226923	ESTs	3.125
	121775	AA421773	Hs.161008	ESTs	3.125
65	114768	AA149007	Hs.182339	Ets homologous factor	3.12
	132381	N48818	Hs.46884	ESTs	3.11
	123105	AA485973	Hs.143947	ESTs	3.104
	121176	AA400080	Hs.97774	ESTs	3.1
	125053	T80620	Hs.188473	ESTs	3.075
	105909	AA401739	Hs.5111	ESTs	3.066

	119767	W72562	Hs.58119	ESTs	3.057
	115776	AA424038	Hs.58197	ESTs	3.056
	111713	R22988	Hs.220950	ESTs	3.05
	115301	AA280047	Hs.43948	ESTs	3.05
5	118448	N66412	Hs.49189	ESTs	3
	106586	AA456598	Hs.256269	ESTs	2.995
	110415	H48239	Hs.29739	ESTs; Weakly similar to RAS-RELATED PROTEIN RAB-3A [H.sapiens]	2.979
	105173	AA182030	Hs.8364	ESTs	2.978
10	101102	L07594	Hs.79059	transforming growth factor; beta receptor III (betaglycan; 300kD)	2.978
	110543	H58383	Hs.258544	ESTs	2.976
	125593	R24464	Hs.202949	KIAA1102 protein	2.964
	100824	HG4058-HT4328		Oncogene Aml1-Evt-1, Fusion Activated	2.957
	106822	AA481068	Hs.31835	ESTs	2.95
15	131983	D11930	Hs.3592	ESTs	2.95
	111221	N68869	Hs.15119	ESTs	2.938
	113820	T93795	Hs.17252	EST	2.917
	105220	AA210695	Hs.17212	ESTs	2.917
	123234	AA490227	Hs.105252	ESTs	2.904
20	125250	W87465	Hs.222926	ESTs; Weakly similar to D2092.2 [C.elegans]	2.9
	116196	AA465160	Hs.63388	ESTs	2.9
	122100	AA432243	Hs.41086	ESTs; Weakly similar to OXYSTEROL-BINDING PROTEIN [H.sapiens]	2.896
	111712	R22905	Hs.113716	ESTs	2.895
	126589	W78107	Hs.187698	ESTs; Weakly similar to Yer140wp [S.cerevisiae]	2.895
25	111132	N64378	Hs.13149	ESTs; Highly similar to unknown function [H.sapiens]	2.894
	115307	AA280300	Hs.191346	ESTs	2.888
	108989	AA152263	Hs.18827	KIAA0849 protein	2.883
	129486	H03686	Hs.220689	Ras-GTPase-activating protein SH3-domain-binding protein	2.879
	119805	W73788	Hs.43213	ESTs	2.875
30	125721	R58881	Hs.7503	ESTs	2.871
	103704	AA028171	Hs.153688	ESTs	2.868
	128420	A1088155	Hs.14146	ESTs; Weakly similar to unknown [H.sapiens]	2.866
	120571	AA280738	Hs.128679	ESTs	2.863
	123059	AA482019	Hs.238202	EST	2.86
35	129462	D84239	Hs.111732	IgG Fc binding protein	2.856
	125166	W45491	Hs.172609	nucleobindin 1	2.854
	125992	W01626		za36e07.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone	2.852
	109431	AA227972	Hs.43635	ESTs	2.85
	105077	AA142919	Hs.5558	ESTs	2.847
40	131388	R34531	Hs.92200	KIAA0480 gene product	2.846
	121080	AA398720	Hs.177953	ESTs	2.838
	112575	R73818	Hs.17385	ESTs	2.836
	130244	R26206	Hs.153293	KIAA0701 protein	2.825
	134698	AA427783	Hs.77910	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 1 (soluble)	2.816
45	116355	AA504356	Hs.88650	ESTs	2.813
	115316	AA280627	Hs.57848	ESTs	2.806
	129577	U48738	Hs.198891	serine/threonine-protein kinase PRP4 homolog	2.8
	130971	H20332	Hs.28707	signal sequence receptor; gamma (translocon-associated protein gamma)	2.799
	115054	AA252863	Hs.87729	ESTs	2.795
50	130285	AA063548	Hs.202968	ESTs	2.792
	124308	H93575	Hs.227146	Homo sapiens mRNA; cDNA DKFZp564J142 (from clone DKFZp564J142)	2.783
	125502	AA732329	Hs.191859	ESTs	2.778
	114800	AA159825	Hs.131887	ESTs; Weakly similar to ORF YNL227c [S.cerevisiae]	2.768
	128625	AA242816	Hs.102652	ESTs; Weakly similar to KIAA0437 [H.sapiens]	2.766
55	130159	H51098	Hs.151310	PDZ domain protein (Drosophila InaD-like)	2.75
	107127	AA620504	Hs.22119	ESTs	2.742
	113547	T80746	Hs.15233	ESTs	2.734
	104639	AA004622	Hs.18214	ESTs	2.727
	127609	AA622559	Hs.150318	ESTs	2.728
60	106922	AA490964	Hs.10056	ESTs	2.725
	124825	R52088		yg85c3.s1 Soares infant brain 1NIB Homo sapiens cDNA clone	2.725
	124333	H98683	Hs.154054	ESTs	2.708
	117634	N36421	Hs.107854	ESTs; Weakly similar to SODIUM- AND CHLORIDE-DEPENDENT GLYCINE TRANSP	2.706
65	101609	M54927	Hs.1787	proteolipid protein 1 (Pelizaeus-Merzbacher disease; spastic paraplegia 2; uncomplicated)	2.704
	117142	H96908	Hs.42251	ESTs	2.7
	112602	R79147	Hs.203365	ESTs	2.695
	106828	AA481505	Hs.13797	ESTs	2.68
	124377	N25996	Hs.179833	ESTs	2.675

	101026	J04970	carboxypeptidase M	2.675
	124560	N66393	Hs.102754 ESTs	2.675
	124068	H02494	Hs.101615 ESTs	2.671
5	130281	R12777	Hs.15395 ESTs; Weakly similar to ARGINYL-TRNA SYNTHETASE [H.sapiens]	2.68
	110949	N49602	Hs.13308 ESTs	2.65
	111031	N54839	Hs.221085 ESTs; Highly similar to mediator [H.sapiens]	2.633
	121770	AA421714	Hs.11469 KIAA0898 protein	2.63
	134132	U32519	Hs.220689 Ras-GTPase-activating protein SH3-domain-binding protein	2.626
	112424	R62452	Hs.191265 ESTs	2.625
10	122544	AA451679	Hs.194410 ESTs	2.625
	134425	X90568	Hs.172004 titin	2.624
	111114	N83391	Hs.9238 ESTs	2.619
	116119	AA459242	Hs.44445 ESTs; Weakly similar to Ketch motif containing protein [H.sapiens]	2.616
	112079	R44184	Hs.23014 ESTs	2.6
15	123033	AA481271	Hs.193945 ESTs	2.591
	124196	H52617	Hs.144167 ESTs	2.588
	125873	H14437	y25a04.r1 Soares breast 3NbHBst Homo sapiens cDNA clone	2.58
	117684	N40184	Hs.45050 ESTs	2.575
	134938	D30037	Hs.168328 phosphatidylinositol transfer protein; beta	2.575
20	131822	AA215847	Hs.200332 ESTs	2.568
	135185	U71203	Hs.96038 Ric (Drosophila)-like; expressed in many tissues	2.564
	117690	N40467	Hs.93834 ESTs	2.557
	118807	N78582	Hs.50732 protein kinase; AMP-activated; beta 2 non-catalytic subunit	2.552
25	121369	AA405657	Hs.128791 Human DNA sequence from clone 967N21 on chromosome 20p12.3-13. Contains	2.55
	114860	AA235112	Hs.106227 ESTs; Moderately similar to similar to murine RNA-binding protein [H.sapiens]	2.549
	121857	AA426017	Hs.62694 ESTs; Highly similar to DNA-REPAIR PROTEIN COMPLEMENTING	2.548
	110180	H20560	Hs.244624 ESTs	2.548
	132573	AA045333	Hs.51743 ESTs; Weakly similar to !! ALU SUBFAMILY SB2 WARNING ENTRY !! [H.sapiens]	2.542
	109708	F09729	Hs.12780 ESTs	2.537
30	135109	AA410391	Hs.94592 klotho	2.525
	132810	R37027	Hs.5737 KIAA0475 gene product	2.525
	124879	R73588	Hs.101533 ESTs	2.525
	103840	AA174190	Hs.50932 ESTs	2.525
	119068	R22198	Hs.34492 ESTs	2.519
35	114833	AA234362	Hs.87310 ESTs; Moderately similar to CGI-66 protein [H.sapiens]	2.507
	112998	T23555	Hs.103288 ESTs	2.5
	123312	AA498258	Hs.99801 ESTs	2.499
	121873	AA426270	Hs.145696 splicing factor (CC1.3)	2.491
	123321	AA498884	Hs.23972 ESTs	2.491
40	107760	AA018042	Hs.95078 EST	2.483
	102580	U60808	Hs.152981 CDP-diacylglycerol synthase (phosphatidate cytidylyltransferase) 1	2.481
	103053	X58741	Hs.5947 mel transforming oncogene (derived from cell line NK14)- RAB8 homolog	2.475
	124758	R38100	Hs.106294 ESTs	2.475
45	112938	T15665	Hs.6185 ESTs; Weakly similar to BcDNA.GH12174 [D.melanogaster]	2.475
	125178	W58202	Hs.125731 ESTs	2.475
	112423	R62447	Hs.22123 ESTs	2.471
	123515	AA600323	Hs.112535 EST	2.462
	102842	U95020	Hs.21903 calcium channel; voltage-dependent; beta 4 subunit	2.457
	102400	U42390	Hs.171957 triple functional domain (PTPRF interacting)	2.455
50	113187	T56058	Hs.9992 ESTs	2.452
	131687	L11066	Hs.3069 heat shock 70kD protein 9B (mortalin-2)	2.448
	115314	AA280583	Hs.256501 ESTs	2.437
	128211	AI208427	Hs.168707 ESTs; Highly similar to Ran-binding protein 2 [H.sapiens]	2.43
55	134281	L11005	Hs.81047 aldehyde oxidase 1	2.425
	115985	AA447709	Hs.132094 ESTs; Moderately similar to putative transcription factor CA150 [H.sapiens]	2.425
	111348	N90041	Hs.9585 ESTs	2.418
	129430	AA258842	Hs.197877 Homo sapiens clone 23777 putative transmembrane GTPase mRNA; partial cds	2.418
	133863	C13990	Hs.76930 synuclein; alpha (non A4 component of amyloid precursor)	2.417
60	111164	N66857	Hs.14808 ESTs; Weakly similar to !! ALU CLASS C WARNING ENTRY !! [H.sapiens]	2.416
	132143	AA257058	Hs.7972 KIAA0871 protein	2.412
	130330	M55047	Hs.154679 synaptotagmin 1	2.408
	114219	Z39451	Hs.27389 ESTs	2.406
	117101	H94043	Hs.24341 DKFZP5861419 protein	2.403
65	125433	AA034325	Hs.54320 ESTs	2.4
	111099	N62506	Hs.21958 ESTs	2.4
	120323	AA195405	Hs.110347 Homo sapiens mRNA for alpha integrin binding protein 80; partial	2.397
	118624	N69998	Hs.21801 ESTs	2.394
	123570	AA608855	Hs.109653 ESTs	2.389
	123562	AA608893	Hs.190065 ESTs	2.388

	131546	AA262821	Hs.28578	muscleblind (Drosophila)-like	2.385
	103143	X66141	Hs.75535	myosin; light polypeptide 2; regulatory; cardiac; slow	2.384
	123645	AA609310	Hs.188691	ESTs	2.383
5	130123	AA001835	Hs.150390	zinc finger protein 262	2.379
	131682	AA428368	Hs.30654	ESTs	2.378
	115909	AA436668	Hs.59761	ESTs	2.375
	125168	W45574	Hs.252497	ESTs	2.372
	123973	C14805	Hs.182151	ESTs	2.361
	135197	U76458		Homo sapiens tissue inhibitor of metalloproteinase 4 mRNA, complete cds	2.357
10	118689	N71545	Hs.184544	ESTs	2.357
	107734	AA018225	Hs.93388	ESTs	2.354
	124590	N69220	Hs.41381	ESTs; Weakly similar to ubiquitin hydrolyzing enzyme I [H.sapiens]	2.35
	111163	N66850	Hs.17606	ESTs	2.348
15	112349	R58877	Hs.22665	ESTs; Moderately similar to dJ83L6.1 [H.sapiens]	2.345
	129078	AA262179	Hs.169343	ESTs	2.345
	134238	R81509	Hs.184571	splicing factor; arginine/serine-rich 11	2.341
	116768	H13260	Hs.95097	ESTs	2.336
	106331	AA436853	Hs.34795	ESTs	2.333
20	129003	AA443752	Hs.10784	ESTs	2.332
	132368	AA599814	Hs.46837	ESTs; Weakly similar to cDNA EST yk289g5.5 comes from this gene [C.elegans]	2.332
	124697	R06273	Hs.186467	ESTs; Modly smir to II ALU SUBFAMILY J WARNING ENTRY II [H.sapiens]	2.322
	120273	AA176688	Hs.221139	ESTs	2.313
	127110	AA304993	Hs.100861	ESTs; Weakly similar to p60 katanin [H.sapiens]	2.307
25	105450	AA252621	Hs.93842	ESTs	2.301
	119819	W74371	Hs.56383	ESTs	2.297
	102302	U33052	Hs.69171	protein kinase C-like 2	2.288
	130596	N74353	Hs.16475	ESTs	2.282
	114161	Z38904	Hs.22385	ESTs; Weakly similar to KIAA0970 protein [H.sapiens]	2.278
30	130542	U84675		Human sperm membrane protein BS-63 mRNA, complete cds	2.277
	104491	N71513	Hs.39328	ESTs	2.275
	116988	H82527		ys69e12.s1 Soares retina N2b4HR Homo sapiens cDNA clone	2.275
	126823	AA370120	Hs.7870	ESTs; Weakly similar to Ylr350wp [S.cerevisiae]	2.273
	108800	AA129731	Hs.90424	ESTs	2.273
35	101310	L41807	Hs.934	glucosaminyl (N-acetyl) transferase 2; branching enzyme	2.269
	126842	W19498	Hs.21085	ESTs	2.255
	127251	AA936428	Hs.128638	ESTs	2.251
	124647	N91947	Hs.125033	ESTs	2.249
	127112	AI143906	Hs.125103	ESTs	2.247
40	101873	S82597	Hs.80120	UDP-N-acetyl-alpha-D-galactosamine:polypeptide	2.246
	120999	AA398302	Hs.127437	ESTs	2.245
	130225	AA598583	Hs.15299	HMBA-inducible	2.243
	119980	W88678	Hs.249247	heterogeneous nuclear protein similar to rat helix destabilizing protein	2.243
	124222	H61053	Hs.222844	ESTs	2.24
	129199	H90914	Hs.128629	ESTs	2.238
45	106802	AA479101	Hs.16570	ESTs; Weakly similar to II ALU SUBFAMILY SQ WARNING ENTRY II [H.sapiens]	2.231
	126160	N90960	Hs.247277	ESTs; Weakly similar to transformation-related protein [H.sapiens]	2.229
	104627	AA001976	Hs.19603	ESTs	2.228
	106474	AA450212	Hs.42484	Homo sapiens mRNA; cDNA DKFZp564C053 (from clone DKFZp564C053)	2.226
50	113096	T40927	Hs.8345	ESTs	2.225
	135336	AA452822	Hs.99027	ESTs	2.225
	135344	R62978	Hs.168491	ESTs; Moderately similar to TRF1-interacting ankyrin-related	2.225
	126156	AA508354	Hs.118448	ESTs; Moderately similar to AKT3 protein kinase [H.sapiens]	2.222
	128885	AA397841	Hs.180141	cofilin 2 (muscle)	2.218
55	107900	AA026385	Hs.176600	ESTs; Moderately similar to II ALU SUBFAMILY SB2 WARNING	2.217
	114481	AA033562	Hs.151572	ESTs	2.212
	109292	AA199828	Hs.188662	ESTs	2.212
	104257	AF006265	Hs.9222	estrogen receptor-binding fragment-associated gene 9	2.209
	132832	T15482	Hs.6093	ESTs	2.204
60	127392	AA262728	Hs.14898	Homo sapiens clone 24590 mRNA sequence	2.204
	104641	AA004652	Hs.18584	ESTs	2.2
	122529	AA449828	Hs.99229	ESTs	2.195
	124307	H93582	Hs.162395	proline synthetase co-transcribed (bacterial homolog)	2.193
	133601	S95938	Hs.75155	transferrin	2.193
65	119904	W85709	Hs.128927	ESTs; Weakly similar to II ALU SUBFAMILY SP WARNING ENTRY II [H.sapiens]	2.192
	100348	D84109	Hs.4994	transducer of ERBB2; 2 (TOB2)	2.185
	126871	AA351778	Hs.200334	ESTs	2.18
	127793	AI298835	Hs.30445	ESTs; Weakly similar to transcription regulator Stat-50 [H.sapiens]	2.178
	105149	AA169253	Hs.8958	ESTs	2.177
	121367	AA405648		zw39g8.s1 Soares_total_fetus_Nb2HF8_9w H sapiens cDNA clone IMAGE:772478	2.177

	111838	R36228	Hs.25119	ESTs	2.175
	133394	R16759	Hs.237225	ribosomal protein S5 pseudogene 1	2.175
	123207	AA489697	Hs.145053	ESTs	2.175
	129801	F11087	Hs.239668	ESTs	2.175
5	103393	X94612	Hs.41749	protein kinase; cGMP-dependent; type II	2.161
	132415	AA043223	Hs.4815	nudix (nucleoside diphosphate linked moiety X)-type motif 3	2.157
	106369	AA443828	Hs.25324	ESTs	2.157
	122963	AA478446	Hs.69559	KIAA1098 protein	2.156
	133473	M19309	Hs.73980	troponin T1; skeletal; slow	2.155
10	134257	C06270	Hs.8078	Homo sapiens mRNA; cDNA DKFZp586L081 (from clone DKFZp586L081)	2.155
	135156	AA056012	Hs.9552	bindin of Axl Two	2.151
	104055	AA393755	Hs.117211	ESTs; Highly similar to CGI-62 protein [H.sapiens]	2.15
	102313	U33921	HSU33921	Clontech adult lung cDNA library (HL1158a) Homo sapiens cDNA	2.15
	109788	F10638	Hs.12432	Homo sapiens clone 24407 mRNA sequence	2.15
15	103507	Y10032	Hs.159640	serum/glucocorticoid regulated kinase	2.15
	116000	AA448710	Hs.41327	ESTs	2.15
	105858	AA399164	Hs.227678	ESTs; Moderately similar to II ALU SUBFAMILY SQ	2.137
	103153	X66534	Hs.75295	guanylate cyclase 1; soluble; alpha 3	2.137
	126202	AA652238	Hs.189726	ESTs	2.135
20	115955	AA446121	Hs.44198	Homo sapiens BAC clone RG054D04 from 7q31	2.134
	104164	AA458770	Hs.27023	KIAA0917 protein	2.132
	108692	AA121270	Hs.82960	ESTs	2.128
	122878	AA465341	Hs.99640	ESTs	2.128
	134771	L13939	Hs.88576	adaptor-related protein complex 1; beta 1 subunit	2.125
25	104298	D31120	Hs.40368	adaptor-related protein complex 1; sigma 2 subunit	2.125
	104840	AA039595	Hs.42458	Homo sapiens mRNA; cDNA DKFZp586C1817 (from clone DKFZp586C1817)	2.125
	122180	AA435798	Hs.98835	ESTs; Moderately similar to putative ring zinc finger protein	2.125
	131012	H01992	Hs.202949	KIAA1102 protein	2.125
	134092	H17490	Hs.7905	ESTs; Highly similar to sorting nexin 9 [H.sapiens]	2.123
30	118617	N89868	Hs.183413	ESTs; Modtly smir to II ALU SUBFAMILY J WARNING ENTRY II [H.sapiens]	2.123
	107155	AA621202	Hs.7948	DKFZP586D1519 protein	2.12
	130925	N71935	Hs.169378	multiple PDZ domain protein	2.12
	135167	U63717	Hs.95821	osteoclast stimulating factor 1	2.118
	105952	AA405263	Hs.181400	ESTs	2.109
35	110308	H38148	Hs.32775	ESTs	2.108
	116368	AA521186	Hs.94217	ESTs	2.107
	132939	U76189	Hs.81152	exostoses (multiple)-like 2	2.102
	117881	N50073	Hs.84926	ESTs; Highly similar to B-IND1 protein [M.musculus]	2.1
	121723	AA419622	Hs.104800	ESTs; Weakly similar to Mouse 19.5 mRNA; complete cds [M.musculus]	2.096
40	103500	Y09443	Hs.22580	alkylglycerone phosphate synthase	2.094
	121429	AA406293	Hs.183498	ESTs	2.093
	134632	AA398710	Hs.174139	chloride channel 3	2.091
	129785	F10980	Hs.184780	ESTs	2.09
	111065	N58193	Hs.18740	ESTs; Weakly similar to 1-evidence	2.089
45	114710	AA129931	Hs.79081	protein phosphatase 1; catalytic subunit; gamma isoform	2.083
	132711	N73702	Hs.238927	ESTs	2.083
	133377	R05490	Hs.7239	SEC24 (S. cerevisiae) related gene family; member B	2.079
	124773	R40923	Hs.106604	ESTs	2.078
	117759	N47587	Hs.97345	ESTs; Weakly similar to TROPOMODULIN [H.sapiens]	2.076
50	127386	AA457411	Hs.106728	ESTs	2.076
	101167	L15309	Hs.193677	zinc finger protein 141 (clone pHZ-44)	2.075
	109597	F02582	Hs.14474	ESTs	2.074
	124390	N29325	Hs.7535	ESTs; Highly similar to COBW-like placental protein [H.sapiens]	2.07
	116225	AA478609	Hs.47278	Human Chromosome 16 BAC clone CIT987SK-A-735G6	2.07
55	131243	R16687	Hs.24752	spectrin SH3 domain binding protein 1	2.069
	130557	T90830	Hs.15981	ESTs; Weakly similar to line-1 protein ORF2 [H.sapiens]	2.067
	134103	D14826	Hs.155924	cAMP responsive element modulator	2.064
	108833	AA131866	Hs.61661	ESTs; Weakly similar to DY3.6 [C.elegans]	2.063
	112286	R53765	Hs.158135	KIAA0981 protein	2.063
60	125624	AA185411	zq49a01.1	Stratagene hNT neuron (#937233) Homo sapiens cDNA clone	2.061
	124612	N72200	Hs.13913	ESTs	2.058
	116335	AA495830	Hs.87013	ESTs	2.057
	112248	R51361	Hs.23423	ESTs	2.056
	115789	AA424754	Hs.43149	ESTs	2.056
65	107029	AA599219	Hs.187492	ESTs; Weakly similar to ALR [H.sapiens]	2.056
	110294	H30270	Hs.165082	ESTs	2.054
	120532	AA262354	Hs.186648	ESTs	2.054
	118180	N59249	Hs.48349	ESTs	2.052
	132018	AA283184	Hs.3737	ESTs	2.052

	132617	AA171913	Hs.5338	carbonic anhydrase XII	2.05
	131526	N36167	Hs.28274	ESTs	2.05
	113254	T64438	Hs.11449	DKFZP564O123 protein	2.05
	122785	AA459978	Hs.99508	ESTs	2.05
5	107203	D20426	Hs.5656	EST	2.05
	105713	AA291321	Hs.184319	ESTs; Moderately similar to KIAA1008 protein [H.sapiens]	2.046
	129385	D82675	Hs.110950	Homo sapiens clone 25007 mRNA sequence	2.042
	119116	R43845	Hs.64595	DKFZP566E2346 protein	2.04
	118405	AA600253	Hs.55601	ESTs; Highly similar to host cell factor 2 [H.sapiens]	2.04
10	125924	AA526849	Hs.82109	syndecan 1	2.039
	105599	AA279442	Hs.143460	protein kinase C; nu	2.037
	119741	W70205	Hs.43870	kinesin family member 3A	2.037
	101449	M21494	Hs.118843	creatine kinase; muscle	2.036
	107109	AA609943	Hs.32793	ESTs	2.034
15	117040	H89112		yw25e5.s1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:25328	2.034
	132906	AA142857	Hs.234896	ESTs; Highly similar to geminin [H.sapiens]	2.031
	105479	AA255546	Hs.23467	ESTs	2.027
	102031	U04898	Hs.2156	RAR-related orphan receptor A	2.027
	119846	W80363	Hs.58446	ESTs	2.024
20	124809	R46482	Hs.106875	ESTs	2.024
	130286	AA041548	Hs.154023	KIAA0573 protein	2.023
	124457	N50114	Hs.128704	ESTs	2.017
	125144	W37899	Hs.24336	ESTs	2.017
	120581	AA281257	Hs.125868	ESTs	2.014
25	104931	AA062731	Hs.108319	thyroid hormone receptor-associated protein; 150 kDa subunit	2.012
	120548	AA278846	Hs.187634	ESTs	2.011
	113933	W81362	Hs.30567	ESTs	2.011
	123072	AA485041	Hs.104308	ESTs	2.009
	123648	AA609323	Hs.112689	ESTs	2.008
30	116875	H67749	Hs.161022	EST	2.003
	103179	X69398	Hs.82685	CD47 antigen (Rb-related antigen; integrin-associated signal transducer)	1.995
	103478	Y07755	Hs.38991	S100 calcium-binding protein A2	1.995
	111007	N53378	Hs.22543	ESTs	1.995
	120470	AA251797		zs1113.s1 NCL_CGAP_GCB1 Homo sapiens cDNA clone	1.989
35	112260	R53457	Hs.26040	ESTs; Weakly similar to fatty acid omega-hydroxylase [H.sapiens]	1.989
	114127	Z38652	Hs.106961	ESTs; Weakly similar to TYL [H.sapiens]	1.988
	129863	AA151005	Hs.129872	sperm surface protein	1.988
	106320	AA436608		ESTs	1.988
40	108933	AA147224	Hs.71814	ESTs	1.988
	105906	AA401633	Hs.22380	ESTs	1.982
	109029	AA157911	Hs.72200	ESTs	1.982
	118470	N66769	Hs.82781	ESTs	1.975
	115358	AA281888	Hs.88923	ESTs	1.975
	115257	AA279060	Hs.183516	B-cell CLL/lymphoma 10	1.974
45	126879	AA719776		zh38g04.s1 Soares_pineal_gland_N3HPG Homo sapiens cDNA clone IMAGE:414390	1.974
	109547	F01479	Hs.26966	ESTs	1.973
	127111	AA805728	Hs.220509	ESTs	1.969
	101268	L36845	Hs.73964	EphA4	1.966
	129319	AA037467	Hs.30340	ESTs	1.965
50	106211	AA428240	Hs.126083	ESTs	1.962
	112753	R93696	Hs.169882	ESTs	1.961
	120489	AA255538	Hs.180504	ESTs	1.959
	129699	AA458578	Hs.12017	KIAA0439 protein; homolog of yeast ubiquitin-protein ligase Rsp5	1.956
	105425	AA251129	Hs.24416	ESTs	1.953
55	134740	L37362	Hs.89455	oploid receptor; kappa 1	1.95
	109324	AA210700	Hs.86405	Homo sapiens mRNA; cDNA DKFZp564P056 (from clone DKFZp564P056)	1.95
	124303	H93043	Hs.107070	ESTs	1.95
	102337	U36922		Human fork head domain protein (FKHR) mRNA, 3' end	1.948
	109441	AA228100	Hs.86998	nuclear factor of activated T-cells 5	1.946
60	127364	AA179573	Hs.90061	progesterone binding protein	1.942
	105255	AA227498	Hs.3623	ESTs	1.942
	130672	L19783	Hs.177	phosphatidylinositol glycan; class H	1.942
	104301	D45332	Hs.6783	ESTs	1.94
	132442	R62589	Hs.167419	ESTs	1.939
65	105519	AA258063	Hs.23438	ESTs	1.937
	132902	AA490969	Hs.168147	ESTs	1.936
	118873	N89881	Hs.44577	ESTs	1.936
	114124	Z38595	Hs.125019	ESTs; Highly similar to KIAA0886 protein [H.sapiens]	1.934
	115075	AA255486	Hs.88045	ESTs	1.933

	110695	H93483	Hs.124777	ESTs	1.931
	105380	AA236209	Hs.187626	ESTs	1.931
	124998	T56013	Hs.77910	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 1 (soluble)	1.929
5	121816	AA424814	Hs.187509	ESTs	1.927
	111717	R23241	Hs.110778	STAT induced STAT Inhibitor-2	1.925
	128874	H06245	Hs.106801	ESTs	1.925
	109391	AA219699	Hs.184245	KIAA0929 protein Mx2 interacting nuclear target (MINT) homolog	1.913
	126129	H82165	Hs.40334	ESTs	1.911
10	115553	AA369027	Hs.71414	ESTs	1.905
	113811	W44928	Hs.4878	ESTs	1.905
	108345	AA070906	zm68d1.s1 Stratagene neuroepithelium (#937231)	Homo sapiens cDNA clone	1.904
	120472	AA251875	Hs.104472	ESTs; Weakly similar to Gag-Pol polyprotein [M.musculus]	1.903
	116602	D80063	Hs.241673	EST	1.901
15	121121	AA399371	Hs.189095	ESTs; Weakly similar to zinc finger protein SALL1 [H.sapiens]	1.9
	125330	AA401804	Hs.114574	ESTs	1.896
	130095	F01831	Hs.14838	ESTs	1.894
	119782	W72982	Hs.58262	ESTs	1.894
	104115	AA428080	Hs.26102	ESTs	1.893
20	131313	C17938	Hs.22370	Homo sapiens mRNA; cDNA DKFZp564O0122 (from clone DKFZp564O0122)	1.891
	105583	AA278907	Hs.24549	ESTs	1.891
	122825	AA461185	Hs.99580	ESTs	1.887
	119495	W35390	Hs.55533	ESTs	1.886
	130309	AA134289	Hs.15423	Homo sapiens BAC clone RG114B19 from 7q31.1	1.886
25	125628	AA418069	Hs.241493	natural killer-tumor recognition sequence	1.886
	110611	H66947	Hs.14671	ESTs; Highly similar to gene ERCC5 protein [H.sapiens]	1.885
	117301	N22569	Hs.43215	ESTs	1.884
	131406	N92239	Hs.26471	Wnt inhibitory factor-1	1.881
	126428	AA013312	Hs.64988	ESTs	1.881
30	120285	AA182882	Hs.111110	titin-cap (telethonin)	1.878
	112724	R91753	Hs.17757	ESTs	1.878
	103121	X63679	Hs.4147	translocating chain-associating membrane protein	1.875
	124381	N26765	Hs.109008	ESTs	1.875
	117226	N20468	Hs.177322	ESTs; Weakly similar to putative p150 [H.sapiens]	1.875
35	105610	AA278991	Hs.124691	ESTs; Weakly similar to trithorax homologue 2 [H.sapiens]	1.875
	111229	N69113	Hs.110855	ESTs	1.875
	120627	AA285079	Hs.190474	ESTs	1.873
	107048	AA600012	Hs.10669	ESTs; Moderately similar to KIAA0400 [H.sapiens]	1.872
	104041	AA381902	Hs.197114	RNA binding protein	1.872
40	115162	AA258368	Hs.227806	ras GTPase activating protein-like	1.872
	102239	U26726	Hs.1376	hydroxysteroid (11-beta) dehydrogenase 2	1.87
	100043	M10098	AFFX control 18S ribosomal RNA		1.868
	120296	AA191353	Hs.22385	ESTs; Weakly similar to KIAA0970 protein [H.sapiens]	1.867
	129011	S72869	Hs.107932	DNA segment; single copy; probe pH4 (transforming sequence; thyroid-1;	1.867
45	134851	R44479	Hs.90232	KIAA0552 gene product	1.866
	117392	N26175	Hs.93405	ESTs	1.864
	114530	AA053027	Hs.191797	ESTs	1.863
	123541	AA608794	Hs.112592	ESTs	1.863
	124890	R78618	Hs.34145	ESTs; Weakly similar to RAS-RELATED PROTEIN RAB-8 [H.sapiens]	1.862
50	105299	AA233511	Hs.194720	ATP-binding cassette; sub-family G (WHITE); member 2	1.861
	103560	Z20656	Hs.182787	myosin; heavy polypept 6; cardiac muscle; alpha (cardiomyopathy; hypertrophic 1)	1.861
	113073	T33637	Hs.6841	ESTs	1.86
	120407	AA235040	Hs.107283	ESTs	1.859
	103892	AA243523	Hs.17155	ESTs	1.858
55	123795	AA620381	Hs.70488	ESTs	1.857
	108524	AA084323	Hs.68138	ESTs	1.857
	113953	W85812	Hs.187554	ESTs	1.856
	110721	H97678	Hs.31319	ESTs	1.856
	129426	AA412087	Hs.168272	EST; Highly smlr to prot inhibitor of activated STAT prot PIASx-alpha [H.sapiens]	1.853
60	112102	R44840	Hs.21303	ESTs	1.852
	118502	N67317	Hs.50150	ESTs	1.852
	107619	AA004955	Hs.60015	ESTs	1.851
	100436	D87446	Hs.75912	KIAA0257 protein	1.85
	120652	AA287312	Hs.191648	ESTs	1.85
65	121643	AA417078	Hs.183767	ESTs	1.843
	117387	N26011	Hs.53810	ESTs	1.843
	132084	Y12394	Hs.3888	karyopherin alpha 3 (importin alpha 4)	1.843
	124449	N48593	Hs.121820	ESTs	1.841
	120263	AA173440	Hs.193919	ESTs	1.838
	127228	AA731038	Hs.3463	ribosomal protein S23	1.838

	111837	R38447	Hs.24453	ESTs	1.835
	128727	M64174	Hs.50651	Janus kinase 1 (a protein tyrosine kinase)	1.834
	114439	AA018937	Hs.128629	ESTs	1.833
	102332	U35637		Human nebulin mRNA, partial cds	1.83
5	126579	W72979	Hs.146082	ESTs	1.83
	102341	U37122	Hs.8110	adducin 3 (gamma)	1.83
	114248	Z39848	Hs.12079	ESTs	1.828
	131757	D17532	Hs.316	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 6 (RNA helicase; 54kD)	1.823
	108904	AA136521	Hs.71148	ESTs; Weakly similar to putative p150 [H.sapiens]	1.823
10	115084	AA255568	Hs.42484	Homo sapiens mRNA; cDNA DKFZp564C053 (from clone DKFZp564C053)	1.823
	131957	AA603008	Hs.183232	ESTs	1.822
	100131	D12485	Hs.11851	phosphodiesterase 1/nucleotide pyrophosphatase 1 (homologous to mouse Ly-41 antigen)	1.822
	124163	H30539	Hs.189838	ESTs	1.821
15	118204	N59859	Hs.48443	ESTs	1.821
	107727	AA016021	Hs.173091	DKFZP434K151 protein	1.82
	100357	D78156	Hs.241548	RAS p21 protein activator 2	1.82
	116295	AA489016	Hs.91216	ESTs; Highly similar to partial CDS; human putative tumor suppressor [H.sapiens]	1.82
	124833	R54112	Hs.128697	ESTs	1.817
20	122587	AA453255	Hs.6968	ESTs	1.817
	114359	Z41589	Hs.153483	ESTs; Moderately similar to H1 chloride channel [H.sapiens]	1.815
	111289	N72253	Hs.238246	ESTs	1.813
	110828	N30068	Hs.15347	ESTs	1.812
	104108	AA422123	Hs.42457	ESTs	1.811
25	130043	AA055404	Hs.193953	ESTs; Weakly similar to II ALU SUBFAMILY J WARNING ENTRY II [H.sapiens]	1.253
	115864	AA432080	Hs.81200	ESTs	1.81
	129737	AA056140	Hs.122684	ESTs	1.81
	124477	N53158	Hs.102682	ESTs	1.809
	100782	HG3740-HT4010		Basic Transcription Factor 2, 34 Kda Subunit	1.806
30	106101	AA421053	Hs.34395	ESTs	1.806
	115479	AA287588		zs52h09.s1 NCI_CGAP_GCB1 H sapiens cDNA clone IMAGE:701153	1.804
	116104	AA456635	Hs.78524	ESTs	1.804
	114173	Z39050	Hs.21963	ESTs	1.804
	132632	N59764	Hs.5398	guanine-monophosphate synthetase	1.803
35	119135	R49548	Hs.169681	death effector domain-containing	1.802
	131559	N91087	Hs.28728	ESTs; Weakly similar to F55A12.9 [C.elegans]	1.801
	125922	AA177138	Hs.161671	ESTs	1.8
	117375	N25427	Hs.108812	ESTs	1.8
	103571	Z25535	Hs.211608	nucleoporin 153kD	1.8
40	105978	AA406367	Hs.15873	ESTs	1.8
	125904	H22372	Hs.163586	ESTs	1.799
	133863	AA397915	Hs.77221	choline kinase	1.798
	105777	AA348412	Hs.23096	ESTs	1.797
	110168	H19480	Hs.174309	ESTs	1.796
45	105038	AA130273	Hs.7584	ESTs; Weakly similar to hypothetical protein; similar to [H.sapiens]	1.796
	105427	AA251330	Hs.28248	ESTs	1.795
	115278	AA279757	Hs.67466	ESTs; Weakly similar to BACN32G11.d [D.melanogaster]	1.794
	133104	L13698	Hs.65029	growth arrest-specific 1	1.794
	131170	N48874	Hs.23796	Human DNA sequence from clone 1052M9 on chromosome Xq25. Contains the	1.792
50	100136	D13540	Hs.22868	protein tyrosine phosphatase; non-receptor type 11	1.791
	127263	AA331157		EST35035 Embryo, 6 week, subtracted (total cDNA) I Homo sapiens cDNA	1.79
	114157	Z38878	Hs.24979	ESTs	1.79
	125601	AI086717	Hs.247043	KIAA0525 protein	1.788
	118472	N66818	Hs.42179	ESTs	1.787
55	112456	R63925	Hs.28484	ESTs	1.787
	130236	N69682	Hs.51857	SC35-interacting protein 1	1.786
	133297	AA600057	Hs.70266	KIAA0905 protein	1.784
	125650	R40096	Hs.176578	ESTs	1.784
	132056	T89386	Hs.38176	KIAA0606 protein; SCN Circadian Oscillatory Protein (SCOP)	1.783
60	129093	AA262710	Hs.108614	KIAA0627 protein	1.783
	123178	AA489020	Hs.193424	ESTs	1.782
	106340	AA441782	Hs.22857	chord domain-containing protein 1	1.781
	100598	HG2463-HT2559		Guanine Nucleotide-Binding Protein G25k	1.779
	104038	AA374532		EST86676 HSC172 cells I Homo sapiens cDNA 5' end, mRNA sequence	1.778
65	122235	AA438475	Hs.190104	ESTs	1.777
	105104	AA151771	Hs.76941	ATPase; Na+/K+ transporting; beta 3 polypeptide	1.776
	107601	AA004638	Hs.50223	ESTs	1.776
	131467	W68255	Hs.27184	DKFZP434K171 protein	1.776
	118449	N66413	Hs.172466	ESTs; Weakly similar to KIAA0775 protein [H.sapiens]	1.776

	107969	AA034030	Hs.155212	methylmalonyl Coenzyme A mutase	1.775
	115527	AA342079	Hs.252055	ESTs	1.775
	132471	T16305	Hs.49349	beta-site APP-cleaving enzyme	1.775
5	105968	AA406105	Hs.5344	adaptor-related protein complex 1; gamma 1 subunit	1.774
	127548	AA373091	Hs.83832	Homo sapiens clone 24483 unknown mRNA; partial cds	1.774
	106217	AA428379	Hs.24870	ESTs	1.773
	131214	N28777	Hs.172635	ESTs	1.773
	106295	AA435664	Hs.8583	similar to APOBEC1	1.773
10	106328	AA436705	Hs.28020	KIAA0766 gene product	1.772
	124661	N93797	Hs.3090	EphB1	1.772
	122988	AA479166	Hs.105633	ESTs	1.772
	115504	AA291946	Hs.42736	ESTs	1.771
	105168	AA180208	Hs.16606	ESTs; Highly similar to CGI-32 protein [H.sapiens]	1.767
15	129153	AA188618	Hs.181461	ariadne; Drosophila; homolog of	1.766
	105829	AA398290	Hs.21965	ESTs	1.764
	101811	M88917	Hs.24734	oxysterol binding protein	1.764
	100138	D13628	Hs.2463	angiotensin 1	1.764
	124704	R07335		ye98c1.s1 Soares fetal liver spleen 1N1LS Homo sapiens cDNA clone	1.763
20	122314	AA442257	Hs.192076	ESTs	1.762
	109865	H02566	Hs.191268	Homo sapiens mRNA; cDNA DKFZp434N174 (from clone DKFZp434N174)	1.761
	106206	AA428069	Hs.89519	KIAA1046 protein	1.758
	107135	AA620782	Hs.23247	ESTs	1.757
	105760	AA336960	Hs.28170	ESTs	1.756
25	106288	AA435538	Hs.24338	ESTs	1.756
	103968	AA304566	Hs.3542	ESTs	1.756
	129559	AA234945	Hs.11360	ESTs	1.756
	117885	N50112	Hs.47023	ESTs	1.754
	107032	AA599472	Hs.247309	succinate-CoA ligase; GDP-forming; beta subunit	1.754
30	124807	R45963	Hs.233811	ESTs; Weakly similar to ORF2 [M.musculus]	1.753
	100276	D42047	Hs.82432	KIAA0089 protein	1.753
	110924	N47938		yy84a09.s1 Soares multiple sclerosis 2NbHMSP Homo sapiens cDNA clone	1.751
	133002	AF006082	Hs.62461	ARP2 (actin-related protein 2; yeast) homolog	1.751
	132530	AA455917	Hs.50785	SEC22; vesicle trafficking protein (S. cerevisiae)-like 1	1.75
35	110759	N21671	Hs.19025	ESTs	1.75
	106138	AA424515	Hs.33264	ESTs	1.75
	107348	U43701	Hs.184776	ribosomal protein L23a	1.75
	115867	AA432162	Hs.165988	DKFZP586B2022 protein	1.749
	135398	AA194075	Hs.99908	nuclear receptor coactivator 4	1.747
40	113783	W19222	Hs.7041	ESTs; Weakly similar to II ALU SUBFAMILY SQ WARNING ENTRY II [H.sapiens]	1.747
	134898	X98330	Hs.90821	ryanodine receptor 2 (cardiac)	1.745
	132215	T10132	Hs.4236	KIAA0478 gene product	1.744
	104229	AB002346	Hs.61289	synaptotagmin 2	1.743
	116166	AA461558	Hs.202949	KIAA1102 protein	1.743
45	115433	AA284252	Hs.58372	ESTs	1.743
	114908	AA236545	Hs.54973	ESTs	1.742
	127425	AA470941	Hs.143162	ESTs	1.741
	131089	Z38807	Hs.22870	ESTs	1.739
	113498	T88908	Hs.189746	ESTs	1.738
50	116710	F10577	Hs.70312	ESTs	1.735
	127210	R51478		yg76f04.r1 Soares infant brain 1N1B Homo sapiens cDNA clone	1.733
	120554	AA279654	Hs.194524	ESTs	1.733
	129940	U18242	Hs.13572	calcium modulating ligand	1.732
	117023	H88157	Hs.41105	ESTs	1.731
55	111700	R22212	Hs.23361	ESTs	1.731
	116911	H72240	Hs.39292	ESTs; Moderately similar to KIAA0745 protein [H.sapiens]	1.731
	106025	AA412063	Hs.6065	ESTs	1.728
	106628	AA101984	Hs.61697	G-protein coupled receptor	1.726
	111614	R12581	Hs.181146	ESTs	1.726
60	134134	L76703	Hs.173328	protein phosphatase 2; regulatory subunit B (B56); epsilon isoform	1.725
	106886	AA489086	Hs.36545	ESTs	1.725
	117998	N52136	Hs.93828	ESTs	1.725
	121204	AA400422	Hs.55896	ESTs	1.725
	121342	AA404995	Hs.192480	ESTs	1.725
65	131129	R27296	Hs.23240	ESTs	1.725
	116235	AA479181	Hs.186726	ESTs	1.725
	102423	U44754	Hs.179312	small nuclear RNA activating complex; polypeptide 1; 43kD	1.724
	110273	H29050	Hs.24096	ESTs	1.722
	108758	AA127395	Hs.222414	ESTs	1.722
	110672	H88477	Hs.191178	ESTs	1.721

	120271	AA176404	Hs.111092	ESTs; Weakly similar to ZINC FINGER PROTEIN 136 [H.sapiens]	1.72
	100227	D28915	Hs.82316	Interferon-induced; hepatitis C-associated microtubular aggregate prot (44kD)	1.719
	129232	W89459	Hs.109655	sex comb on midleg (Drosophila)-like 1	1.719
5	134663	W73367	Hs.8750	ESTs	1.717
	104902	AA055475	Hs.104143	clathrin; light polypeptide (Lca)	1.717
	120582	AA281290	Hs.125287	ESTs; Weakly similar to BC331191_1 [H.sapiens]	1.717
	134891	F03517	Hs.80787	ESTs	1.716
	106219	AA428567	Hs.26613	Homo sapiens mRNA; cDNA DKFZp586F1323 (from clone DKFZp586F1323)	1.715
10	116372	AA521311	Hs.13854	ESTs	1.713
	107570	AA001870	Hs.237323	N-acetylglucosamine-phosphate mutase; DKFZP434B187 protein	1.713
	106188	AA427816	Hs.11803	ESTs	1.712
	125138	W31479	Hs.129051	ESTs	1.712
	104973	AA085676	Hs.6763	KIAA0942 protein	1.712
15	128710	J04813	Hs.104117	cytochrome P450; subfamily IIA (naphedipine oxidase); polypeptide 5	1.711
	123934	D20899	Hs.107127	Homo sapiens mRNA; cDNA DKFZp564G022 (from clone DKFZp564G022)	1.711
	127871	AA766511	Hs.128848	ESTs	1.71
	116089	AA455933	Hs.41324	ESTs	1.709
	123337	AA504153	Hs.132797	ESTs; Weakly similar to ORF YGL050w [S.cerevisiae]	1.708
	123619	AA609200	Hs.162686	ESTs	1.708
20	104781	AA026617	Hs.21610	ESTs; Highly similar to BAI1-associated protein 1 [H.sapiens]	1.707
	115114	AA258488	Hs.88148	ESTs	1.705
	117852	N49408	Hs.136102	KIAA0853 protein	1.705
	127644	T57570	Hs.77039	ribosomal protein S3A	1.704
	111359	N91273	Hs.27179	ESTs	1.702
25	131721	L36644	Hs.31092	EphA5	1.7
	132438	F08925	Hs.48810	ESTs	1.7
	132476	N67192	Hs.49476	Homo sapiens clone TUA8 Cri-du-chat region mRNA	1.7
	130890	F02488	Hs.21917	KIAA0768 protein	1.7
30	128499	AA487503	Hs.100636	ESTs	1.698
	120780	AA342337	Hs.241569	ESTs; Modfly smir to II ALU SUBFAMILY SQ WARNING ENTRY II [H.sapiens]	1.697
	132920	L06133	Hs.606	ATPase; Cu++ transporting; alpha polypeptide (Menkes syndrome)	1.696
	135037	U77948	Hs.184122	general transcription factor II; I	1.696
	110024	H11297	Hs.31050	ESTs	1.695
35	134415	AA329274	Hs.82911	protein tyrosine phosphatase type IVA; member 2	1.694
	102223	U24685	Hs.148228	Human anti-B cell autoantibody IgM heavy chain variable V-D-J region (VH4) gene; clone E11; VH4-63 non-productive rearrangement	1.694
	126712	AA205862	Hs.7942	ESTs	1.694
	101507	M27492	Hs.82112	Interleukin 1 receptor; type I	1.692
40	106291	AA435551	Hs.30824	ESTs	1.691
	116826	H58691	Hs.8215	ESTs; Weakly similar to double-stranded RNA-binding nuclear protein DRBP76 [H.sapiens]	1.69
	135339	D59269	Hs.127842	Homo sapiens mRNA full length insert cDNA clone EUROIMAGE 763848	1.69
	118250	N62602		yz75b6.s1 Soares_multiple_sclerosis_2NbHMSP Homo sapiens cDNA clone IMAGE:288851 3' similar to contains Alu repetitive element; mRNA sequence	1.689
45	106470	AA450116	Hs.188180	ESTs	1.688
	108203	AA057678	Hs.63408	ESTs	1.687
	119748	W70313	Hs.126906	ESTs	1.686
	116576	D51228	Hs.79404	neuron-specific protein	1.683
50	123035	AA481392	Hs.105166	ESTs	1.683
	126668	AA011616	Hs.184086	ESTs	1.681
	101512	M28209	Hs.250716	RAB1; member RAS oncogene family	1.678
	102704	U76638	Hs.54089	BRCA1 associated RING domain 1	1.677
	126218	AA256386	Hs.13649	Novel human gene mapping to chromosome 13; similar to rat RhoGAP	1.676
55	111180	N67277	Hs.9403	ESTs	1.676
	105937	AA404342	Hs.173531	ESTs	1.675
	114118	Z38520	Hs.175930	ESTs	1.675
	109203	AA190834	Hs.108787	endoplasmic reticulum membrane protein	1.675
	125245	W86608	Hs.7243	ubiquitin specific protease 24	1.675
60	102906	X06958	Hs.75318	tubulin; alpha 1 (testis specific)	1.675
	125914	AA262925	Hs.180034	cleavage stimulation factor; 3' pre-RNA; subunit 3; 77kD	1.674
	134294	U63289	Hs.81248	CUG triplet repeat; RNA-binding protein 1	1.674
	109742	F10108	Hs.183333	ESTs	1.673
	134674	D63878	Hs.87726	KIAA0154 protein	1.673
65	104079	AA402937	Hs.103238	ESTs	1.671
	107554	AA001388	Hs.59844	ESTs	1.671
	132439	AA243139	Hs.4863	Homo sapiens clone 25088 mRNA sequence	1.669
	124515	N58172	Hs.109370	ESTs	1.668
	124300	H92575	Hs.105959	ESTs; Weakly similar to II ALU SUBFAMILY SQ WARNING ENTRY II [H.sapiens]	1.668
	126809	AA743476	Hs.171693	ESTs	1.667

	106095	AA419547	Hs.11713	ESTs	1.664
	101754	M77142	Hs.239489	TIA1 cytotoxic granule-associated RNA-binding protein	1.663
	105188	AA192306	Hs.23926	ESTs	1.663
	113582	T91371	Hs.16824	EST	1.661
5	119559	W38197		Accession not listed in Genbank	1.661
	119961	W87535	Hs.59015	ring finger protein 9	1.657
	123255	AA490890	Hs.105273	ESTs	1.657
	111078	N59230	Hs.186574	ESTs	1.655
10	113082	T40528	Hs.8246	ESTs	1.654
	119589	W44692	Hs.124177	ESTs	1.652
	104308	D53639	Hs.77904	ribosomal protein S26	1.65
	103073	X59417	Hs.74077	proteasome (prosome; macropain) subunit; alpha type; 6	1.65
	124424	N35314	Hs.107265	ESTs	1.65
15	128890	AA096157	Hs.182364	ESTs; Weakly similar to 25 kDa trypsin inhibitor [H.sapiens]	1.65
	119400	T92767		ye27d06.s1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:118955 3', mRNA sequence.	1.65
	131631	AA486868	Hs.29802	slit (Drosophila) homolog 2	1.65
	118229	N62339	Hs.180532	heat shock 90kD protein 1; alpha	1.649
20	118533	N67954	Hs.49413	ESTs	1.648
	130666	AA476307	Hs.194035	KIAA0737 gene product	1.647
	103093	X60708	Hs.44926	dipeptidylpeptidase IV (CD26; adenosine deaminase complexing protein 2)	1.647
	128667	U69140	Hs.103419	fasciculation and elongation protein zeta 2 (zyglin II)	1.646
	112933	T15530	Hs.221439	ESTs	1.646
25	114546	AA056263	Hs.132747	ESTs	1.645
	126705	AA579377	Hs.180532	heat shock 90kD protein 1; alpha	1.644
	114399	AA007595	Hs.220937	ESTs	1.642
	118836	N79820	Hs.50854	ESTs	1.64
	100401	D85423		Homo sapiens mRNA for Cdc5, partial cds	1.64
30	105681	AA284865	Hs.171228	KIAA1040 protein	1.639
	132526	AA460128	Hs.5074	similar to S. pombe dim1+	1.639
	133809	AA034002	Hs.76359	catalase	1.639
	115968	AA447083	Hs.134522	ESTs	1.637
	116370	AA521258	Hs.236204	ESTs; Moderately similar to NUCLEAR PORE COMPLEX PROTEIN NUP107 [R.norvegicus]	1.631
35	109644	F04477	Hs.204802	ESTs; Moderately similar to GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE; LIVER [H.sapiens]	1.627
	103427	X97303		H.sapiens mRNA for Ptg-12 protein	1.627
	132186	T33888	Hs.221040	KIAA1038 protein	1.626
40	131428	U17838	Hs.26719	PR domain containing 2; with ZNF domain	1.626
	126838	AA649257	Hs.188602	ESTs	1.625
	114503	AA039568	Hs.188083	ESTs	1.625
	121242	AA400857	Hs.97509	EST	1.625
	122414	AA446885	Hs.99087	ESTs; Moderately similar to ZINC FINGER PROTEIN 141 [H.sapiens]	1.625
45	110632	H72344	Hs.171635	ESTs	1.624
	111389	N95837	Hs.169111	ESTs; Weakly similar to L82A [D.melanogaster]	1.624
	112449	R63802	Hs.124186	ring finger protein 2	1.623
	113070	T33464	Hs.6298	ESTs	1.622
	107229	D59284	Hs.34644	ESTs	1.618
50	132710	W93726	Hs.55279	protease inhibitor 5 (maspin)	1.617
	124664	N94814	Hs.33540	ESTs; Weakly similar to KIAA0765 protein [H.sapiens]	1.617
	130168	AA350690	Hs.151411	KIAA0916 protein	1.616
	125040	T78451	Hs.189961	ESTs	1.615
	132972	H39627	Hs.164967	ESTs; Weakly similar to II ALU SUBFAMILY SB WARNING ENTRY II [H.sapiens]	1.615
55	115873	AA433916	Hs.90093	heat shock 70kD protein 4	1.611
	120408	AA235045	Hs.190151	ESTs	1.61
	120934	AA383773	Hs.191500	ESTs	1.61
	115259	AA279071	Hs.13453	splicing factor 3b; subunit 1; 155kD	1.609
60	134330	D20113	Hs.8185	ESTs; Highly similar to CGI-44 protein [H.sapiens]	1.607
	115117	AA256492	Hs.49007	poly(A) polymerase	1.606
	125162	W44682	Hs.109896	ESTs	1.605
	103946	AA285246	Hs.111650	ESTs; Weakly similar to Prt1 homolog [H.sapiens]	1.604
	133389	AA166917	Hs.72639	ESTs	1.603
	115528	AA342301	Hs.53929	ESTs; Weakly similar to II ALU CLASS B WARNING ENTRY II [H.sapiens]	1.602
65	129704	W81301	Hs.12064	ubiquitin specific protease 22	1.602
	109313	AA206800	Hs.86276	ESTs; Moderately similar to zinc finger protein dp [H.sapiens]	1.601
	130457	U58091	Hs.155976	cullin 4B	1.6
	123076	AA485211	Hs.190046	ESTs	1.6
	115113	AA256480	Hs.44810	ESTs	1.6
	117731	N48433	Hs.46609	ESTs	1.6

5	123344	AA504338	Hs.171857	ESTs	1.599
	131798	X86098	Hs.3238	adenovirus 5 E1A binding protein	1.597
	125370	AA256743	Hs.151791	KIAA0092 gene product	1.596
	114918	AA236813	Hs.72324	ESTs; Highly similar to unknown [H.sapiens]	1.596
	114807	AA160805	Hs.189832	ESTs	1.596
10	105103	AA151593	Hs.10130	ESTs	1.594
	125004	T60120		yb68f02.s1 Stratagene ovary (#937217) Homo sapiens cDNA clone IMAGE:76347 3', mRNA sequence.	1.592
	105658	AA282914	Hs.10176	ESTs	1.589
	110455	H52172		yt85e8.s1 Soares_pineal_gland_N3HPG Homo sapiens cDNA clone IMAGE:23111 3' similar to contains Alu repetitive element; mRNA sequence	1.589
	119780	W72967	Hs.181381	ESTs; Weakly similar to hypothetical protein [H.sapiens]	1.587
15	126983	AA211537		zn55d01.r1 Stratagene muscle 937209 Homo sapiens cDNA clone IMAGE:562081 5', mRNA sequence.	1.588
	134675	AA250745	Hs.87773	protein kinase; cAMP-dependent; catalytic; beta	1.584
	105431	AA252033	Hs.15036	ESTs; Weakly similar to II ALU SUBFAMILY J WARNING ENTRY II [H.sapiens]	1.584
	120187	Z40251	Hs.56974	ESTs	1.584
	115830	AA428137	Hs.86434	ESTs	1.581
20	135069	AA456311	Hs.93961	ESTs; Weakly similar to II ALU CLASS A WARNING ENTRY II [H.sapiens]	1.581
	122897	AA479285	Hs.106290	Kelch motif containing protein	1.581
	119707	W67569	Hs.44143	ESTs; Weakly similar to SNF2alpha protein [H.sapiens]	1.58
	131934	D80948	Hs.34922	ESTs	1.58
	106141	AA424558	Hs.9302	phosphatidylcholine	1.58
25	115271	AA279422	Hs.5724	ESTs	1.579
	131468	R27598	Hs.27197	KIAA0787 protein	1.577
	131165	R98173	Hs.23763	Max-interacting protein	1.575
	117273	N21680	Hs.43047	ESTs	1.575
	101569	M33772	Hs.182421	troponin C2; fast	1.575
30	116127	AA459703	Hs.78070	v-myc avian myelocytomatosis viral oncogene homolog	1.575
	120022	W90625	Hs.58432	ESTs	1.575
	117512	N32157	Hs.82207	ESTs	1.574
	106511	AA452865	Hs.206713	UDP-Gal4betaGlcNAc beta 1,4- galactosyltransferase; polypeptide 2	1.573
	116415	AA609204	Hs.27973	KIAA0874 protein	1.573
35	127879	AA810215	Hs.189079	ESTs	1.571
	125211	W72798	Hs.103177	ESTs; Wkly smlr to cDNA EST EMBL:D32579 comes from this gene [C.elegans]	1.571
	114748	AA135638	Hs.223756	ESTs	1.571
	122698	AA456112	Hs.99410	ESTs	1.57
	116765	H12636	Hs.121585	ESTs; Weakly similar to reverse transcriptase [H.sapiens]	1.568
40	130895	AA609828	Hs.21015	ESTs; Highly similar to tetracycline transporter-like protein [M.musculus]	1.568
	114338	Z41368	Hs.40109	KIAA0872 protein	1.567
	111005	N53078	Hs.5998	ESTs	1.567
	128135	AA913491	Hs.189143	ESTs; Modrtly smlr to II ALU SUBFAMILY J WARNING ENTRY II [H.sapiens]	1.567
	112048	R43365	Hs.22273	ESTs	1.566
45	132160	AA281770	Hs.184081	seven in absentia (Drosophila) homolog 1	1.566
	111568	R10153	Hs.20561	ESTs	1.566
	127775	H04106	Hs.179902	ESTs; Weakly similar to NG22 [H.sapiens]	1.566
	115359	AA281936	Hs.88914	ESTs	1.566
	121845	AA425734	Hs.165066	ESTs; Weakly similar to hypothetical protein [H.sapiens]	1.565
50	127854	AA769520		ESTs; Weakly similar to REGULATOR OF MITOTIC SPINDLE ASSEMBLY 1 [H.sapiens]	1.564
	120287	AA187679	Hs.111114	ESTs	1.563
	114940	AA243012	Hs.75928	ESTs	1.562
	126716	AA031700	Hs.251962	ESTs	1.562
	134161	U97188	Hs.79440	IGF-II mRNA-binding protein 3	1.561
55	125390	H95094	Hs.75187	translocase of outer mitochondrial membrane 20 (yeast) homolog	1.561
	115334	AA281244	Hs.65300	ESTs	1.559
	113721	T97831	Hs.18180	EST	1.558
	114895	AA238177	Hs.76591	KIAA0887 protein	1.558
	119341	T62571	Hs.146388	microtubule-associated protein 7	1.558
60	108012	AA039616	Hs.61933	ESTs	1.558
	130335	AA158499	Hs.8454	protein kinase; cAMP-dependent; regulatory; type II; alpha	1.557
	134351	R82074	Hs.82109	syndecan 1	1.557
	133300	D51401	Hs.70333	ESTs	1.553
	106920	AA490899	Hs.24462	ESTs	1.553
65	118744	N74075	Hs.94293	EST	1.552
	128489	W20016	Hs.144228	ESTs; Weakly similar to ZINC FINGER PROTEIN 83 [H.sapiens]	1.55
	115913	AA436720	Hs.65487	ESTs	1.55
	107868	AA025234	Hs.61260	ESTs	1.55
	134520	N21407	Hs.257325	ESTs	1.55

	109703	F09684	Hs.24782	ESTs; Weakly similar to ORF YOR283w [S.cerevisiae]	1.55
	120288	AA187938	Hs.55189	ESTs; Weakly similar to F25B5.3 [C.elegans]	1.548
	106356	AA443277	Hs.31034	peroxisomal biogenesis factor 11A	1.548
5	129460	AA235627	Hs.11171	APG5 (autophagy 5; S. cerevisiae)-like	1.547
	133950	D11861	Hs.77823	ESTs	1.546
	128172	AJ400862	Hs.142607	ESTs	1.546
	114162	Z38909	Hs.22265	ESTs	1.545
	101803	M86546	Hs.155691	pre-B-cell leukemia transcription factor 1	1.544
10	113817	T93630	Hs.17207	ESTs	1.542
	104896	AA054228	Hs.23165	ESTs	1.541
	114477	AA032013	Hs.144260	EST	1.54
	110731	H98653	Hs.188006	KIAA0878 protein	1.54
	130367	Z38501	Hs.8768	ESTs; Wkly smlr to II ALU SUBFAMILY SQ WARNING ENTRY II [H.sapiens]	1.538
15	130539	L07044	Hs.250857	Homo sapiens calcium/calmodulin-dependent protein kinase II mRNA; partial cds	1.538
	134921	W60186	Hs.169487	Kreisler (mouse) maf-related leucine zipper homolog	1.537
	130583	W24957	Hs.16281	ESTs; Moderately similar to similar to C.elegans protein encoded in cosmid T20D3 [H.sapiens]	1.537
	133723	AA088851	Hs.75744	S-adenosylmethionine decarboxylase 1	1.537
20	106450	AA449469	Hs.11859	ESTs	1.536
	104120	AA429838	Hs.89519	KIAA1046 protein	1.536
	100533	HG1879-HT1919		Ras-Like Protein Tc10	1.535
	130664	R09049	Hs.17625	ESTs	1.535
	127122	AA279153	Hs.190049	ESTs	1.535
25	134264	T03391	Hs.8087	ESTs	1.535
	132319	AA418682	Hs.44625	ESTs	1.535
	115465	AA286941	Hs.43891	ESTs	1.533
	125003	T59442	Hs.100445	ESTs	1.532
	102273	U30888	Hs.75981	ubiquitin specific protease 14 (tRNA-guanine transglycosylase)	1.532
30	121875	AA426299	Hs.98510	ESTs	1.532
	114366	Z41747	Hs.469	succinate dehydrogenase complex; subunit A; flavoprotein (Fp)	1.531
	132944	AA054515	Hs.6127	ESTs; Weakly similar to prostate-specific transglutaminase [H.sapiens]	1.53
	111199	N68210	Hs.29822	ESTs	1.53
	113494	T88878	Hs.258738	ESTs	1.529
35	129515	AA490882	Hs.112227	ESTs	1.528
	133124	AA158049	Hs.65490	ESTs	1.528
	104785	AA027163	Hs.7942	ESTs	1.526
	105595	AA279408	Hs.25866	ESTs	1.526
	130198	U67156	Hs.151988	mitogen-activated protein kinase kinase kinase 5	1.526
40	114297	Z40758	Hs.173091	DKFZP434K151 protein	1.525
	112876	T03488	Hs.4842	ESTs	1.525
	127500	AA525014	Hs.162115	ESTs	1.525
	120519	AA258585	Hs.129887	cadherin 19 (NOTE: redefinition of symbol)	1.525
	119859	W80702	Hs.58481	ESTs	1.525
45	129944	L00389	Hs.1361	cytochrome P450; subfamily I (aromatic compound-inducible); polypeptide 2	1.524
	118864	N89670	Hs.42148	ESTs; Weakly similar to Su(P) [D.melanogaster]	1.523
	123984	C13961	Hs.210115	EST	1.523
	111676	R19414	Hs.166459	ESTs	1.522
	128332	AI079523	Hs.134173	ESTs	1.522
50	130455	X17059	Hs.155956	N-acetyltransferase 1 (arylamine N-acetyltransferase)	1.521
	125181	W58461	Hs.12396	ESTs	1.521
	127093	AA768241		oa72d02.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1317795 3', mRNA sequence.	1.521
	132156	AA157401	Hs.4113	S-adenosylhomocysteine hydrolase-like 1	1.521
55	125303	Z39821	Hs.107295	ESTs	1.52
	132697	AA281951	Hs.5518	Homo sapiens mRNA; cDNA DKFZp566J2146 (from clone DKFZp566J2146)	1.52
	117086	H93135	Hs.41840	ESTs	1.519
	113355	T79203	Hs.14480	ESTs	1.518
	108621	AA101811	Hs.69506	ESTs	1.518
60	109384	AA219172	Hs.88849	EST	1.518
	128510	X94703	Hs.100816	RAB28; member RAS oncogene family	1.517
	132868	N77151	Hs.61638	myosin X	1.515
	117035	H88798	Hs.41182	ESTs	1.515
	116781	H22985	Hs.52132	ESTs	1.513
65	108677	AA115629	Hs.118531	ESTs	1.513
	130214	H78003	Hs.15288	ESTs	1.513
	134700	AA481414	Hs.8888	golgi SNAP receptor complex member 1	1.512
	116818	D80783	Hs.45224	ESTs	1.508
	126257	N99638		tumor necrosis factor receptor superfamily; member 10b	1.508
	125859	AA806808	Hs.118797	ubiquitin-conjugating enzyme E2D 3 (homologous to yeast UBC4/5)	1.508

	113837	W57698	Hs.8888	ESTs	1.507
	114317	Z41038	Hs.469	succinate dehydrogenase complex; subunit A; flavoprotein (Fp)	1.507
	100311	D50640	Hs.184653	phosphodiesterase 3B; cGMP-inhibited	1.507
	126802	AA947601	Hs.97056	ESTs	1.508
5	128681	R82837	Hs.103329	KIAA0970 protein	1.506
	134194	AA233231	Hs.79828	ESTs	1.508
	108953	AA149652	Hs.42128	ESTs	1.504
	133240	D31161	Hs.68613	ESTs	1.502
	132671	X76302	Hs.54849	putative nucleic acid binding protein RY-1	1.501
10	132609	Z48923	Hs.53250	bone morphogenetic protein receptor, type II (serine/threonine kinase)	1.501
	105574	AA278678	Hs.258567	ESTs	1.5
	113718	T97782	Hs.256268	ESTs	1.5
	127824	AI208365	Hs.127811	ESTs	1.5
	130132	U55938	Hs.184376	synaposomal-associated protein; 23kD	1.5
15	127394	AA453224		ESTs; Weakly similar to II ALU SUBFAMILY J WARNING ENTRY II [H.sapiens]	1.5
	100485	HG11111-HT1111		Ras-Like Protein Tc21	1.5
	101078	L04510	Hs.782	ADP-ribosylation factor domain protein 1; 64kD	1.5
	128611	AA456845	Hs.102471	KIAA0680 gene product	1.5

TABLE 12A shows the accession numbers for those primekeys lacking unigeneID's for Table 12. For each probeset we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

10	Pkey: CAT number: Accession:	Unique Eos probeset identifier number Gene cluster number Genbank accession numbers	
15	Pkey	CAT number	Accession
20	108536 117040 100782	119811_1 46956_1 18457_1	AA084524 AA339253 AW986289 AW970600 AA503323 H89218 AF086031 H89112 AA355435 NM_001516 Z30093 T28405 AW949486 AA461142 AA410532 AI652073 AA521208 AI970141 AI968234 AI026102 AA713583 AW135876 AA936614 AA770300 AI242635 AA377033 AW960263 AW607683 AI273803 AA410287 AI040513 AA460838 AI803916 AW294095 AW448680 AW798677 AW675048 BE542116 AL120521 L34840 NM_003241 U31905 AI546931 AJ791616 AI973065 AI792321 AI546937 AI685880 AI732835 AI682360 AA420653 AA564047 AI682323 AI824614 AI659889 AI680052 AI970887 AI623108 AA420692 AI418074 AA631018 AI810595 AW291463 AW449930 AI668908 AI970818
25	100819 100824	3022_1 5_38	AI393237 AI521317 AI761348 AF025841 D43968 AW994987 L34598 AF025841 D89789 D89788 D89780 AW998932 AI971742 AI310238 X90976 AW139668 AW674280 AI385552 AA877452 AV657554 C75229 AA376077 AI798056 AW609213 W25586 H30149 BE075089 BE075190 AW580858 H99598 AA425238 AA133916 AW363478 BE158121 BE158127 AW467960 BE158135 BE158126 BE158145 N92860 AA847246 AI981688 AI381423 AA878154 AA043767 AI863712 AI559226 AW339007 AI371266 AI368901 AA046824 AA134739 AW449154 AA130232 AI458720 AA962511 AI700627 R70437 AW004008 AA045228 AI671572 H99599 AA043768 AI685454 AI871685 N29937 X90977 AA524240 AI142114 AI825750 AI587805 AI631385 AI347893 AA134740 F20669 AA046707 AW793216 AW983298 AW959380 AA363265 AI784593 AI268201 R69451 AV657618 AI695588 BE312163 AI230798 AA374482 AI926059 AA822653 AI860704 BE139185 AW296884 T60238 T60120 U33921 AI190489 AA573311
30	125004 102313 102337	264197_1 27608_1 553_1	AI814663 AA806761 AA765241 AA019317 AA092255 AA035405 T85079 AA890151 AI373959 T85080 BE153728 AA740848 BE080582 AL048137 AW182316 AI699488 AW274481 AW407538 AA306562 AW950024 AW949943 AL045703 AW843199 W25132 BE612794 AA304266 AW958054 H25673 AV646563 AV646573 BE172890 AW593488 AA385181 AA164998 AI246476 AA345406 AI277554 AA134749 AA856624 BE613247 AA299003 AL048138 AA028121 T92510 AI923835 AW020440 AI401594 AI889401 N93290 AA044247 AA028100 AI582845 AA811151 AI741811 AI925878 AA448277 AA172221 AI214783 BE220783 AA022746 AI082882 AA022849 AI928385 AA573472 AI420686 AW072902 AI799493 AI873506 AI468977 AI192079 AI468976 AA044272 AW015701 AW316979 AA933042 AA609017 AI318393 AI424571 AI934945 AA172023 AW050917 AA848180 AA134748 AI003947 AI766769 AW008697 AA653517 AW575680 AI474214 AA401478 U36922 AA927064 AA868000 D62654 T91745 AW500202 AA194764 AA746346 AA130464 AW117498 AA054526 N26432 H02534 H04964 AW303367 BE300931 AI218049 AI208073 AW182749 AA983630 AI147585 AA194765 AA054534 AA922720 AI438585 AI348535 AA134289 AA280923 AA897422 AA019559 AW274010 AA035406 AA917879 H99327 W32908 AI216048 AW496823 AA018414 H82288 W35284 AI936621 AI767113 AA866177 AW367874 H82398 AF032685 AW300151 AW467069 AA809346 AI188507 AI494178 AA872752 AI631631 U02310 NM_002015 AA815006 AI382453 AW197658 AI761654 AI804396 AI382221 AI813840 AI439635 AI523901 AW517242 AI221705 AW298104 AW204560 AW573095 AW028783 AW014650 AI766744 AI808294 AI698758 AI041809 AI766667 AI479103 AA872797 AA769305 AA765080 AA334166 AI472322
35	124704 116988 124825 110455 126257 125624 104038 103427	282319_1 185904_1 330773_1 46874_1 182217_1 154135_1 264235_1 43892_1	R07335 R07640 AW953679 AW953680 AA244436 H82527 AA381046 AA244483 H82526 AA501669 R52088 H52576 AF085971 H52172 N99638 AW973750 AA328271 H80994 AA558020 AA234435 N59599 R94815 AW968383 AA465492 R34539 AA165411 AA374532 AA421255 BE514383 AA071273 AW247987 AW673286 BE312102 AW749824 BE071985 AW577383 BE071945 BE072005 AW577355 BE071965 AW239231 BE072000 BE071960 AW577360 AW749830 AW373020 X97303 AW999522 BE000182 BE562219 BE266555 BE264970 AA074713 AA447006 AW977549 AA256038 AL365415 AW500455 AA768241 AW968097 Z17849 AA256104
40			
45			
50			
55			
60			

125873	10492_1	AW271838 AL133605 C01646 H29959 AA999896 D60676 AW999454 AW961178 AA315244 H14437 AW386118 N46512 AW272021 A1768516 BE466421 A1082809 A1804454 AA905101 AW173368 N38942 AW614169 A1080483 N29489 A1500550 AA994475 AA614464 AA707368 AA593145 AA569473 AW627815 A1828244 N63228 N42300
5	125954	4457_1 NM_016353 AB023584 W44753 R09585 AA382865 R23772 A1814257 AA974046 AK001608 A1935838 AW440609 A1420022 AA777388 AA806969 A1554876 A1584006 A1688556 A1688634 A1687897 A1014540 A1806683 A1741202 AW263154 AW297238 A1149951 A1589078 AW082158 AW614265 AA931887 AA781969 R09490 AA484543 A1207121 A1088390 A1538065 A1619547 A1741925 A1702846 H40846 R93943 AW747979 AA461348 U30163 AA326023 A1535992 AW242870 A1244025 A1222558 W38425 AW473630 A1624599 A1821226 A1683152 A1086458 A1123822 AW170802 C16447 A1337674 D25726 AW339368 AW771259 AA461174 H48372 W01626 AA305278 AA223833 110924 6443_1 AW058463 AF195768 AA680145 T86901 W60373 W60281 NM_007222 AF106862 A1000795 AA167188 AW884503 AW891313 AW891332 AW891312 A1984924 A1123518 N75170 AA131614 H25330 A1913358 A1742277 W25576 R58771 AW445159 AW888628 AW888627 AW274674 A1088482 N52314 N34282 AW001769 A1338943 T66784 A288983 AW468676 AW237528 H25289 N71690 AA610128 A1143458 A1082599 N49144 AA854773 AW663411 AW610151 N47938 AW601626 AA167189 AA918304 AA805205 BE069496 AA652836 BE069499 A1699298 AW249528 AW888578 BE567635 T10728 AW604715 D54245 D53062 D55610 D55555 AA301376 A1133498 N77788 A1936320 AW090734 A1269877 N50828 AA550814 A1421893 A1005384 N50813 D60282 D59349 AA131710 D81698 D81699 AA331156 AA331157 AA331155 U76456 NM_003256 AF057532 AA183414 AW293304 AW963378 AA313095 A1359841 A1968312 A1080163 AW448928 A1671136 BE466399 A1637867 A1671873 AW196583 AW071635 A1634427 AW298872 AW292470 AA193650 BE161832 AA453224 AA485772 D90391 M55575 A1652268 AA719776 AA524888 AW971347 AA211537 AW971327 AA524988 AW628653 AA251787 AW976796 AA769520 AA432071 AA405648 AW000908 T16347 AB028957 AL120001 A1267678 H10928 R19844 AW970334 AA393182 F05472 F11711 H09908 N50250 A1815411 BE463679 D61468 AW970253 D60889 C15548 D61011 D60867 A1815795 AA534831 D81386 AW235039 A1382158 D81174 AA416899 AA852310 H09789 H10929 H09813 F09369 R44721 D51515 Z38458 R14004 T68255 F12148 F12139 AW351702 M85350 A1018713 AW972450 AW972645 AA514964 T66172 F09785 F09776 AA436608 T05327 T07118 AA339352 AW301608 N46706 AA849093 AA287595 AW811753 AA287596 N39260 NM_001874 J04970 T91426 AW205201 T84979 AA255727 AA847837 R02164 T91339 AV651884 AV651835 AV651350 AV650118 AV651338 A1272002 A1367796 AA830651 AA262112 AW151188 A1076696 AA219720 AL135197 AA305877 N56376 AA318063 AA130725 AW954903 BE541230 AW383312 U86753 D85423 A1679458 A1122932 AB007892 A1583918 BE160134 F08104 R34903 F13440 AA095444 AA262453 AA191036 R17895 T81268 BE149776 A1279537 A1143113 AA361072 AW959030 AW268817 AA811533 BE275179 A1221677 T65147 R49293 AA249176 BE000290 AA768053 F09494 BE092845 BE172099 Z41177 AA044750 A1909768 BE140795 BE140574 AW845210 R1752452 BE243244 AA843664 A1300080 BE169032 AW189979 BE004869 AA621872 A1951772 A1678897 A1926598 N62813 A1350912 AW608791 A1309602 A1983138 AW875592 A1655073 AW875626 AA130606 A1370827 C75528 C75554 AW263335 A1344426 BE004788 AA576220 AA604824 A1431405 AA749378 R38882 AW955075 AA173821 C75657 AA219672 AW768408 R43141 A1431414 AA483343 A1673792 T17294 AW770187 N74285 AA76404 A1088288 AA654152 AW974864 BE817311 BE243328 BE168049 U64676 AW167507 AW167508 BE218568 AA779360 W85722 AL044843 BE159404 AF012088 AW898611 AW898610 BE159405 BE092191 AW890826 AW369841 AW368064 AW606702 AL044731 R82691 AA419346 AA416558 H96045 AL040450 A1640531 A1808434 AL048613 AW855784 AW362489 AL048881 AL049015 AA094272 AA888908 AA417294 AW237786 R59793 AL044916 D82402 A1216854 A1079342 H96406 AL037845 A1915900 AA972133 A1478783 T31074 Z21135 Z21396 AA352182 R13918 AA430178 C17811 A1371824 A1742256 AA826801 N79156 AA350610 AA081971 N83639 R35544 AA312292 AW952080 N42322 AA171957 AA565297 R89207 AA504106 A1630782 AA826482 A1301579 T36241 AW966618 Z28426 AL043480 A1124636 AA393449 T19504 AW887823 A1289814 N53979 AL043571 A1632764 A1859613 A1986308 A1683212 A1984499 A1133258 C05898 AW512761 A1041280 BE466240 Z19161 A1351190 N67549 A1373374 AA400873 AW440914 AW514879 AA770146 A1358754 R51113 A1283773 AA649888 T30543 D54358 R37750 T03358 T15451 T15880 AA999689 N67396 A1056289 T85587 N62441 R89099 R00035 T85596 R61335 R00128 N63359 A1535964 A1207768 M31468 NM_012250 W01322 AA253280 AA253233 AA293148 AW582106 R79880 AA459547 AA363459 AA234396 N31669 H44468 AA434587 AW363088 AW993541 AA070906 AA070934 X51501 NM_002652 Y10179 J03460 A1791818 A1821473 AA916588 AA564296 AA916110 A1972286 A1420470 A1568790 A1597724 AW205207 A1659305 A1791620 AA532383 A1821475 AA526498 NM_012249 M31470 AL043108 AA282561 AA178883 T29433 AA313329 W48807 AW404323 AA453560 AW403227 H94816 W17101 AA165152 W23989 AA091310 AL121734 D54896 AA424269 BE242906 AA362118 BE018454 A1280348 AL048769 M35543 AA757734 A1128865 H20289 H23728 A1203445 H41481 H18237 H44081 H92839 A1928621 H75675 D51148 A1796188 AW390453 D55579 D54145 D53996 D54015 R37664 H17541 AA668681 T55061 R15887 AW468123 R16049 H69030 AA054226 H16070 F09655 R92144 T03521 R05473 H92840 AA018186 R91707 U35637 AA112989 Z19308
10	125992	1589048_1 127210 15307_6
15	127263	232161_1 135197 28440_1
20	127394	304844_1 126879 1860_2 126983 171841_1 120470 188975_1
25	127854	443883_1 121367 280429_1 106320 6435_1
30	115479	201515_1 101026 11075_1
35	100401	24827_1
40	130542	28089_3
45	100485	30576_2 108345 112277_6 100522 19669_1
50	100533	32905_1 100598 23902_2
55	102332	14745_3 118250 genbank_N62602 N62602 103678 entrez_Z84483 Z84483 119400 genbank_T82767 T82767 119559 entrez_W38197 W38197
60	102332	14745_3 118250 genbank_N62602 N62602 103678 entrez_Z84483 Z84483 119400 genbank_T82767 T82767 119559 entrez_W38197 W38197
65	102332	14745_3 118250 genbank_N62602 N62602 103678 entrez_Z84483 Z84483 119400 genbank_T82767 T82767 119559 entrez_W38197 W38197

MISSING AT THE TIME OF PUBLICATION

TABLE 13: shows genes, including expression sequence tags, up-regulated in prostate tumor tissue compared to normal prostate tissue as analyzed using Affymetrix/Eos Hu02 GeneChip array. Shown are the ratios of "average" normal prostate to "average" prostate cancer tissues.

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10 Pkey: Unique Eos probe set identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigenID: Unigene number
 Unigene Title: Unigene gene title
 R1: Background subtracted normal prostate : prostate tumor tissue

	Pkey	ExAccn	UnigenID	Unigene Title	R1
15	333516			CH22_FGENES.173_1	0.028
	337954			CH22_EM:AC005500.GENSCAN.96-3	0.029
	332498	R73299	Hs.204354	ras homolog gene family; member B	0.03
	337944			CH22_EM:AC005500.GENSCAN.69-7	0.033
	334111			CH22_FGENES.330_10	0.033
20	333657			CH22_FGENES.241_2	0.034
	327718			CH.04_hs gl[6525284	0.034
	336355			CH22_FGENES.817_5	0.035
	322011	AL137354		EST cluster (not in UniGene)	0.035
	336377			CH22_FGENES.821_6	0.036
25	300254	AW079607	Hs.188417	ESTs; Weakly similar to ZnT-3 [H.sapiens]	0.037
	330096			CH.19_p2 gl[6016278	0.037
	335191			CH22_FGENES.507_6	0.038
	334040			CH22_FGENES.322_8	0.039
	333586			CH22_FGENES.204_2	0.04
30	333285			CH22_FGENES.132_2	0.042
	313326	AI088120	Hs.122329	ESTs	0.043
	329517			CH.10_p2 gl[3983513	0.043
	333403			CH22_FGENES.144_21	0.043
	335228			CH22_FGENES.513_11	0.044
35	335976			CH22_FGENES.652_11	0.045
	333637			CH22_FGENES.229_2	0.046
	334582			CH22_FGENES.407_5	0.046
	336437			CH22_FGENES.826_4	0.047
	337461			CH22_FGENES.782-1	0.047
40	302892	N58545	Hs.6975	histone deacetylase 3	0.049
	338689			CH22_EM:AC005500.GENSCAN.475-3	0.049
	334721			CH22_FGENES.421_32	0.049
	305887	AA864572		EST singleton (not in UniGene) with exon hit	0.049
	335498			CH22_FGENES.571_7	0.05
45	311596	AI682088	Hs.223368	ESTs	0.05
	326959			CH.21_hs gl[6469838	0.051
	311688	AW025661	Hs.240090	ESTs	0.052
	317298	AI922374	Hs.158549	ESTs	0.052
	332884			CH22_FGENES.54_6	0.052
50	321039	AW247083		EST cluster (not in UniGene)	0.053
	335844			CH22_FGENES.623_4	0.053
	325371			CH.12_hs gl[5866920	0.054
	335667			CH22_FGENES.590_18	0.054
	333635			CH22_FGENES.228_2	0.054
55	336736			CH22_FGENES.110-2	0.055
	335893			CH22_FGENES.635_1	0.055
	333170			CH22_FGENES.94_5	0.055
	329768			CH.14_p2 gl[6015501	0.055
	334030			CH22_FGENES.320_2	0.055
60	323359	AA234172	Hs.137418	ESTs	0.055
	300453	AW051431	Hs.113029	ribosomal protein S25	0.055
	334282			CH22_FGENES.367_12	0.055
	306590	AI000246		EST singleton (not in UniGene) with exon hit	0.055
	331087	R22520	Hs.233398	ESTs	0.055
65	338620			CH22_EM:AC005500.GENSCAN.450-18	0.056
	339045			CH22_DA59H18.GENSCAN.28-5	0.056
	308023	AI452732		EST singleton (not in UniGene) with exon hit	0.057

	339067		CH22_DA59H18.GENSCAN.33-3	0.057
	335889		CH22_FGENES.598_4	0.057
	339069		CH22_DA59H18.GENSCAN.33-5	0.057
	338176		CH22_EM:AC005500.GENSCAN.219-4	0.057
5	328159		CH.08_hs gij5868065	0.058
	335655		CH22_FGENES.590_6	0.058
	336371		CH22_FGENES.820_1	0.058
	336558		CH22_FGENES.842_3	0.059
	337738		CH22_EM:AC000097.GENSCAN.100-4	0.059
10	334273		CH22_FGENES.369_2	0.059
	335889		CH22_FGENES.833_3	0.059
	327807		CH.05_hs gij5867968	0.059
	333315		CH22_FGENES.138_7	0.059
	338825		CH22_DJ246D7.GENSCAN.4-6	0.06
15	337612		CH22_C20H12.GENSCAN.22-5	0.06
	333897		CH22_FGENES.293_4	0.06
	335990		CH22_FGENES.855_4	0.06
	334264		CH22_FGENES.367_15	0.06
	338653		CH22_EM:AC005500.GENSCAN.460-39	0.061
20	322303	W07459	EST cluster (not in UniGene)	0.061
	333498		CH22_FGENES.168_8	0.061
	338522		CH22_FGENES.839_3	0.061
	301357	AW295677	Hs.137840 ESTs; Moderately similar to HOMEBOX PROTEIN SIX1 [H.sapiens]	0.062
25	305917	AA876469	Hs.181357 laminin receptor 1 (67kD; ribosomal protein SA)	0.062
	338143		CH22_FGENES.705_5	0.063
	333493		CH22_FGENES.168_2	0.063
	332533	M99487	Hs.1915 folate hydrolase (prostate-specific membrane antigen) 1	0.063
	325844		CH.16_hs gij6552453	0.063
30	336402		CH22_FGENES.823_17	0.063
	335767		CH22_FGENES.607_1	0.064
	301893	T80334	EST cluster (not in UniGene) with exon hit	0.064
	324019	AW177009	EST cluster (not in UniGene)	0.064
	305801	AA845997	EST singleton (not in UniGene) with exon hit	0.064
35	335188		CH22_FGENES.507_3	0.065
	337533		CH22_FGENES.828-2	0.065
	333311		CH22_FGENES.138_3	0.065
	335688		CH22_FGENES.590_19	0.065
40	306786	AI041589	EST singleton (not in UniGene) with exon hit	0.066
	306365	AA962086	EST singleton (not in UniGene) with exon hit	0.066
	306249	AA933840	EST singleton (not in UniGene) with exon hit	0.066
	335018		CH22_FGENES.474_6	0.066
	333594		CH22_FGENES.210_3	0.066
45	333900		CH22_FGENES.293_7	0.066
	325207		CH.10_hs gij6552430	0.067
	328888		CH.15_p2 gij6067149	0.067
	328238		CH.17_hs gij5867260	0.067
	333858		CH22_FGENES.241_4	0.067
	335809		CH22_FGENES.617_6	0.068
50	307427	AI243437	EST singleton (not in UniGene) with exon hit	0.068
	318428	AI949409	Hs.224583 ESTs	0.069
	327005		CH.21_hs gij5867664	0.069
	330483	HQ998-HT998	Sulfotransferase, Phenol-Preferring	0.069
55	333318		CH22_FGENES.138_10	0.07
	333313		CH22_FGENES.138_5	0.07
	325937		CH.16_hs gij5867132	0.07
	335863		CH22_FGENES.590_14	0.07
	335349		CH22_FGENES.539_2	0.07
60	303396	AA224470	Hs.25426 ESTs; Weakly similar to unknown [H.sapiens]	0.07
	332603	N66681	Hs.33470 ESTs	0.07
	333310		CH22_FGENES.138_2	0.071
	309924	AW340812	EST singleton (not in UniGene) with exon hit	0.071
	336340		CH22_FGENES.814_15	0.071
65	308025	AI453365	Hs.172928 collagen; type I; alpha 1	0.071
	306805	AI055968	EST singleton (not in UniGene) with exon hit	0.071
	335499		CH22_FGENES.571_8	0.071
	328669		CH.14_p2 gij6272129	0.071
	321666	D28390	EST cluster (not in UniGene)	0.071
	338174		CH22_EM:AC005500.GENSCAN.219-2	0.072

	336558		CH22_FGENES.842_1	0.072
	305451 AA738105	Hs.140	immunoglobulin gamma 3 (Gm marker)	0.072
	336684		CH22_FGENES.46_1	0.072
5	326943		CH.21_hs g 58004448	0.073
	333947		CH22_FGENES.303_1	0.074
	333214		CH22_FGENES.104_5	0.074
	331817 AA446572	Hs.174007	ESTs; Moderately similar to III ALU SUBFAMILY J WARNING	0.074
	339102		CH22_DA59H18.GENSCAN.44-9	0.074
10	328122		CH.06_hs g 5868031	0.075
	332250 N62712	Hs.226223	KIAA0618 gene product	0.075
	328506		CH.07_hs g 5868471	0.075
	331758 AA291468	Hs.98504	ESTs	0.075
	335193		CH22_FGENES.507_8	0.076
15	317729 AA971718	Hs.128141	ESTs	0.076
	304515 AA458708	Hs.251577	hemoglobin; alpha 2	0.076
	313644 AI565768	Hs.124960	ESTs	0.076
	326145		CH.17_hs g 5867204	0.076
	336394		CH22_FGENES.823_6	0.077
20	306516 AA989542		EST singleton (not in UniGene) with exon hit	0.077
	300629 AA152119	Hs.155101	ATP synthase; H+ transporting; mitochondrial F1 complex; alpha subunit; isoform 1; cardiac muscle	0.077
	333160		CH22_FGENES.91_2	0.077
	337490		CH22_FGENES.789-5	0.077
25	305403 AA723748		EST singleton (not in UniGene) with exon hit	0.077
	331747 AA281765	Hs.183689	ESTs	0.077
	332792		CH22_FGENES.3_2	0.078
	330513 M81057	Hs.180884	carboxypeptidase B1 (tissue)	0.078
	308905 AI859636	Hs.8102	ribosomal protein S20	0.078
30	337419		CH22_FGENES.759-4	0.078
	333459		CH22_FGENES.157_8	0.078
	334851		CH22_FGENES.440_3	0.078
	329046		CH.X_hs g 5868569	0.078
	327879		CH.06_hs g 5868142	0.079
35	305830 AA857665		EST singleton (not in UniGene) with exon hit	0.079
	302928 AL137719		EST cluster (not in UniGene) with exon hit	0.079
	304321 AA136698	Hs.113029	ribosomal protein S25	0.079
	326390		CH.19_hs g 5867340	0.079
	335230		CH22_FGENES.514_2	0.08
40	334622		CH22_FGENES.412_6	0.08
	335331		CH22_FGENES.535_4	0.08
	304753 AA578840	Hs.77981	major histocompatibility complex; class I; B	0.08
	301863 AI418863		EST cluster (not in UniGene) with exon hit	0.081
	336561		CH22_FGENES.842_6	0.081
	335611		CH22_FGENES.583_5	0.081
45	305060 AA635771		EST singleton (not in UniGene) with exon hit	0.081
	306051 AA906130		EST singleton (not in UniGene) with exon hit	0.082
	308269 AI571211		EST singleton (not in UniGene) with exon hit	0.082
	334365		CH22_FGENES.378_13	0.082
50	335496		CH22_FGENES.571_4	0.082
	332634 S38953		Human unidentified gene complementary to P450c21 gene; partial cds	0.082
	337824		CH22_EM:AC005500.GENSCAN.13-18	0.082
	335822		CH22_FGENES.619_7	0.082
55	334758		CH22_FGENES.428_7	0.082
	309641 AW194230	Hs.253100	EST	0.082
	333064		CH22_FGENES.75_7	0.083
	338695		CH22_EM:AC005500.GENSCAN.477-25	0.083
	331809 AA402482	Hs.97312	ESTs	0.083
60	328138		CH.17_hs g 5867203	0.083
	328304		CH.07_hs g 58004478	0.083
	330570 U60276	Hs.165439	arsA (bacterial) arsenite transporter; ATP-binding; homolog 1	0.083
	334305		CH22_FGENES.373_8	0.083
	335885		CH22_FGENES.632_3	0.083
65	325839		CH.16_hs g 6552452	0.083
	333531		CH22_FGENES.175_18	0.084
	330385 AA449749	Hs.31388	ESTs; Highly similar to secreted apoptosis related protein 1 [H.sapiens]	0.084
	323305 AA811351	Hs.25307	Homo sapiens clone 24812 mRNA sequence	0.084
	331698 Z39929	Hs.65843	ESTs	0.084

	335888		CH22_FGENES.633_2	0.084
	306008 AA894390		EST singleton (not in UniGene) with exon hit	0.084
	334249		CH22_FGENES.385_15	0.084
5	318303 AW451197	Hs.113418	ESTs	0.084
	330171		CH.02_p2 gi 6648220	0.084
	336662		CH22_FGENES.41-1	0.085
	320506 AI815668	Hs.157478	suc1-associated neurotrophic factor target 2 (FGFR signalling adaptor)	0.085
	316974 AI740721	Hs.128282	ESTs	0.085
10	336492		CH22_FGENES.832_9	0.085
	335750		CH22_FGENES.602_4	0.085
	335678		CH22_FGENES.594_1	0.086
	336093		CH22_FGENES.691_2	0.086
15	310932 AI933861	Hs.222852	ESTs	0.086
	335160		CH22_FGENES.502_4	0.086
	334306		CH22_FGENES.373_9	0.086
	334793		CH22_FGENES.433_5	0.086
	333936		CH22_FGENES.301_2	0.087
	336413		CH22_FGENES.823_35	0.087
20	333775		CH22_FGENES.272_6	0.087
	335971		CH22_FGENES.652_4	0.087
	301737 AI815981		EST cluster (not in UniGene) with exon hit	0.087
	339101		CH22_DA59H18.GENSCAN.44-6	0.087
25	327612		CH.04_hs gi 6525283	0.087
	326241		CH.17_hs gi 5867260	0.088
	338388		CH22_EM:AC005500.GENSCAN.331-4	0.088
	327762		CH.05_hs gi 5867961	0.088
	305266 AA679772		EST singleton (not in UniGene) with exon hit	0.088
30	334359		CH22_FGENES.378_4	0.088
	335500		CH22_FGENES.571_10	0.088
	329687		CH.14_p2 gi 8117856	0.088
	333654		CH22_FGENES.240_2	0.088
	324430 AA464018		EST cluster (not in UniGene)	0.088
	325999		CH.16_hs gi 5867073	0.089
35	334832		CH22_FGENES.439_1	0.089
	339115		CH22_DA59H18.GENSCAN.49-3	0.089
	300896 AI916902	Hs.213882	ESTs	0.089
	328784		CH.07_hs gi 5868309	0.089
40	335044		CH22_FGENES.480_1	0.089
	329791		CH.14_p2 gi 6468354	0.089
	333656		CH22_FGENES.240_4	0.089
	326180		CH.17_hs gi 5867211	0.089
	333391		CH22_FGENES.144_6	0.089
	338324		CH22_EM:AC005500.GENSCAN.306-3	0.089
45	305396 AA721052		EST singleton (not in UniGene) with exon hit	0.089
	337483		CH22_FGENES.795-7	0.09
	326424		CH.19_hs gi 5867389	0.09
	306454 AA977992		EST singleton (not in UniGene) with exon hit	0.09
	338893		CH22_DJ32110.GENSCAN.7-6	0.09
50	327470		CH.02_hs gi 5887772	0.09
	333165		CH22_FGENES.81_7	0.09
	307155 AI186738	Hs.182426	ribosomal protein S2	0.09
	330717 AA233926	Hs.23635	ESTs	0.09
55	335334		CH22_FGENES.535_10	0.09
	335907		CH22_FGENES.638_2	0.09
	333885		CH22_FGENES.292_7	0.09
	331034 N51868	Hs.31965	ESTs; Moderately similar to 40S RIBOSOMAL PROTEIN S20 [H.sapiens]	0.09
	304660 AA534418	Hs.162185	ESTs	0.09
60	328217		CH.08_hs gi 5888096	0.091
	336068		CH22_FGENES.684_13	0.091
	302833 AA295381	Hs.44423	ESTs	0.091
	328668		CH.07_hs gi 5888254	0.091
	335309		CH22_FGENES.532_2	0.091
65	338481		CH22_EM:AC005500.GENSCAN.377-5	0.091
	306266 AA936892		EST singleton (not in UniGene) with exon hit	0.091
	305070 AA639783		EST singleton (not in UniGene) with exon hit	0.091
	304870 AA594811	Hs.119122	ribosomal protein L13a	0.091
	303858 AA968589	Hs.944	glucose phosphate isomerase	0.091

	323769	AI459812	Hs.170460	ESTs; Weakly similar to KIAA0990 protein [H.sapiens]	0.092
	334910			CH22_FGENES.455_3	0.092
	326382			CH.19_hs gl 5867327	0.092
5	332467	AA489630	Hs.119004	KIAA0665 gene product	0.092
	338534			CH22_EM:AC005500.GENSCAN.402-7	0.092
	336449			CH22_FGENES.829_6	0.092
	333709			CH22_FGENES.250_24	0.092
	336559			CH22_FGENES.842_4	0.092
10	333230			CH22_FGENES.107_10	0.093
	333133			CH22_FGENES.83_9	0.093
	334885			CH22_FGENES.451_11	0.093
	330605	X02419	Hs.77274	plasminogen activator; urokinase	0.093
	338392			CH22_FGENES.823_4	0.093
15	334083			CH22_FGENES.327_38	0.093
	325469			CH.12_hs gl 6017034	0.093
	331077	R09531	Hs.19039	ESTs	0.093
	303701	AW500732		EST cluster (not in UniGene) with exon hit	0.093
	334218			CH22_FGENES.358_3	0.093
20	336542			CH22_FGENES.840_6	0.093
	337151			CH22_FGENES.548-1	0.093
	333642			CH22_FGENES.231_2	0.093
	336863			CH22_FGENES.297-4	0.093
	334680			CH22_FGENES.419_2	0.093
25	326365			CH.18_hs gl 5867297	0.093
	338952			CH22_DJ32110.GENSCAN.23-22	0.093
	337639			CH22_FGENES.832-4	0.094
	333546			CH22_FGENES.180_2	0.094
	335258			CH22_FGENES.518_3	0.094
30	336786			CH22_FGENES.168-19	0.094
	321644	AI204177	Hs.237396	ESTs	0.094
	335943			CH22_FGENES.646_17	0.094
	327918			CH.06_hs gl 5868165	0.094
	306398	AA970548		EST singleton (not in UniGene) with exon hit	0.094
35	335671			CH22_FGENES.592_3	0.094
	335033			CH22_FGENES.475_11	0.094
	338277			CH22_EM:AC005500.GENSCAN.290-2	0.094
	332061	AA504812	Hs.192824	early B-cell factor	0.094
	305153	AA654582	Hs.77039	ribosomal protein S3A	0.094
40	333680			CH22_FGENES.292_2	0.094
	323940	AI864428	Hs.170880	ESTs	0.094
	313779	AA848798	Hs.129771	ESTs	0.095
	323109	AA169345		EST cluster (not in UniGene)	0.095
	332930			CH22_FGENES.38_4	0.095
45	335368			CH22_FGENES.543_6	0.095
	303887	R72672	Hs.193484	ESTs; Weakly similar to Similarity with yeast gene L3502.1 [C.elegans]	0.095
	336223			CH22_FGENES.727_3	0.095
	311280	AI767957	Hs.197737	ESTs; Weakly similar to Y38A8.1 gene product [C.elegans]	0.095
50	337256			CH22_FGENES.648-3	0.095
	308814	AI819263		EST singleton (not in UniGene) with exon hit	0.095
	334659			CH22_FGENES.418_7	0.095
	335895			CH22_FGENES.635_3	0.095
	321697	AW388061	Hs.4953	golgi autoantigen; golgin subfamily a; 3	0.095
55	336010			CH22_FGENES.668_8	0.096
	302824	U21260		EST cluster (not in UniGene) with exon hit	0.096
	333612			CH22_FGENES.217_7	0.096
	304823	AA584837		EST singleton (not in UniGene) with exon hit	0.096
	335665			CH22_FGENES.590_16	0.096
60	306518	AA989598		EST singleton (not in UniGene) with exon hit	0.096
	335243			CH22_FGENES.518_4	0.096
	335436			CH22_FGENES.559_5	0.096
	300243	AI420256	Hs.161271	ESTs	0.096
	332810			CH22_FGENES.7_12	0.097
65	308612	AI735834		EST singleton (not in UniGene) with exon hit	0.097
	335818			CH22_FGENES.618_6	0.097
	325838			CH.16_hs gl 6552452	0.097
	337482			CH22_FGENES.795-6	0.097
	336645			CH22_FGENES.26-1	0.097
	337293			CH22_FGENES.675-1	0.098

	329893		CH.16_p2 gi 5525313	0.098
	326533		CH.19_hs gi 5867441	0.098
	334905		CH22_FGENES.452_20	0.098
5	306347	AA961144	EST singleton (not in UniGene) with exon hit	0.098
	336676		CH22_FGENES.43-4	0.098
	339186		CH22_DA59H18.GENSCAN.69-7	0.098
	335774		CH22_FGENES.607_10	0.098
	339216		CH22_FF113D11.GENSCAN.6-11	0.098
10	335311		CH22_FGENES.532_4	0.098
	329632		CH.11_p2 gi 5729060	0.098
	326595		CH.07_hs gi 5868224	0.098
	326928		CH.21_hs gi 5456782	0.098
	315234	AI079680	Hs.120770 ESTs	0.098
15	306082	AA908508	EST singleton (not in UniGene) with exon hit	0.098
	305710	AA826544	EST singleton (not in UniGene) with exon hit	0.098
	318540	T30280	EST cluster (not in UniGene)	0.099
	337553		CH22_C4G1.GENSCAN.2-1	0.099
	320951	AA344069	Hs.202699 neurexophilin 4	0.099
20	303845	T08033	EST cluster (not in UniGene) with exon hit	0.099
	338981		CH22_DA59H18.GENSCAN.2-5	0.099
	321313	R87385	Hs.26058 ESTs; Weakly similar to p532 [H.sapiens]	0.099
	328348		CH.07_hs gi 5868383	0.099
	332203	H49388	Hs.102082 EST	0.099
25	301780	R07064	EST cluster (not in UniGene) with exon hit	0.099
	332095	AA608838	Hs.162681 EST	0.099
	333227		CH22_FGENES.107_5	0.099
	316442	AA760894	Hs.153023 ESTs	0.099
30	326001		CH.16_hs gi 5867073	0.099
	334383		CH22_FGENES.378_11	0.099
	338895		CH22_DJ32110.GENSCAN.9-2	0.099
	327460		CH.02_hs gi 5004455	0.099
	332705	T59161	Hs.76293 thymosin; beta 10	0.1
	307806	AI351739	EST singleton (not in UniGene) with exon hit	0.1
35	322800	F25037	Hs.225175 ESTs	0.1
	304918	AA602697	EST singleton (not in UniGene) with exon hit	0.1
	334327		CH22_FGENES.375_4	0.1
	318359	AI097439	Hs.135548 ESTs	0.1
	326644		CH.20_hs gi 5867559	0.1
40	334454		CH22_FGENES.388_3	0.1
	327859		CH.06_hs gi 5868210	0.1
	323783	AA330588	Hs.131819 ESTs	0.1
	309198	AI955915	Hs.248038 major histocompatibility complex; class I; C	0.1
	339265		CH22_BA354112.GENSCAN.10-3	0.1
45	320576	AL049977	Hs.162209 Homo sapiens mRNA; cDNA DKFZp564C122 (from clone DKFZp564C122)	0.1
	338132		CH22_EM:AC005500.GENSCAN.200-2	0.1
	333163		CH22_FGENES.91_5	0.101
	337584		CH22_C20H12.GENSCAN.5-1	0.101
50	307588	AI285535	EST singleton (not in UniGene) with exon hit	0.101
	336969		CH22_FGENES.378-2	0.101
	327535		CH.02_hs gi 5525279	0.101
	328732		CH.07_hs gi 5868289	0.101
	338686		CH22_FGENES.46-3	0.101
55	335777		CH22_FGENES.607_13	0.101
	332944		CH22_FGENES.47_3	0.101
	333174		CH22_FGENES.95_1	0.101
	336380		CH22_FGENES.821_8	0.101
	330571	U60800	Hs.79089 sema domain; immunoglobulin domain (Ig); cytoplasmic domain; (semaphorin) 4D	0.101
60	331789	AA398721	Hs.186749 ESTs	0.101
	338915		CH22_DJ32110.GENSCAN.12-1	0.101
	334844		CH22_FGENES.439_24	0.101
	336642		CH22_FGENES.23-4	0.101
	334906		CH22_FGENES.452_21	0.101
65	333188		CH22_FGENES.88_8	0.101
	300088	AW299993	EST cluster (not in UniGene) with exon hit	0.101
	329373		CHX_hs gi 5682537	0.102
	331120	R46576	Hs.23239 ESTs	0.102
	335856		CH22_FGENES.628_1	0.102

	331888	AA431337	Hs.98017	ESTs	0.102
	333154			CH22_FGENES.89_4	0.102
	335889			CH22_FGENES.655_2	0.102
5	304385	AA235802		EST singleton (not in UniGene) with exon hit	0.102
	338016			CH22_EM:AC005500.GENSCAN.133-1	0.102
	335190			CH22_FGENES.507_5	0.102
	318595	T39486	Hs.6137	ESTs	0.102
	333897			CH22_FGENES.250_11	0.102
10	306526	AA989713		EST singleton (not in UniGene) with exon hit	0.103
	328734			CH.07_hs g 5888289	0.103
	307294	AI205612	Hs.73742	ribosomal protein; large; P0	0.103
	327424			CH.02_hs g 5867751	0.103
	335872			CH22_FGENES.630_3	0.103
15	333572			CH22_FGENES.189_1	0.103
	334774			CH22_FGENES.430_6	0.103
	338660			CH22_EM:AC005500.GENSCAN.462-1	0.103
	326713			CH.20_hs g 5867595	0.103
	333694			CH22_FGENES.310_18	0.103
	335800			CH22_FGENES.613_4	0.103
20	318113	AI187943	Hs.132322	ESTs	0.103
	337278			CH22_FGENES.685-1	0.103
	336386			CH22_FGENES.822_6	0.103
	334790			CH22_FGENES.432_15	0.103
25	303778	AW505368		EST cluster (not in UniGene) with exon hit	0.104
	336524			CH22_FGENES.839_5	0.104
	328836			CH.08_hs g 5868500	0.104
	335102			CH22_FGENES.494_7	0.104
	300935	AA513844	Hs.222815	ESTs; Weakly similar to Wiskott-Aldrich Syndrome protein [H.sapiens]	0.104
30	307581	AI284415		EST singleton (not in UniGene) with exon hit	0.104
	317301	AW291683	Hs.226056	ESTs	0.104
	335330			CH22_FGENES.535_3	0.104
	337668			CH22_EM:AC005500.GENSCAN.103-2	0.104
35	335627			CH22_FGENES.584_7	0.104
	336274			CH22_FGENES.762_2	0.104
	334730			CH22_FGENES.424_6	0.105
	334409			CH22_FGENES.383_6	0.105
	327237			CH.01_hs g 5867544	0.105
40	333321			CH22_FGENES.138_13	0.105
	303181	AA452368		EST cluster (not in UniGene) with exon hit	0.105
	333738			CH22_FGENES.261_2	0.105
	338255			CH22_EM:AC005500.GENSCAN.276-3	0.105
	334282			CH22_FGENES.369_12	0.105
	330190			CH.05_p2 g 6165182	0.105
45	310748	AW014249	Hs.158698	ESTs	0.105
	338150			CH22_EM:AC005500.GENSCAN.207-2	0.105
	336719			CH22_FGENES.82-6	0.105
	330228			CH.05_p2 g 6013527	0.105
50	327801			CH.05_hs g 5867824	0.105
	330525	S75168	Hs.274	megakaryocyte-associated tyrosine kinase	0.105
	334972			CH22_FGENES.468_2	0.105
	335111			CH22_FGENES.494_19	0.106
	334483			CH22_FGENES.395_5	0.106
	328829			CH.07_hs g 5868337	0.106
55	302753	M74299		EST cluster (not in UniGene) with exon hit	0.106
	334512			CH22_FGENES.398_10	0.106
	330024			CH.18_p2 g 8671908	0.106
	321030	AI769930	Hs.233617	Homo sapiens (clone B3B3E13) Huntington's disease candidate region	0.107
60	338410			CH22_EM:AC005500.GENSCAN.341-8	0.107
	334353			CH22_FGENES.376_5	0.107
	338276			CH22_EM:AC005500.GENSCAN.288-9	0.107
	329053			CH.X_hs g 5868574	0.107
	336560			CH22_FGENES.842_5	0.107
65	332158	AA621363	Hs.112980	EST	0.107
	336447			CH22_FGENES.829_4	0.107
	333703			CH22_FGENES.250_17	0.107
	326207			CH.17_hs g 5867222	0.107
	333232			CH22_FGENES.108_1	0.107

	334802		CH22_FGENES.435_1	0.107
	303784 AA704983		EST cluster (not in UniGene) with exon hit	0.107
	338847		CH22_DJ246D7.GENSCAN.10-2	0.107
5	339407		CH22_DJ579N16.GENSCAN.1-9	0.108
	337635		CH22_C20H12.GENSCAN.32-8	0.108
	334650		CH22_FGENES.417_17	0.108
	308511 AI687580		EST singleton (not in UniGene) with exon hit	0.108
	333392		CH22_FGENES.144_8	0.108
	325840		CH.16_hs g 5552452	0.108
10	315044 AW205664	Hs.129568	ESTs	0.108
	333298		CH22_FGENES.133_4	0.108
	335157		CH22_FGENES.501_7	0.108
	333305		CH22_FGENES.137_2	0.108
15	326379		CH.19_hs g 5867327	0.108
	335050		CH22_FGENES.482_1	0.108
	305185 AA663985	Hs.248038	major histocompatibility complex, class I; C	0.108
	335558		CH22_FGENES.590_9	0.108
	323040 AA336809	Hs.10882	ESTs	0.108
20	337328		CH22_FGENES.699-6	0.108
	339262		CH22_BA354112.GENSCAN.9-6	0.108
	321202 H54052	Hs.163639	ESTs; Weakly similar to INTERCELLULAR ADHESION MOLECULE-1 PRECURSOR [H.sapiens]	0.109
	331782 AA398968	Hs.97548	EST	0.109
25	333808		CH22_FGENES.278_2	0.109
	321325 AB033100		EST cluster (not in UniGene)	0.109
	331373 AA435513	Hs.178170	ESTs; Weakly similar to DUAL SPECIFICITY PROTEIN PHOSPHATASE 3	0.87
	328775		CH.07_hs g 5868309	0.109
	335105		CH22_FGENES.494_10	0.109
30	300975 AI283548	Hs.149668	ESTs	0.109
	324893 T31940		EST cluster (not in UniGene)	0.109
	333397		CH22_FGENES.144_15	0.109
	338484		CH22_FGENES.831_3	0.109
	335507		CH22_FGENES.571_22	0.109
35	336373		CH22_FGENES.820_3	0.109
	336188		CH22_FGENES.717_12	0.109
	313455 AW081702	Hs.137329	ESTs	0.109
	335185		CH22_FGENES.506_4	0.109
40	306814 AI068577		EST singleton (not in UniGene) with exon hit	0.109
	311130 AI632322	Hs.195306	ESTs	0.109
	310882 AW080339	Hs.211911	ESTs	0.109
	323383 AI348359	Hs.135209	ESTs	0.11
	300212 AW135925	Hs.184552	biphenylhydrolase-like (serine hydrolase; breast epithelial mucin-assoc.	0.11
45	325675		CH.14_hs g 5867014	0.11
	330095		CH.19_p2 g 6015278	0.11
	331942 AA453261	Hs.99309	ESTs	0.11
	334723		CH22_FGENES.421_34	0.11
	333614		CH22_FGENES.217_9	0.11
50	337318		CH22_FGENES.692-1	0.11
	305057 AA635628	Hs.62954	ferritin; heavy polypeptide 1	0.11
	338704		CH22_EM:AC005500.GENSCAN.480-3	0.11
	335385		CH22_FGENES.543_27	0.11
	338012		CH22_EM:AC005500.GENSCAN.128-10	0.11
55	329449		CH.Y_hs g 5868888	0.11
	338980		CH22_DA59H18.GENSCAN.2-4	0.11
	336553		CH22_FGENES.841_10	0.111
	330021		CH.18_p2 g 6671889	0.111
	327579		CH.03_hs g 5867824	0.111
60	333089		CH22_FGENES.79_4	0.111
	337078		CH22_FGENES.453-4	0.111
	331388 AA456852	Hs.43543	suppressor of white apricot homolog 2	0.111
	306674 AI005542	Hs.180414	heat shock 70kD protein 10 (HSC71)	0.111
	305949 AA884409		EST singleton (not in UniGene) with exon hit	0.111
65	330748 AA418217	Hs.15911	DKFZP586E1422 protein	0.111
	333780		CH22_FGENES.273_2	0.111
	323676 AI702835		EST cluster (not in UniGene)	0.111
	308952 AI868157	Hs.224226	EST	0.111
	309338 AW026946	Hs.181185	eukaryotic translation elongation factor 1 alpha 1	0.111

	329317		CH.X_hs g 6381976	0.112
	333518		CH22_FGENES.173_3	0.112
	306982	AI127883	EST singleton (not in UniGene) with exon hit	0.112
5	338225		CH22_FGENES.728_2	0.112
	333688		CH22_FGENES.250_12	0.112
	302173	AI417947	ESTs	0.112
	335510		CH22_FGENES.571_25	0.112
	328042		CH.06_hs g 5902482	0.112
10	338512		CH22_FGENES.834_7	0.112
	328541		CH.07_hs g 5868486	0.112
	311265	AW205118	ESTs	0.112
	323218	AF131848	Homo sapiens clone 25028 mRNA sequence	0.112
	302002	AF013956	chromobox homolog 4 (Drosophila Pc class)	0.112
15	315088	AA557351	ESTs; Moderately similar to MULTIFUNCTIONAL PROTEIN ADE2	0.112
	312581	AI937242	ESTs	0.112
	322246	AW384710	ESTs	0.112
	333659		CH22_FGENES.241_5	0.113
	327510		CH.02_hs g 6117815	0.113
20	338520		CH22_FGENES.839_1	0.113
	338682		CH22_EM:AC005500.GENSCAN.472-1	0.113
	334508		CH22_FGENES.398_8	0.113
	322533	T59538	EST cluster (not in UniGene)	0.113
	306873	AI086929	EST singleton (not in UniGene) with exon hit	0.113
	338040		CH22_FGENES.679_2	0.113
25	303898	T23215	EST cluster (not in UniGene) with exon hit	0.113
	312011	AW294868	ESTs	0.113
	335188		CH22_FGENES.506_5	0.113
	333607		CH22_FGENES.216_2	0.113
30	305549	AA773530	EST singleton (not in UniGene) with exon hit	0.113
	333688		CH22_FGENES.249_4	0.113
	334352		CH22_FGENES.376_3	0.113
	338185		CH22_EM:AC005500.GENSCAN.233-18	0.114
	333588		CH22_FGENES.206_2	0.114
35	339233		CH22_BA354112.GENSCAN.2-3	0.114
	337455		CH22_FGENES.777-1	0.114
	309101	AI925108	EST singleton (not in UniGene) with exon hit	0.114
	328522		CH.07_hs g 5868477	0.114
	323999	AI537333	ESTs	0.114
40	333517		CH22_FGENES.173_2	0.114
	329935		CH.16_p2 g 6165200	0.114
	326226		CH.17_hs g 5867230	0.114
	335890		CH22_FGENES.633_4	0.114
	336715		CH22_FGENES.77-1	0.114
45	327640		CH.04_hs g 5867890	0.114
	338842		CH22_DJ248D7.GENSCAN.7-1	0.114
	306534	AA991487	EST singleton (not in UniGene) with exon hit	0.114
	338597		CH22_FGENES.266_1	0.114
	321010	Y17456	Homo sapiens LSFR2 gene; last exon	0.114
50	302294	AA159213	isocitrate dehydrogenase 2 (NADP+); mitochondrial	0.114
	324895	N44238	Inositol 1,4,5-triphosphate receptor, type 3	0.114
	327358		CH.01_hs g 58552411	0.114
	308782	AI815153	glyceraldehyde-3-phosphate dehydrogenase	0.115
	325888		CH.16_hs g 5867087	0.115
	336850		CH22_FGENES.272-11	0.115
55	305858	AA863103	EST singleton (not in UniGene) with exon hit	0.115
	302569	AC004472	multiple UniGene matches	0.115
	336158		CH22_FGENES.707_2	0.115
	327666		CH.06_hs g 5868131	0.115
60	339157		CH22_DA59H18.GENSCAN.67-3	0.115
	339258		CH22_BA354112.GENSCAN.8-3	0.115
	336129		CH22_FGENES.701_17	0.115
	333684		CH22_FGENES.249_2	0.115
	309618	AW190162	ribosomal protein L23a	0.115
65	312826	AA954097	ESTs	0.115
	302640	AB035698	EST cluster (not in UniGene) with exon hit	0.115
	328968		CH.08_hs g 6456775	0.115
	327902		CH.08_hs g 5868158	0.115
	321927	AJ223366	EST cluster (not in UniGene)	0.115
	335962		CH22_FGENES.651_4	0.115

	334827		CH22_FGENES.460_1	0.115
	330535	U11872	Human Interleukin-8 receptor type B (IL8RB) mRNA, splice variant IL8RB1	0.858
5	328591		CH.07_hs g 5868227	0.115
	334902		CH22_FGENES.452_16	0.115
	328525		CH.07_hs g 5868482	0.115
	325870		CH.16_hs g 6682492	0.116
	337522		CH22_FGENES.819-1	0.116
10	305078	AA641329	EST singleton (not in UniGene) with exon hit	0.116
	327343		CH.01_hs g 6017017	0.116
	333918		CH22_FGENES.298_7	0.116
	333600		CH22_FGENES.213_2	0.116
	335848		CH22_FGENES.623_8	0.116
	333510		CH22_FGENES.171_4	0.116
15	327629		CH.04_hs g 5887872	0.116
	333470		CH22_FGENES.181_6	0.116
	326855		CH.20_hs g 6552460	0.116
	327008		CH.21_hs g 5867684	0.117
	337480		CH22_FGENES.795-3	0.117
20	338425		CH22_FGENES.824_10	0.117
	321964	AL079687	Hs.171065 ESTs	0.117
	335651		CH22_FGENES.590_2	0.117
	308164	AI245174	Hs.181165 eukaryotic translation elongation factor 1 alpha 1	0.117
	337827		CH22_EM:AC005500.GENSCAN.80-3	0.117
25	300341	H45095	Hs.153524 ESTs	0.117
	300154	AI245127	Hs.179331 ESTs	0.117
	306295	AA937331	EST singleton (not in UniGene) with exon hit	0.117
	329670		CH.14_p2 g 6272128	0.117
	335612		CH22_FGENES.583_6	0.117
30	307845	AI363450	EST singleton (not in UniGene) with exon hit	0.117
	330401	D28383	Human mRNA for ATP synthase B chain, 5'UTR (sequence from the 5'cap to the start codon)	0.117
	327127		CH.21_hs g 6682520	0.117
	333843		CH22_FGENES.290_1	0.117
35	331083	R17762	Hs.22282 ESTs	0.117
	329140		CH.X_hs g 6017060	0.117
	339338		CH22_BA354H12.GENSCAN.27-3	0.117
	331974	AA464518	Hs.89816 ESTs	0.117
	338631		CH22_EM:AC005500.GENSCAN.454-2	0.117
40	330299		CH.08_p2 g 2905881	0.117
	330351		CH.09_p2 g 3058822	0.117
	305377	AA715714	Hs.181357 laminin receptor 1 (67kD; ribosomal protein SA)	0.117
	333106		CH22_FGENES.79_12	0.117
	338514		CH22_EM:AC005500.GENSCAN.392-4	0.117
45	327335		CH.01_hs g 5902477	0.117
	301970	AB028962	Hs.120245 KIAA1039 protein	0.118
	326339		CH.17_hs g 6056311	0.118
	330612	X15673	Hs.83174 Human endogenous retrovirus pHE.1 (ERV9)	0.118
	334178		CH22_FGENES.350_8	0.118
50	328008		CH.08_hs g 5902482	0.118
	329978		CH.16_p2 g 4878063	0.118
	320952	AA897432	Hs.130411 ESTs	0.118
	305621	AA789095	EST singleton (not in UniGene) with exon hit	0.118
	337850		CH22_EM:AC005500.GENSCAN.34-3	0.118
55	333628		CH22_FGENES.224_2	0.118
	337672		CH22_EM:AC000097.GENSCAN.67-1	0.118
	328803		CH.07_hs g 6004475	0.118
	325922		CH.16_hs g 5867122	0.118
	334489		CH22_FGENES.397_1	0.118
60	320638	R54768	Hs.101120 ESTs	0.118
	321932	AA569229	EST cluster (not in UniGene)	0.118
	336958		CH22_FGENES.367-1	0.118
	332082	AA600176	Hs.112345 ESTs	0.118
	306004	AA889992	EST singleton (not in UniGene) with exon hit	0.118
65	336803		CH22_FGENES.194-1	0.118
	309107	AI925823	EST singleton (not in UniGene) with exon hit	0.118
	336859		CH22_FGENES.293-9	0.118
	337935		CH22_EM:AC005500.GENSCAN.85-6	0.118
	326492		CH.19_hs g 5867422	0.118

	327289		CH.01_hs g 5867481	0.119
	325818		CH.14_hs g 5862490	0.119
	310787	AW262580	Hs.159040 ESTs	0.119
5	330028		CH.16_p2 g 58671908	0.119
	325317		CH.11_hs g 5866878	0.119
	335279		CH22_FGENES.523_7	0.119
	331720	AA192173	Hs.221530 ESTs	0.118
	329188		CHX_hs g 5868711	0.119
10	318012	AA764950	Hs.119898 ESTs	0.119
	338316		CH22_EM:AC005500.GENSCAN.304-2	0.119
	326033		CH.17_hs g 5867178	0.119
	334745		CH22_FGENES.426_3	0.119
	333051		CH22_FGENES.73_5	0.119
15	301763	R01279	EST cluster (not in UniGene) with exon hit	0.12
	304502	AA454809	Hs.172928 collagen; type I; alpha 1	0.12
	335680		CH22_FGENES.594_5	0.12
	304678	AA548558	EST singleton (not in UniGene) with exon hit	0.12
	335441		CH22_FGENES.560_4	0.12
20	336187		CH22_FGENES.717_11	0.12
	309422	AW087175	EST singleton (not in UniGene) with exon hit	0.12
	336047		CH22_FGENES.679_9	0.12
	309651	AW185850	EST singleton (not in UniGene) with exon hit	0.12
	308547	AI695385	Hs.201903 EST	0.12
25	304443	AA399444	EST singleton (not in UniGene) with exon hit	0.12
	336245		CH22_FGENES.746_3	0.12
	302703	H72333	EST cluster (not in UniGene) with exon hit	0.12
	335690		CH22_FGENES.596_5	0.12
	328941		CH.08_hs g 6456785	0.12
30	333873		CH22_FGENES.291_9	0.12
	317248	AW105092	Hs.155690 ESTs	0.12
	339288		CH22_BA354112.GENSCAN.16-6	0.12
	337896		CH22_EM:AC005500.GENSCAN.116-3	0.12
	333304		CH22_FGENES.137_1	0.121
35	308332	AI591235	EST singleton (not in UniGene) with exon hit	0.121
	329319		CHX_hs g 6381976	0.121
	302086	X57138	multiple UniGene matches	0.121
	333290		CH22_FGENES.129_2	0.121
	323825	AI793080	Hs.123525 ESTs; Weakly similar to NEUTROPHIL GELATINASE-ASSOCIATED LIPOCALIN PRECURSOR [R.norvegicus]	0.121
40	330575	U64105	Hs.252280 Rho guanine nucleotide exchange factor (GEF) 1	0.121
	305274	AA679890	Hs.181165 eukaryotic translation elongation factor 1 alpha 1	0.121
	333647		CH22_FGENES.235_2	0.121
	302251	AA333340	EST cluster (not in UniGene) with exon hit	0.121
45	329777		CH.14_p2 g 6002090	0.121
	333155		CH22_FGENES.89_5	0.121
	326122		CH.17_hs g 5867194	0.121
	335310		CH22_FGENES.532_3	0.121
	335453		CH22_FGENES.562_13	0.122
50	305103	AA643329	Hs.111334 ferritin; light polypeptide	0.122
	337284		CH22_FGENES.667-2	0.122
	337418		CH22_FGENES.768-4	0.122
	313073	AI963740	Hs.46826 ESTs	0.122
	303759	AW504164	EST cluster (not in UniGene) with exon hit	0.122
55	300017			
	M33197		AFFX control: GAPDH	0.122
	316725	AW135084	Hs.127264 ESTs	0.122
	330738	AA293153	Hs.120980 nuclear receptor co-repressor 2	0.122
	338466		CH22_FGENES.829_25	0.122
60	335956		CH22_FGENES.647_3	0.122
	315308	AA780564	Hs.189053 ESTs	0.122
	338925		CH22_DJ32110.GENSCAN.14-3	0.122
	334969		CH22_FGENES.466_2	0.122
	322050	AL137589	EST cluster (not in UniGene)	0.122
65	339084		CH22_DA59H18.GENSCAN.38-2	0.122
	338323		CH22_EM:AC005500.GENSCAN.306-2	0.122
	337003		CH22_FGENES.418-7	0.122
	325470		CH.12_hs g 6017034	0.123
	338503		CH22_FGENES.833_10	0.123
	330786	D60374	Hs.258712 EST	0.123

	329446		CH.Y_hs gij586888	0.123
	303326	AA229433	Hs.222634 ESTs; Moderately similar to ubiquitin-like protein / ribosomal protein S30	0.123
5	309067	AI916313	Hs.212788 EST	0.123
	317464	AA968472	Hs.130463 ESTs	0.123
	328755		CH.07_hs gij5868301	0.123
	326036		CH.17_hs gij5867178	0.123
	327208		CH.01_hs gij5867447	0.123
10	326124		CH.17_hs gij5916395	0.123
	327509		CH.02_hs gij5117815	0.123
	338398		CH22_EM.AC005500.GENSCAN.336-5	0.123
	304652	AA527782	Hs.84298 CD74 antigen (invariant polypeptide of major histocompatibility complex; class II antigen-associated)	0.123
15	335797		CH22_FGENES.612_6	0.124
	336714		CH22_FGENES.76-29	0.124
	327204		CH.01_hs gij5867447	0.124
	331881	AA430672	Hs.123778 ESTs	0.124
	306971	AI126509	EST singleton (not in UniGene) with exon hit	0.124
20	336174		CH22_FGENES.710_1	0.124
	336126		CH22_FGENES.701_13	0.124
	329129		CH.X_hs gij6588026	0.124
	303049	AW407562	EST cluster (not in UniGene) with exon hit	0.124
	335778		CH22_FGENES.607_14	0.124
25	336601		CH22_FGENES.369_2	0.124
	334340		CH22_FGENES.375_17	0.124
	337436		CH22_FGENES.787-1	0.124
	306013	AA898990	EST singleton (not in UniGene) with exon hit	0.124
	339213		CH22_FF113D11.GENSCAN.6-8	0.124
30	335355		CH22_FGENES.541_2	0.124
	336552		CH22_FGENES.641_9	0.124
	336384		CH22_FGENES.822_4	0.124
	310485	AI286202	Hs.149800 ESTs	0.125
	335840		CH22_FGENES.622_3	0.125
	336444		CH22_FGENES.827_10	0.125
35	315703	N38070	EST cluster (not in UniGene)	0.125
	327763		CH.05_hs gij5867961	0.125
	336383		CH22_FGENES.822_3	0.125
	333498		CH22_FGENES.168_6	0.125
40	328662		CH.07_hs gij6004473	0.125
	336966		CH22_DA59H18.GENSCAN.5-1	0.125
	328311		CH.07_hs gij5868371	0.125
	337241		CH22_FGENES.644-2	0.125
	336933		CH22_FGENES.350-7	0.125
45	313483	AW294432	Hs.144252 ESTs	0.125
	326116		CH.17_hs gij5867193	0.125
	330450	HG363-HT383	Epidermal Growth Factor Receptor-Related Protein	0.125
	307491	AI268539	EST singleton (not in UniGene) with exon hit	0.125
	331852	AA418988	Hs.98314 Homo sapiens mRNA; cDNA DKFZp586L0120 (from clone DKFZp586L0120)	0.125
50	330462	HG944-HT944	Dopamine Receptor D4	0.125
	304410	AA284508	EST singleton (not in UniGene) with exon hit	0.125
	336385		CH22_FGENES.822_5	0.125
	336783		CH22_FGENES.176-3	0.125
55	326243		CH.17_hs gij5867261	0.125
	327266		CH.01_hs gij5867482	0.125
	320753	AF070579	Hs.181544 Homo sapiens clone 24487 mRNA sequence	0.125
	336960		CH22_FGENES.369-5	0.125
	329667		CH.14_p2 gij6272129	0.125
60	328168		CH.06_hs gij5868071	0.125
	338534		CH22_FGENES.839_18	0.125
	339289		CH22_BA354H12.GENSCAN.16-9	0.126
	309230	AI970747	EST singleton (not in UniGene) with exon hit	0.126
	339190		CH22_FF113D11.GENSCAN.1-2	0.126
	337088		CH22_FGENES.458-14	0.126
65	319233	R21054	Hs.211522 ESTs	0.126
	339396		CH22_BA232E17.GENSCAN.6-8	0.126
	331830	AA449077	Hs.179765 Homo sapiens mRNA; cDNA DKFZp586H1821 (from clone DKFZp586H182)	0.126
	308099	AI475914	EST singleton (not in UniGene) with exon hit	0.126

	338477		CH22_EM:AC005500.GENSCAN.373-5	0.128
	334288		CH22_FGENES.369_18	0.128
	317245	AI025039	Hs.131732 ESTs	0.126
5	335249		CH22_FGENES.516_10	0.126
	333327		CH22_FGENES.136_20	0.126
	304240	AA009802	EST singleton (not in UniGene) with exon hit	0.126
	335464		CH22_FGENES.562_26	0.126
	335236		CH22_FGENES.515_8	0.126
	334154		CH22_FGENES.340_4	0.126
10	309257	AI984183	EST singleton (not in UniGene) with exon hit	0.126
	310015	AI220122	Hs.201981 ESTs; Weakly similar to breast carcinoma-associated antigen [H.sapiens]	0.126
	328280		CH.07_hs gij5868352	0.126
15	305744	AA831819	EST singleton (not in UniGene) with exon hit	0.126
	327430		CH.02_hs gij5867754	0.126
	328323		CH.07_hs gij5868373	0.126
	333274		CH22_FGENES.123_2	0.126
	337193		CH22_FGENES.575-3	0.127
	334820		CH22_FGENES.437_2	0.127
20	328708		CH.07_hs gij5868270	0.127
	331228	W67267	Hs.174911 ESTs	0.127
	307205	AI192479	EST singleton (not in UniGene) with exon hit	0.127
	337123		CH22_FGENES.519-3	0.127
	326201		CH.17_hs gij5867216	0.127
25	335276		CH22_FGENES.523_2	0.127
	331202	T81115	Hs.191136 ESTs	0.127
	330532	U03187	Hs.121544 interleukin 12 receptor; beta 1	0.127
	321235	N49521	EST cluster (not in UniGene)	0.127
	301743	F12605	Hs.204529 ESTs; Weakly similar to reverse transcriptase [H.sapiens]	0.127
30	328175		CH.06_hs gij5868073	0.127
	306407	AA971985	EST singleton (not in UniGene) with exon hit	0.127
	327145		CH.01_hs gij5867548	0.127
	327649		CH.04_hs gij5867899	0.127
	335142		CH22_FGENES.498_12	0.127
35	333909		CH22_FGENES.285_2	0.127
	330608	X04325	Hs.2679 gap junction protein; beta 1; 32kD (connexin 32; Charcot-Marie-Tooth neuropathy; X-linked)	0.127
	330158		CH.21_p2 gij6580367	0.127
	320153	AF064594	Hs.120360 phospholipase A2; group VI	0.127
40	314407	AA098835	Hs.224432 ESTs	0.127
	333383		CH22_FGENES.143_22	0.127
	320663	AI734242	Hs.244473 ESTs	0.128
	326233		CH.17_hs gij5867232	0.128
	326598		CH.20_hs gij5867634	0.128
45	335174		CH22_FGENES.504_4	0.128
	319843	H29920	Hs.99486 ESTs; Weakly similar to aralar1 [H.sapiens]	0.128
	335458		CH22_FGENES.562_18	0.128
	332997		CH22_FGENES.58_4	0.128
	334188		CH22_FGENES.352_3	0.128
50	329759		CH.14_p2 gij6048280	0.128
	330348		CH.09_p2 gij4544475	0.128
	326958		CH.21_hs gij6469836	0.128
	305263	AA679467	EST singleton (not in UniGene) with exon hit	0.128
	337693		CH22_EM:AC000097.GENSCAN.78-14	0.128
55	326812		CH.20_hs gij6682504	0.128
	333237		CH22_FGENES.108_7	0.128
	333699		CH22_FGENES.250_13	0.128
	311498	AI768677	Hs.209888 ESTs; Weakly similar to phosphatidylserine synthase-2 [M.musculus]	0.128
60	338499		CH22_FGENES.833_4	0.128
	320087	AF032387	Hs.113265 small nuclear RNA activating complex; polypeptide 4; 190kD	0.128
	309989	AI184188	Hs.197813 ESTs	0.128
	301490	AW298468	Hs.250461 ESTs	0.128
	337011		CH22_FGENES.427-6	0.128
65	315052	AA876910	Hs.134427 ESTs	0.128
	301611	W22172	Hs.59038 ESTs	0.128
	336497		CH22_FGENES.833_2	0.129
	302068	Y16280	Hs.132049 endothelin type b receptor-like protein 2	0.129
	334502		CH22_FGENES.397_18	0.129

5	304332	AA158884	EST singleton (not in UniGene) with exon hit	0.129
	304522	AA485405	EST singleton (not in UniGene) with exon hit	0.129
	312407	R46180	Hs.153485 ESTs	0.129
	310098	AI685841	Hs.161354 ESTs	0.129
	301119	AF142579	EST cluster (not in UniGene) with exon hit	0.129
10	309268	AI985821	Hs.62954 ferritin; heavy polypeptide 1	0.129
	330989	H42142	Hs.226396 DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 19 (Dbp5; yeast; homolog)	0.129
	336949		CH22_FGENES.361-4	0.129
	330115		CH.19_p2 g 6015202	0.129
	339212		CH22_FF113D11.GENSCAN.6-7	0.129
15	326951		CH.21_hs g 6004446	0.129
	305165	AA682939	EST singleton (not in UniGene) with exon hit	0.129
	308238	AI559492	EST singleton (not in UniGene) with exon hit	0.129
	337140		CH22_FGENES.537-5	0.13
	321758	U29112	EST cluster (not in UniGene)	0.13
20	304619	AA515554	Hs.119598 ribosomal protein L3	0.13
	312469	AA745289	Hs.173088 ESTs	0.13
	339017		CH22_DA59H18.GENSCAN.20-6	0.13
	330116		CH.19_p2 g 6015202	0.13
	333312		CH22_FGENES.138_4	0.13
25	338004		CH22_EM:AC005500.GENSCAN.121-1	0.13
	314141	AA232134	Hs.190028 ESTs	0.13
	300509	AI239845	Hs.128494 ESTs; Weakly similar to EG-95B7.2 [D.melanogaster]	0.13
	338530		CH22_EM:AC005500.GENSCAN.398-11	0.13
	335968		CH22_FGENES.652_1	0.13
30	314121	AI732100	Hs.187619 ESTs	0.13
	337593		CH22_C20H12.GENSCAN.8-8	0.13
	332881		CH22_FGENES.33_1	0.13
	305836	AA858043	EST singleton (not in UniGene) with exon hit	0.13
	339059		CH22_DA59H18.GENSCAN.30-5	0.13
35	305610	AA782319	EST singleton (not in UniGene) with exon hit	0.13
	305852	AA862455	EST singleton (not in UniGene) with exon hit	0.13
	327409		CH.02_hs g 5887750	0.13
	312751	AI613089	Hs.164178 ESTs	0.13
	308726	AI789268	Hs.209929 EST	0.13
40	325961		CH.16_hs g 5887147	0.13
	311159	AW025919	Hs.187636 ESTs	0.13
	322715	AA057230	Hs.182135 ESTs	0.13
	338441		CH22_FGENES.827_7	0.13
	336339		CH22_FGENES.814_12	0.13
45	306911	AI095365	EST singleton (not in UniGene) with exon hit	0.13
	333613		CH22_FGENES.217_8	0.13
	338489		CH22_EM:AC005500.GENSCAN.384-17	0.131
	326904		CH.21_hs g 5867684	0.131
	337337		CH22_FGENES.717-1	0.131
50	326752		CH.20_hs g 5867615	0.131
	303977	AW512978	EST singleton (not in UniGene) with exon hit	0.131
	301373	AA595235	EST cluster (not in UniGene) with exon hit	0.131
	338448		CH22_EM:AC005500.GENSCAN.359-22	0.131
	333774		CH22_FGENES.272_5	0.131
55	332988		CH22_FGENES.54_8	0.131
	335362		CH22_FGENES.541_12	0.131
	335898		CH22_FGENES.635_4	0.131
	337825		CH22_EM:AC005500.GENSCAN.13-19	0.131
	325257		CH.11_hs g 5866895	0.131
60	331188	T50240	Hs.167837 ESTs	0.131
	330645	Y08302	Hs.144879 dual specificity phosphatase 9	0.131
	331760	AA292721	Hs.154434 ESTs; Weakly similar to unknown [H.sapiens]	0.131
	322995	AA513829	Hs.28797 ribosomal protein L10	0.131
	335497		CH22_FGENES.571_5	0.131
65	334824		CH22_FGENES.437_6	0.131
	319480	R06933	Hs.184221 ESTs	0.131
	334842		CH22_FGENES.439_21	0.131
	333335		CH22_FGENES.139_4	0.131
	317252	AA905178	Hs.130124 ESTs	0.131
	329034		CH.X_hs g 5868561	0.131
	305188	AA664230	EST singleton (not in UniGene) with exon hit	0.131
	335755		CH22_FGENES.604_4	0.131

	302143	H15270	Hs.189847	putative neuronal cell adhesion molecule	0.131
	334939			CH22_FGENES.465_3	0.131
	318994	C15110	Hs.17802	ESTs	0.131
5	334498			CH22_FGENES.397_14	0.131
	333413			CH22_FGENES.146_2	0.132
	329676			CH.14_p2 gi 8272128	0.132
	327277			CH.01_hs gi 5867473	0.132
	305022	AA627416		EST singleton (not in UniGene) with exon hit	0.132
10	336805			CH22_FGENES.196-3	0.132
	320121	T83657		EST cluster (not in UniGene)	0.132
	334761			CH22_FGENES.428_10	0.132
	339400			CH22_BA232E17.GENSCAN.7-6	0.132
	330301			CH.06_p2 gi 2905862	0.132
15	316822	AA827691	Hs.129957	ESTs; Weakly similar to neuronal thread protein	
				AD7c-NTP [H.sapiens]	0.132
	328020			CH.06_hs gi 5902482	0.132
	325327			CH.11_hs gi 5866875	0.132
	321163	AA209530		EST cluster (not in UniGene)	0.132
20	336393			CH22_FGENES.823_5	0.132
	325905			CH.18_hs gi 5867104	0.132
	305237	AA676286	Hs.2186	eukaryotic translation elongation factor 1 gamma	0.132
	339048			CH22_DA59H18.GENSCAN.28-6	0.132
	325375			CH.12_hs gi 5866920	0.132
25	333981			CH22_FGENES.304_7	0.132
	335450			CH22_FGENES.562_8	0.133
	302286	R58438		EST cluster (not in UniGene) with exon hit	0.133
	335116			CH22_FGENES.496_3	0.133
	327333			CH.01_hs gi 5902477	0.133
30	308070	A470948		EST singleton (not in UniGene) with exon hit	0.133
	308311	AI581855		EST singleton (not in UniGene) with exon hit	0.133
	320813	AW360847	Hs.208839	ESTs	0.133
	323665	AW248307		EST cluster (not in UniGene)	0.133
	328318			CH.07_hs gi 5868373	0.133
35	320603	R51419		EST cluster (not in UniGene)	0.133
	332791			CH22_FGENES.3_1	0.133
	314976	AA524725	Hs.162108	ESTs	0.133
	303309	AL134164	Hs.224868	ESTs	0.133
	320581	R39763	Hs.170187	ESTs	0.133
40	333944			CH22_FGENES.302_2	0.133
	317992	AI733512	Hs.130901	ESTs	0.133
	330935	F02383	Hs.26492	beta-1,3-glucuronyltransferase 3 (glucuronosyltransferase I)	0.133
	336659			CH22_FGENES.36-5	0.133
	338887			CH22_DJ32I10.GENSCAN.6-10	0.133
45	305273	AA679979	Hs.181165	eukaryotic translation elongation factor 1 alpha 1	0.133
	333566			CH22_FGENES.183_2	0.134
	316952	AW450033	Hs.163312	ESTs	0.134
	333818			CH22_FGENES.283_1	0.134
	328687			CH.07_hs gi 5868262	0.134
50	302879	H11802		EST cluster (not in UniGene) with exon hit	0.134
	336557			CH22_FGENES.842_2	0.134
	335222			CH22_FGENES.513_5	0.134
	338094			CH22_EM:AC005500.GENSCAN.179-3	0.134
	337384			CH22_FGENES.745-1	0.134
55	327360			CH.01_hs gi 6552411	0.134
	328132			CH.06_hs gi 5868038	0.134
	323604	AI751438	Hs.182827	ESTs; Weakly similar to !!!! ALU SUBFAMILY SQ	
				WARNING ENTRY !!!!	0.134
	337591			CH22_C20H12.GENSCAN.6-6	0.134
60	307018	AI140639		EST singleton (not in UniGene) with exon hit	0.134
	326898			CH21_hs gi 5867680	0.134
	333479			CH22_FGENES.163_5	0.134
	337915			CH22_EM:AC005500.GENSCAN.61-3	0.134
	335110			CH22_FGENES.494_18	0.134
65	333481			CH22_FGENES.163_9	0.134
	327512			CH.02_hs gi 8117815	0.134
	300096	AW328639	Hs.83575	ESTs; Weakly similar to ZC328.3 [C.elegans]	0.134
	330163			CH.02_p2 gi 6042042	0.135
	335752			CH22_FGENES.604_1	0.135
	334857			CH22_FGENES.443_1	0.135

	301872	H84730	EST cluster (not in UniGene) with exon hit	0.135
	337529		CH22_FGENES.823-29	0.135
	335734		CH22_FGENES.601_4	0.135
	337551		CH22_FGENES.847-8	0.135
5	309078	AI920965	Hs.77961 major histocompatibility complex, class I; B	0.135
	335513		CH22_FGENES.571_28	0.135
	339078		CH22_DA59H18.GENSCAN.37-6	0.135
	321807	N56660	Hs.148722 ESTs; Weakly similar to large tumor suppressor 1 [H.sapiens]	0.135
	337189		CH22_FGENES.571-32	0.135
10	329635		CH.12_p2 gi 5302817	0.135
	308601	AI718930	EST singleton (not in UniGene) with exon hit	0.135
	305020	AA627248	Hs.2084 vimentin	0.135
	333894		CH22_FGENES.293_1	0.135
15	322465	AA137152	Hs.3784 ESTs; Highly similar to phosphoserine aminotransferase [H.sapiens]	0.135
	305601	AA780975	EST singleton (not in UniGene) with exon hit	0.135
	332186	H10781	Hs.141051 ESTs; Moderately similar to IIII ALU SUBFAMILY SB WARNING ENTRY	0.135
	327822		CH.05_hs gi 5867868	0.135
20	310087	AI393914	Hs.160624 ESTs; Weakly similar to similar to CR16; SH3 domain binding protein	0.135
	328752		CH.07_hs gi 5868298	0.135
	337611		CH22_C20H12.GENSCAN.19-4	0.135
25	334470		CH22_FGENES.394_1	0.136
	335115		CH22_FGENES.496_2	0.136
	328730		CH.07_hs gi 5868289	0.136
	330350		CH.09_p2 gi 3056622	0.136
	336971		CH22_FGENES.378-6	0.136
30	308258	AI565612	EST singleton (not in UniGene) with exon hit	0.136
	326745		CH.20_hs gi 5867611	0.136
	335440		CH22_FGENES.560_3	0.136
	320257	AA330746	EST cluster (not in UniGene)	0.136
	328677		CH.07_hs gi 5868256	0.136
	329731		CH.14_p2 gi 6065783	0.136
35	315950	AA700553	Hs.208974 ESTs	0.136
	330049		CH.17_p2 gi 4567182	0.136
	337070		CH22_FGENES.448-3	0.136
	304095	H11324	Hs.31059 EST	0.136
40	309304	AW005527	Hs.232820 EST	0.136
	333458		CH22_FGENES.157_7	0.136
	329899		CH.15_p2 gi 6563505	0.136
	322202	AI275056	Hs.200133 ESTs	0.136
	333991		CH22_FGENES.310_15	0.136
45	318617	AW247252	Hs.75514 nucleoside phosphorylase	0.136
	310623	AI341586	Hs.185588 ESTs	0.136
	330489	M23323	Hs.3003 CD3E antigen; epsilon polypeptide (TTT3 complex)	0.136
	309646	AW194694	EST singleton (not in UniGene) with exon hit	0.136
	331068	R00071	Hs.191199 ESTs	0.136
	334285		CH22_FGENES.369_15	0.136
50	332178	F13689	Hs.100725 EST	0.136
	305724	AA827608	EST singleton (not in UniGene) with exon hit	0.136
	303158	AL138110	Hs.8594 Homo sapiens mRNA containing (CAG)4 repeat; clone CZ-CAG-7	0.136
	334543		CH22_FGENES.403_8	0.136
55	335384		CH22_FGENES.543_26	0.136
	338527		CH22_FGENES.839_8	0.136
	334951		CH22_FGENES.485_20	0.136
	325882		CH.16_hs gi 5867087	0.137
	305134	AA653159	EST singleton (not in UniGene) with exon hit	0.137
	307058	AI148709	EST singleton (not in UniGene) with exon hit	0.137
60	331943	AA453418	Hs.178272 ESTs	0.137
	331116	R44780	Hs.22634 ESTs	0.137
	306094	AA908877	EST singleton (not in UniGene) with exon hit	0.137
	333581		CH22_FGENES.180_18	0.137
65	321439	H61962	EST cluster (not in UniGene)	0.137
	324594	AA497090	EST cluster (not in UniGene)	0.137
	337926		CH22_EM:AC005500.GENSCAN.77-4	0.137
	337353		CH22_FGENES.728-1	0.137
	331838	AA412295	Hs.104774 EST	0.137
	308981	AI873242	EST singleton (not in UniGene) with exon hit	0.137

	329424		CH.Y_hs g 5868879	0.137
	325829		CH.15_hs g 5867052	0.137
	331845	AA416863	Hs.98183 ESTs	0.137
	333854		CH22_FGENES.290_13	0.137
5	306591	AI000248	EST singleton (not in UniGene) with exon hit	0.137
	328948		CH.08_hs g 58456765	0.137
	338935		CH22_DJ3210.GENSCAN.18-12	0.137
	325960		CH.18_hs g 5867147	0.137
	328377		CH.07_hs g 5868390	0.138
10	308851	AI829820	EST singleton (not in UniGene) with exon hit	0.138
	314620	AA424352	Hs.210588 ESTs	0.138
	337592		CH22_C20H12.GENSCAN.6-7	0.138
	338684		CH22_EM:AC005500.GENSCAN.472-3	0.138
15	331800	AA400498	Hs.97543 ESTs	0.138
	304587	AA505535	EST singleton (not in UniGene) with exon hit	0.138
	333981		CH22_FGENES.310_4	0.138
	332452	AA040369	SYT interacting protein	0.138
	305752	AA835278	EST singleton (not in UniGene) with exon hit	0.138
	311947	T65554	Hs.251591 EST	0.138
20	333783		CH22_FGENES.273_5	0.138
	337406		CH22_FGENES.754-14	0.138
	327976		CH.08_hs g 5868212	0.138
	325593		CH.13_hs g 5866892	0.138
	339425		CH22_DJ579N16.GENSCAN.14-4	0.138
25	304475	AA428879	EST singleton (not in UniGene) with exon hit	0.138
	309488	AW131104	EST singleton (not in UniGene) with exon hit	0.138
	337532		CH22_FGENES.827-8	0.138
	317234	AA804448	Hs.126368 ESTs	0.138
	312261	AA854425	Hs.144455 ESTs	0.138
30	328927		CH.08_hs g 5868500	0.138
	336424		CH22_FGENES.824_9	0.138
	326867		CH.20_hs g 5552455	0.138
	325988		CH.16_hs g 5867064	0.138
	318446	AW300287	EST cluster (not in UniGene)	0.139
35	338511		CH22_FGENES.834_6	0.139
	335204		CH22_FGENES.508_13	0.139
	303244	AA147472	EST cluster (not in UniGene) with exon hit	0.139
	330870	AA115804	Hs.187593 ESTs	0.139
	329378		CH.X_hs g 5868859	0.139
40	304703	AA563898	EST singleton (not in UniGene) with exon hit	0.139
	333653		CH22_FGENES.239_2	0.139
	306799	AI051696	EST singleton (not in UniGene) with exon hit	0.139
	304872	AA595289	EST singleton (not in UniGene) with exon hit	0.139
	330812	AA013001	Hs.60563 ESTs	0.139
45	329568		CH.10_p2 g 3982490	0.139
	319210	AA253074	Hs.146261 ESTs	0.139
	334320		CH22_FGENES.374_5	0.139
	300860	AI916949	Hs.149748 ESTs; Weakly similar to weak similarity to collagens [C.elegans]	0.139
	305868	AA864533	EST singleton (not in UniGene) with exon hit	0.139
50	312943	AA984364	Hs.119064 ESTs	0.139
	330523	M99439	Hs.83958 transducin-like enhancer of split 4; homolog of Drosophila E(sp1)	0.139
	312708	AI076204	Hs.135440 ESTs	0.139
	309366	AW072970	EST singleton (not in UniGene) with exon hit	0.139
	303273	AA316069	EST cluster (not in UniGene) with exon hit	0.139
55	317484	AW274696	Hs.143921 ESTs	0.139
	333239		CH22_FGENES.111_1	0.139
	307126	AI184951	EST singleton (not in UniGene) with exon hit	0.139
	316813	AA826505	Hs.124517 ESTs	0.139
	331746	AA281365	Hs.121640 ESTs; Weakly similar to KIAA0386 [H.sapiens]	0.139
60	308558	AI700145	Hs.172182 poly(A)-binding protein; cytoplasmic 1	0.139
	310784	AW086142	Hs.159017 ESTs	0.139
	323831	AA335715	Hs.200299 ESTs	0.139
	307692	AI318342	EST singleton (not in UniGene) with exon hit	0.139
	310570	AI318327	EST cluster (not in UniGene)	0.139
65	327834		CH.06_hs g 5868184	0.139
	305232	AA670052	Hs.195188 glyceraldehyde-3-phosphate dehydrogenase	0.139
	334756		CH22_FGENES.428_5	0.139
	331938	AA451867	Hs.99255 ESTs	0.139
	301393	AA474722	Hs.150898 ESTs; Weakly similar to KIAA0644 protein [H.sapiens]	0.139

	312005	T78450	Hs.13941	ESTs	0.139
	338431			CH22_EM:AC005500.GENSCAN.351-4	0.14
	331214	T90496	Hs.16757	ESTs	0.14
	333601			CH22_FGENES.213_4	0.14
5	323481	AA278449	Hs.137429	ESTs	0.14
	336911			CH22_FGENES.344-4	0.14
	338157			CH22_EM:AC005500.GENSCAN.209-5	0.14
	327845			CH.05_hs g 5531962	0.14
10	319109	Z45662	Hs.90797	Homo sapiens clone 23620 mRNA sequence	0.14
	334763			CH22_FGENES.428_12	0.14
	329384			CH.X_hs g 5868869	0.14
	302986	AF054663		EST cluster (not in UniGene) with exon hit	0.14
	323751	AW452656	Hs.209824	ESTs	0.14
	329916			CH.16_p2 g 6223624	0.14
15	301983	N49826	Hs.18602	ESTs	0.14
	338129			CH22_EM:AC005500.GENSCAN.197-2	0.14
	325704			CH.14_hs g 5867028	0.14
	335656			CH22_FGENES.590_7	0.14
	331673	W72366	Hs.40033	ESTs	0.14
20	316807	AJ018331	Hs.172444	ESTs; Highly similar to transcription regulator [M.musculus]	0.14
	310743	AW449754	Hs.158665	ESTs	0.14
	326941			CH.21_hs g 6004446	0.14
	328809			CH.07_hs g 5868327	0.14
	323855	AJ653164	Hs.128665	ESTs	0.14
25	304705	AA564064		EST singleton (not in UniGene) with exon hit	0.14
	325666			CH.14_hs g 6469822	0.14
	333747			CH22_FGENES.265_6	0.14
	318287	AW015616	Hs.143321	ESTs	0.141
	332972			CH22_FGENES.51_5	0.141
30	305704	AA825266		EST singleton (not in UniGene) with exon hit	0.141
	315699	AW182805	Hs.189183	ESTs; Weakly similar to Nod1 [H.sapiens]	0.141
	327286			CH.01_hs g 5867492	0.141
	336400			CH22_FGENES.823_15	0.141
	321033	H26214	Hs.20733	ESTs; Weakly similar to IIII ALU SUBFAMILY SX WARNING ENTRY	0.141
35	316522	AJ475995	Hs.122910	ESTs	0.141
	335715			CH22_FGENES.599_15	0.141
	335959			CH22_FGENES.650_2	0.141
	333259			CH22_FGENES.118_7	0.141
40	337382			CH22_FGENES.744-8	0.141
	322346	AA227618	Hs.10882	HMG-box containing protein 1	0.141
	325378			CH.12_hs g 5866920	0.141
	338500			CH22_EM:AC005500.GENSCAN.390-1	0.141
	338460			CH22_EM:AC005500.GENSCAN.362-5	0.141
45	315279	AW511138	Hs.256581	ESTs	0.141
	314439	AJ539443	Hs.137447	ESTs	0.141
	333624			CH22_FGENES.222_3	0.141
	329237			CH.X_hs g 5868729	0.141
	330117			CH.19_p2 g 6015201	0.141
50	338017			CH22_EM:AC005500.GENSCAN.134-1	0.141
	337854			CH22_EM:AC005500.GENSCAN.38-12	0.142
	329984			CH.16_p2 g 4646193	0.142
	305004	AA622328	Hs.162762	EST	0.142
55	302815	N40373		EST cluster (not in UniGene) with exon hit	0.142
	327823			CH.05_hs g 5867968	0.142
	326753			CH.20_hs g 5867616	0.142
	301201	AA904482	Hs.197775	ESTs	0.142
	334303			CH22_FGENES.373_6	0.142
	326453			CH.19_hs g 5867399	0.142
60	311050	AJ864581	Hs.215477	ESTs	0.142
	308740	AJ802711	Hs.210337	EST; Weakly similar to aldolase A [H.sapiens]	0.142
	331003	H63959	Hs.142722	ESTs	0.142
	338010			CH22_EM:AC005500.GENSCAN.128-8	0.142
	336326			CH22_FGENES.812_4	0.142
65	318100	R44308	Hs.242302	ESTs	0.142
	320641	R55421		EST cluster (not in UniGene)	0.142
	325855			CH.16_hs g 5867067	0.142
	330425	HG1728-HT1734		Non-Specific Cross Reacting Antigen (Gb:D90277), Alt. Splice Form 2	0.142

	324583	AA425411	Hs.22581	ESTs	0.142
	326268			CH.17_hs gij5867267	0.142
	331390	AA460341	Hs.45008	ESTs	0.142
5	338904			CH22_DJ32110.GENSCAN.10-18	0.143
	333098			CH22_FGENES.79_1	0.143
	331919	AA446869	Hs.119316	ESTs	0.143
	312214	AI248004	Hs.125187	ESTs	0.143
	323198	AW179174	Hs.7984	ESTs	0.143
10	316107	AI204001	Hs.184014	ribosomal protein L31	0.143
	301335	AA885317	Hs.180511	ESTs	0.143
	337392			CH22_FGENES.747-3	0.143
	325543			CH.12_hs gij6682452	0.143
	305903	AA873085		EST singleton (not in UniGene) with exon hit	0.143
15	332707	L35594	Hs.174185	phosphodiesterase 1/nucleotide pyrophosphatase 2 (autotaxin)	0.143
	337913			CH22_EM:AC005500.GENSCAN.59-10	0.143
	301438	AA961061	Hs.131696	ESTs	0.143
	335078			CH22_FGENES.488_5	0.143
	338451			CH22_EM:AC005500.GENSCAN.359-39	0.143
20	302777	AI230640		EST cluster (not in UniGene) with exon hit	0.143
	330464	J03068	Hs.78223	N-acylaminocaprylate-peptide hydrolase	0.143
	330988	H41411	Hs.33855	ESTs	0.143
	328939			CH.08_hs gij6004481	0.143
	308015	AI440174	Hs.228907	EST; Weakly similar to GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE PROTEIN	0.143
25				12.3 [H.sapiens]	0.143
	328504			CH.07_hs gij5868471	0.143
	332589	AA402891	Hs.32951	solute carrier family 29 (nucleoside transporters); member 2	0.143
	335744			CH22_FGENES.601_15	0.143
30	322394	AF077208		EST cluster (not in UniGene)	0.143
	323892	AL042661		EST cluster (not in UniGene)	0.143
	318443	AI939323	Hs.157714	ESTs; Weakly similar to NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN; ALPHA-5 CHAIN PRECURSOR	0.143
				[H.sapiens]	0.143
35	338588			CH22_FGENES.843_7	0.143
	330958	H08815	Hs.159824	EST	0.143
	327672			CH.04_hs gij5867843	0.143
	335900			CH22_FGENES.635_8	0.144
	336044			CH22_FGENES.679_6	0.144
40	318845	AI815951	Hs.33183	ESTs; Weakly similar to estrogen-responsive finger protein; efp [H.sapiens]	0.144
	333483			CH22_FGENES.165_2	0.144
	333337			CH22_FGENES.139_6	0.144
	305993	AA889197		EST singleton (not in UniGene) with exon hit	0.144
45	335719			CH22_FGENES.599_22	0.144
	325682			CH.14_hs gij6138823	0.144
	327350			CH.01_hs gij6249563	0.144
	339291			CH22_BA354112.GENSCAN.18-1	0.144
	326358			CH.18_hs gij5867293	0.144
50	330316			CH.08_p2 gij6007576	0.144
	308150	AI499348	Hs.174131	ribosomal protein L6	0.144
	338065			CH22_EM:AC005500.GENSCAN.184-1	0.144
	339009			CH22_DA59H18.GENSCAN.18-7	0.144
	327776			CH.05_hs gij5867964	0.145
55	338664			CH22_FGENES.41-8	0.145
	321921	AF070619		EST cluster (not in UniGene)	0.145
	318348	T70147	Hs.12024	ESTs	0.145
	304265	AA062892		EST singleton (not in UniGene) with exon hit	0.145
	303818	Z45986	Hs.250178	copine II	0.145
60	327498			CH.02_hs gij6017023	0.145
	335227			CH22_FGENES.513_13	0.145
	339022			CH22_DA59H18.GENSCAN.22-1	0.145
	302597	H55681	Hs.33026	ESTs; Weakly similar to similar to Enterococcus faecalis TRAB [C.elegans]	0.145
65	308550	AI697008	Hs.201811	EST	0.145
	302175	AA262760	Hs.156015	Homo sapiens chromosome 19; cosmid R29381	0.145
	303252	AA158760		EST cluster (not in UniGene) with exon hit	0.145
	337414			CH22_FGENES.757-2	0.145
	310382	AI734009		EST cluster (not in UniGene)	0.145
	329333			CH.X_hs gij5868808	0.145

	336857		CH22_FGENES.291-7	0.145
	332585	AA234896	Hs.25272 E1A binding protein p300	0.145
	318634	AI928098	Hs.156832 ESTs	0.145
5	336318		CH22_FGENES.801_1	0.145
	310960	AI923551	Hs.170843 ESTs	0.145
	335346		CH22_FGENES.537_2	0.145
	331196	T65416	Hs.12826 ESTs	0.145
	337607		CH22_C20H12.GENSCAN.17-3	0.146
10	331206	T84096	Hs.15284 ESTs	0.146
	301793	T80698	EST cluster (not in UniGene) with exon hit	0.146
	319590	AA210878	EST cluster (not in UniGene)	0.146
	311394	AI695374	Hs.256231 ESTs	0.146
	324773	AA632554	Hs.163401 ESTs	0.146
15	324841	AI142359	Hs.155316 ESTs	0.146
	332260	N70088	Hs.138467 ESTs	0.146
	329276		CHX_hs gjl5868762	0.146
	335887		CH22_FGENES.633_1	0.146
	338294		CH22_EM:AC005500.GENSCAN.297-1	0.146
20	336993		CH22_FGENES.409-4	0.146
	334135		CH22_FGENES.336_2	0.146
	326251		CH.17_hs gjl5867263	0.146
	337396		CH22_FGENES.749-1	0.146
	339167		CH22_DA59H18.GENSCAN.69-8	0.146
25	316838	AW135418	Hs.161210 ESTs	0.146
	325313		CH.11_hs gjl5866865	0.146
	331047	N68918	Hs.32205 ESTs	0.146
	323915	AL043362	EST cluster (not in UniGene)	0.146
	302747	AF062275	EST cluster (not in UniGene) with exon hit	0.146
30	306317	AA947909	EST singleton (not in UniGene) with exon hit	0.146
	334399		CH22_FGENES.382_5	0.146
	326472		CH.19_hs gjl5867404	0.146
	333061		CH22_FGENES.75_4	0.146
	337072		CH22_FGENES.448-5	0.146
35	334328		CH22_FGENES.375_5	0.146
	327039		CH.21_hs gjl6531965	0.146
	325576		CH.12_hs gjl6552443	0.147
	315935	AI075804	Hs.132660 ESTs	0.147
	319638	AA323758	EST cluster (not in UniGene)	0.147
40	334501		CH22_FGENES.397_17	0.147
	336238		CH22_EM:AC005500.GENSCAN.264-4	0.147
	308636	AI744063	EST singleton (not in UniGene) with exon hit	0.147
	336557		CH22_FGENES.843_6	0.147
	335819		CH22_FGENES.619_2	0.147
45	336950		CH22_FGENES.381-8	0.147
	307055	AI148477	EST singleton (not in UniGene) with exon hit	0.147
	315134	AW504854	Hs.126714 ESTs	0.147
	335834		CH22_FGENES.621_1	0.147
	327870		CH.06_hs gjl5868131	0.147
50	323802	AA332011	Hs.250138 protein phosphatase 2C; magnesium-dependent; catalytic subunit	0.147
	329412		CHX_hs gjl6882553	0.147
	323791	AA333068	EST cluster (not in UniGene)	0.147
	324126	AA385315	EST cluster (not in UniGene)	0.147
	327865		CH.06_hs gjl5868130	0.147
	333445		CH22_FGENES.154_2	0.147
55	321302	AA021351	Hs.158497 KIAA0724 gene product	0.147
	336744		CH22_FGENES.118-9	0.147
	323731	AA323414	EST cluster (not in UniGene)	0.148
	320289	H07989	EST cluster (not in UniGene)	0.148
60	305488	AA749000	EST singleton (not in UniGene) with exon hit	0.148
	305592	AA780594	Hs.62954 ferritin; heavy polypeptide 1	0.148
	304094	H11295	EST singleton (not in UniGene) with exon hit	0.148
	325040	AW296368	EST cluster (not in UniGene)	0.148
	339034		CH22_DA59H18.GENSCAN.26-2	0.148
65	334504		CH22_FGENES.398_2	0.148
	334778		CH22_FGENES.431_2	0.148
	320148	U77494	Hs.119687 RAN binding protein 8	0.148
	303584	AW173759	Hs.203401 ESTs	0.148
	325828		CH.15_hs gjl5867048	0.148
	331192	T55182	Hs.152571 ESTs; Highly similar to IGF-II mRNA-binding protein 2 [H.sapiens]	0.148

	325785		CH.14_hs gi 6381957	0.148
	333168		CH22_FGENES.91_8	0.148
	336548		CH22_FGENES.841_5	0.148
	337552		CH22_C4G1.GENSCAN.1-4	0.148
5	331775	AA382742	Hs.97151 EST	0.148
	338938		CH22_DJ3210.GENSCAN.19-6	0.148
	331869	AA428554	Hs.104894 ESTs; Weakly similar to fibronectin precursor [H.sapiens]	0.148
	332885		CH22_FGENES.28_5	0.148
10	328663		CH.07_hs gi 6004473	0.148
	328438		CH.07_hs gi 5868417	0.148
	311158	AI634884	Hs.250789 ESTs; Highly similar to similar to NEDD-4 [H.sapiens]	0.148
	338942		CH22_FGENES.354-2	0.148
	302262	R53169	Hs.246091 ESTs	0.149
	333296		CH22_FGENES.132_3	0.149
15	333385		CH22_FGENES.142_2	0.149
	311706	AW452392	Hs.252854 ESTs	0.149
	337109		CH22_FGENES.489-2	0.149
	315082	AW173300	Hs.180201 ESTs	0.149
20	333454		CH22_FGENES.157_3	0.149
	334784		CH22_FGENES.432_9	0.149
	333255		CH22_FGENES.118_3	0.149
	337618		CH22_FGENES.814-7	0.149
	320651	AA489268	EST cluster (not in UniGene)	0.149
25	323437	AA287567	EST cluster (not in UniGene)	0.149
	328761		CH.07_hs gi 5868302	0.149
	328787		CH.07_hs gi 5868309	0.149
	335261		CH22_FGENES.520_2	0.149
	300827	R16689	Hs.106004 ESTs	0.149
30	339283		CH22_BA354112.GENSCAN.10-1	0.149
	337412		CH22_FGENES.756-6	0.149
	334414		CH22_FGENES.384_1	0.149
	332931		CH22_FGENES.38_5	0.149
	310801	AW270980	Hs.106346 novel centrosomal protein RanBPM	0.149
35	305216	AA669058	EST singleton (not in UniGene) with exon hit	0.149
	314779	AA470122	Hs.180261 ESTs	0.149
	338414		CH22_EM:AC005500.GENSCAN.341-27	0.149
	303342	AW247361	EST cluster (not in UniGene) with exon hit	0.149
	337609		CH22_FGENES.806-4	0.149
40	306631	AI001149	EST singleton (not in UniGene) with exon hit	0.149
	302533	L36149	Hs.248116 chemokine (C motif) XC receptor 1	0.149
	336538		CH22_FGENES.839_18	0.149
	324666	T32458	Hs.14285 ESTs	0.149
	310173	AI767433	Hs.170013 ESTs	0.149
45	333595		CH22_FGENES.211_2	0.149
	335975		CH22_FGENES.652_9	0.15
	306654	AI003854	EST singleton (not in UniGene) with exon hit	0.15
	335025		CH22_FGENES.475_3	0.15
	328711		CH.07_hs gi 5868271	0.15
50	328274		CH.07_hs gi 5868219	0.15
	325505		CH.12_hs gi 6682451	0.15
	329641		CH.14_p2 gi 6468233	0.15
	304955	AA613504	EST singleton (not in UniGene) with exon hit	0.15
	339103		CH22_DA59H18.GENSCAN.44-10	0.15
	329638		CH.12_p2 gi 5302817	0.15
55	310118	AI203293	Hs.157489 ESTs	0.15
	326056		CH.17_hs gi 5867184	0.15
	303773	AA769074	EST cluster (not in UniGene) with exon hit	0.15
	303153	U09759	Hs.8325 mitogen-activated protein kinase 9	0.15

TABLE 13A shows the accession numbers for those primekeys lacking unigeneID's for Table 13. For each probeset we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

Pkey:	CAT number:	Accession:	Unique Eos probeset identifier number
			Gene cluster number
			Genbank accession numbers
Pkey	CAT number	Accession	
322050	24275_1	AL137589 AA423949 BE222949 BE222694 A1189615 AW873116 A1277950 AW044290 AW630096	
321439	1599424_1	H61982 W01567 N75711	
321666	13853_22	BE259906 AA232518 AA013359 AL035788 AW160822 BE387134 BE002954 BE391839 AW161565 A1878841 BE616458	
		BE409981 BE387308 BE297436 BE315536 AA206924 R12012 AA214169 BE312812 BE337093 H11710 BE312009	
		BE260569 AA343566 AA219526 R34757 AA219749 BE338733 AA219751 AW411099 AA232408 BE018716 BE398089	
		AA206253 AA053487 AA114224 AV655868 AW732566 BE394087 AW732574 AA313442 BE336875 AA070548 BE259840	
		BE019828 AW732341 AA289916 BE018253 BE018238 BE387109 AA232304 BE255589 AW732585 AA181436 AA308777	
		AA075802 AW732521 AA314526 AA226747 BE409513 AA206168 BE388292 BE298782 BE387086 AA305310 AV652723	
		AA314918 BE615510 AW951783 BE398104 BE385195 BE407165 BE391336 BE390187 BE389189 BE540650 BE249884	
		BE385985 BE274245 BE391124 BE260080 AA182600 BE512821 BE390090 BE279398 BE279589 BE263454 BE515194	
		BE293569 BE272531 BE388814 BE384659 BE271685 BE561043 BE278449 BE302572 AW239076 A1750583 AA376179	
		AA112632 BE266324 BE266614 R13105 AA132286 BE296305 A1220355 AA205606 AA219527 AA219519 AW804310	
		AA083286 BE171208 T18693 AA338328 BE185868 AA903024 T92162 AA330119 BE410404 BE314668	
	300088 622937_1	AW576245 BE207878 AW299993 A1199558 A1285442 AW299994 AW394242 AW394184	
	322303 704603_1	A1357412 A1870708 A1590539 W07459	
	322394 27492_1	AW068287 AA310079 BE336702 AA356318 AA306059 AA346785 AW402633 AA311210 AW402809 N76879 AW402913	
		AW401920 AA321636 AA354474 C17297 C16938 AA311774 M29871 NM_002872 ZB2188 AW405674 H94176 R89281	
		AA214723 A1014482 AW949347 T27749 AW804226 AW796954 AW404581 AF077208 NM_014029 W68830 W79652	
		AA353375 AW575218 AA552182 AA521232 AA702695 AA033975 AW407827 AA829948 N94402 AW628604 A1523308	
		N57605 AA641662 H42477 N52784 A1753478 AA768493 AA845729 W47391 N55270 A1090117 R89282 BE206172	
		AA076650 AA595650 A1218931 BE049397 A1433110 W74114 H94277 A1358627 A1085221 A1862818 AA835967 AW103905	
		A1840644 AA835507 AA856887 AA694392 AW337542 A1524410 BE045500 A1440060 A1358801 AW028238 AW205248	
		A1718264 R48618 AA357358 A1695002 AA897549 AW081065 A1433360 A1810783 A1620963 ZB2188 AA360224	
	321758 44275_1	U29112 A1656540 A1364875 A1656248 A8990940	
	323109 155498_1	AA169345 A1762857 A1949997 A1809601 A1681948 A1221079 AW167404 A1347614 A1611090 A1023472 A1347683 A1027487	
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		A1766842	
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	321821 34680_1	AF070619 R20302 T80358	
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		AA621975 A1587036 AA665743 AW204003 A1692234 A1002242 A1692219 AW137282 AW268783 AW285910 A1308015	
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		AW732776	
	321932 265316_1	N72324 N52825 W19526 BE143484 AA376060	
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		A1401544 BE327023 A1693383 A1769874 A1744003 AW082273 A1688501 A1798177 A1985196 A1090033 A1432342 A1589918	
		A1638308 BE468080 BE219588 A1912119 BE219787 AW005392 BE326564 A1589039 A1860187 A1758143 A1338168	
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5 AI498018 AI554124 AI239893 AI884054 AI280099 AI192815 AI620465 AI080201 AW002057 BE500988 AI341131 AI818991
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 AI275071 AA888601 BE042933 BE045713 AW087176
 60 324430 312113_1 AA464018 AA464079 AA468142
 323892 477253_1 AA846318 W15478 AL042661
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 302251 27218_4 AA333340 AW955834 R49755 U33428
 302286 22717_6 R58438 AA358612
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	338174 CH22_3567FG_710_1_LINK_DA	
	306094	AA908877
	304823	AA584837
20	304872	AA585289
	304818	AA602697
	304855	AA613504
	306249	AA833840
	306286	AA936892
25	306295	AA937331
	306317	AA947809
	306347	AA961144
	306365	AA962086
	306398	AA970548
30	330401 entrez_D28383	D28383
	330463 460_2	NM_001055 AA332848 U26309 U09031 L19855 L10819 AI366043 X84654 U71088 AV654451 AJ007418 AA053825
		BE168856 AA376730 H12694 AA810348 AA621972 AI818950 AV845387 AI818966 AA910602 AW512449 H67893 AI310497
		AJ304330 AI339217 AW193588 AW438688 AI818970 AW316799 AA906527 AA777570 N47673 AI336428 AW945133
		AI038608 R29692 AW194197 AI304748 H12639 AA053178 AA493213 AA676958 AA113154 AI313469 AI368239 R93183
		W24532 U52852 U54701 AL046864 AA365795
35	330535 1374_-8	U11872
	332634 10404_2	U24488 NM_007116

TABLE 13B shows the genomic positioning for those primekeys lacking unigene ID's and accession numbers in Table 13. For each predicted exon, we have listed the genomic sequence source used for prediction. Nucleotide locations of each predicted exon are also listed.

10 Pkey: Unique number corresponding to an Eos probeset
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers
 Strand: Indicates DNA strand from which exons were predicted.
 Nt_position: Indicates nucleotide positions of predicted exons.

	Pkey	Ref	Strand	Nt_position
15	332791	Dunham, I. et al.	Plus	72720-73315
	332792	Dunham, I. et al.	Plus	73381-73768
	332810	Dunham, I. et al.	Plus	304296-304384
20	332944	Dunham, I. et al.	Plus	2414825-2414932
	332972	Dunham, I. et al.	Plus	2572152-2572238
	333133	Dunham, I. et al.	Plus	3360058-3360195
	333154	Dunham, I. et al.	Plus	3615887-3616019
	333155	Dunham, I. et al.	Plus	3616832-3617003
	333227	Dunham, I. et al.	Plus	3992866-3992968
25	333230	Dunham, I. et al.	Plus	3995507-3996507
	333298	Dunham, I. et al.	Plus	4581537-4581947
	333304	Dunham, I. et al.	Plus	4629943-4630242
	333305	Dunham, I. et al.	Plus	4630388-4630645
	333365	Dunham, I. et al.	Plus	4786883-4787283
30	333383	Dunham, I. et al.	Plus	4907179-4907277
	333391	Dunham, I. et al.	Plus	4916697-4916780
	333392	Dunham, I. et al.	Plus	4918294-4918433
	333397	Dunham, I. et al.	Plus	4922466-4922635
	333403	Dunham, I. et al.	Plus	4925140-4925258
35	333413	Dunham, I. et al.	Plus	4943824-4943974
	333445	Dunham, I. et al.	Plus	5097827-5097885
	333479	Dunham, I. et al.	Plus	5272855-5272939
	333481	Dunham, I. et al.	Plus	5286358-5286505
40	333483	Dunham, I. et al.	Plus	5297945-5298105
	333516	Dunham, I. et al.	Plus	5570204-5570390
	333517	Dunham, I. et al.	Plus	5570729-5570925
	333518	Dunham, I. et al.	Plus	5571761-5572025
	333531	Dunham, I. et al.	Plus	5622622-5622684
	333566	Dunham, I. et al.	Plus	5954226-5954473
45	333572	Dunham, I. et al.	Plus	6026896-6027189
	333588	Dunham, I. et al.	Plus	6246834-6247314
	333588	Dunham, I. et al.	Plus	6255445-6255778
	333594	Dunham, I. et al.	Plus	6308990-6309450
	333595	Dunham, I. et al.	Plus	6323103-6323348
50	333600	Dunham, I. et al.	Plus	6355629-6355925
	333601	Dunham, I. et al.	Plus	6360075-6360442
	333607	Dunham, I. et al.	Plus	6504431-6504690
	333612	Dunham, I. et al.	Plus	6549563-6549697
	333613	Dunham, I. et al.	Plus	6550643-6550748
55	333614	Dunham, I. et al.	Plus	6551227-6551389
	333624	Dunham, I. et al.	Plus	6595146-6595244
	333626	Dunham, I. et al.	Plus	6614174-6614467
	333635	Dunham, I. et al.	Plus	6663683-6663973
	333637	Dunham, I. et al.	Plus	6674968-6675134
60	333642	Dunham, I. et al.	Plus	6708760-6709139
	333647	Dunham, I. et al.	Plus	6772502-6772779
	333653	Dunham, I. et al.	Plus	6811130-6811392
	333654	Dunham, I. et al.	Plus	6816731-6816893
	333656	Dunham, I. et al.	Plus	6822087-6822406
65	333657	Dunham, I. et al.	Plus	6831369-6831445
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	333684	Dunham, I. et al.	Plus	7168561-7169742
	333686	Dunham, I. et al.	Plus	7177117-7177302
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	333698	Dunham, I. et al.	Plus	7205279-7205383
	333699	Dunham, I. et al.	Plus	7206101-7206175
	333703	Dunham, I. et al.	Plus	7215559-7215663
	333709	Dunham, I. et al.	Plus	7229730-7229835
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10	333774	Dunham, I. et al.	Plus	7716509-7716636
	333775	Dunham, I. et al.	Plus	7729983-7730149
	333806	Dunham, I. et al.	Plus	7877475-7877666
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	333854	Dunham, I. et al.	Plus	8029446-8029524
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	333885	Dunham, I. et al.	Plus	8154352-8154437
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	333994	Dunham, I. et al.	Plus	8852749-8852894
	334030	Dunham, I. et al.	Plus	9288463-9288782
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	334111	Dunham, I. et al.	Plus	10279365-10279531
	334135	Dunham, I. et al.	Plus	10457085-10457183
	334218	Dunham, I. et al.	Plus	12680289-12680378
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	334328	Dunham, I. et al.	Plus	13588868-13589936
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	334851	Dunham, I. et al.	Plus	17820110-17820810
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	336568	Dunham, I. et al.	Plus	34428521-34428637
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	337109	Dunham, I. et al.	Plus	21166580-21166850
	337123	Dunham, I. et al.	Plus	22052874-22052942
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	337337	Dunham, I. et al.	Plus	30395182-30395285
	337353	Dunham, I. et al.	Plus	30804824-30804780
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	337532	Dunham, I. et al.	Plus	34187269-34187388
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	337835	Dunham, I. et al.	Plus	6534661-6534782
45	337944	Dunham, I. et al.	Plus	6589383-6589450
	337954	Dunham, I. et al.	Plus	6831483-6831620
	337996	Dunham, I. et al.	Plus	7445532-7445633
	338004	Dunham, I. et al.	Plus	7601363-7601520
	338016	Dunham, I. et al.	Plus	7863131-7863310
50	338174	Dunham, I. et al.	Plus	12771102-12771268
	338176	Dunham, I. et al.	Plus	12774072-12774223
	338238	Dunham, I. et al.	Plus	14681938-14682015
	338277	Dunham, I. et al.	Plus	16167622-16167962
	338294	Dunham, I. et al.	Plus	16463958-16464539
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	338324	Dunham, I. et al.	Plus	17155309-17155574
	338386	Dunham, I. et al.	Plus	18611213-18611407
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	338500	Dunham, I. et al.	Plus	21253847-21253974
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	338653	Dunham, I. et al.	Plus	24219427-24219509

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	338925	Dunham, I. et al.	Plus	28883892-28884036
	338936	Dunham, I. et al.	Plus	29148022-29148160
	338952	Dunham, I. et al.	Plus	29418831-29418968
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	339166	Dunham, I. et al.	Plus	32210902-32211008
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30	339288	Dunham, I. et al.	Plus	33169611-33169691
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	339291	Dunham, I. et al.	Plus	33205057-33205247
	339407	Dunham, I. et al.	Plus	34189461-34189620
	332865	Dunham, I. et al.	Minus	1391482-1391218
35	332881	Dunham, I. et al.	Minus	1563520-1563184
	332930	Dunham, I. et al.	Minus	2022585-2022497
	332931	Dunham, I. et al.	Minus	2023851-2023562
	332984	Dunham, I. et al.	Minus	2632606-2632457
	332986	Dunham, I. et al.	Minus	2635398-2635208
40	332997	Dunham, I. et al.	Minus	2710509-2710375
	333051	Dunham, I. et al.	Minus	2891873-2891840
	333061	Dunham, I. et al.	Minus	3029631-3029527
	333064	Dunham, I. et al.	Minus	3030722-3030623
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	329632	6729060	Plus	192813-193017
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	325375	5866920	Minus	1165503-1165810
10	325378	5866920	Minus	1187981-1188167
	325469	6017034	Plus	286823-286991
	325470	6017034	Plus	287578-287663
	325576	6552443	Minus	137769-137894
	325505	6682451	Minus	240852-240946
15	325543	6682452	Plus	151873-152057
	329635	5302817	Minus	62522-62622
	329636	5302817	Minus	64969-65078
	325593	5866992	Minus	469726-469860
	325675	5867014	Plus	955517-955711
20	325704	5867028	Plus	156198-156387
	325682	6138923	Plus	370618-370763
	325785	6381957	Plus	61849-62003
	325666	6469822	Plus	16769-16857
	325818	6682490	Minus	120278-120559
25	329777	6002090	Minus	191389-191479
	329768	6015501	Plus	118315-118422
	329769	6048280	Minus	37647-37730
	329731	6065783	Plus	158772-158900
	329687	6117856	Minus	22165-22288
30	329676	6272128	Minus	142207-142359
	329667	6272129	Plus	101355-101745
	329669	6272129	Plus	131223-131291
	329670	6272129	Plus	131351-131485
	329641	6468233	Minus	105995-106107
35	329791	6469354	Minus	131982-132089
	325826	5867048	Minus	46361-46458
	325829	5867052	Plus	232674-233060
	329888	6067149	Minus	37227-37473
	329893	6525313	Minus	166123-166791
40	329899	6563505	Minus	111058-111783
	325988	5867064	Plus	17349-17606
	325855	5867067	Plus	276141-276251
	325999	5867073	Plus	149115-149182
	326001	5867073	Plus	155223-155348
45	325886	5867087	Plus	194694-194915
	325882	5867087	Minus	8178-8347
	325905	5867104	Plus	78779-78876
	325922	5867122	Minus	329063-329134
	325937	5867132	Minus	152633-152902
50	325960	5867147	Minus	162506-162635
	325961	5867147	Minus	165106-165209
	325838	6552452	Plus	171451-171532
	325839	6552452	Plus	181964-182037
55	325840	6552452	Plus	184380-184547
	325844	6552453	Minus	14188-14332
	325870	6682492	Plus	228209-228297
	329984	4646193	Minus	139780-139890
	329976	4878063	Minus	62584-62691
	329935	6165200	Minus	69059-69127
60	329916	6223624	Plus	36396-37195
	330021	6671889	Plus	120938-121032
	330024	6671908	Minus	1005-1270
	330028	6671908	Minus	30015-30144
	326033	5867178	Plus	37261-37333
65	326036	5867178	Minus	120215-120273
	326056	5867184	Minus	181553-181690
	326118	5867193	Plus	45548-45604
	326122	5867194	Plus	144397-144683
	326138	5867203	Minus	179374-179436

	326145	5867204	Minus	52599-52814
	326180	5867211	Minus	182758-183222
	326201	5867216	Minus	166168-166959
	326207	5867222	Plus	48139-48219
5	326228	5867230	Plus	52644-52705
	326233	5867232	Plus	124788-124863
	326238	5867260	Plus	64282-64338
	326241	5867260	Minus	181648-181916
	326243	5867261	Plus	123838-123978
10	326251	5867283	Minus	82716-82822
	326268	5867267	Plus	122114-122765
	326124	5916395	Plus	407102-407560
	326339	6056311	Minus	164637-165251
	330049	4567182	Minus	314662-315210
15	326358	5867293	Plus	9122-9185
	326365	5867297	Minus	96630-96764
	326379	5867327	Plus	32289-32402
	326382	5867327	Minus	50420-50503
	326390	5867340	Minus	108814-110592
20	326424	5867369	Minus	168329-168409
	326453	5867399	Plus	86222-86423
	326472	5867404	Plus	293739-293940
	326492	5867422	Plus	120768-120991
	326533	5867441	Minus	532153-532280
25	330117	6015201	Minus	7340-7680
	330115	6015202	Plus	11403-11677
	330116	6015202	Plus	12109-12418
	330095	6015278	Plus	15343-15814
	330098	6015278	Plus	49370-49458
30	326644	5867559	Plus	42684-42819
	326713	5867595	Plus	121511-121798
	326745	5867611	Plus	127130-127318
	326752	5867615	Minus	1214-1582
	326753	5867618	Plus	12454-12511
35	326598	5867634	Plus	68955-69014
	326667	6552455	Plus	142311-142441
	326855	6552480	Minus	111390-111463
	326812	6682504	Plus	189811-189941
	327005	5867664	Plus	610847-610907
40	327008	5867664	Plus	928737-928811
	326996	5867680	Minus	12032-12122
	326904	5867684	Minus	9280-9608
	326951	6004446	Plus	183812-183998
	326941	6004446	Plus	62018-62898
45	326943	6004446	Minus	89242-89427
	326928	6456782	Minus	291007-291219
	326958	6468838	Minus	42952-43082
	326959	6468838	Minus	43159-43301
	327039	6531965	Plus	694486-694998
50	327127	6682520	Plus	41825-42083
	330158	6580387	Plus	81966-82458
	327204	5867447	Plus	165135-165239
	327208	5867447	Plus	180805-180864
	327268	5867482	Minus	82400-82615
55	327277	5867473	Minus	165816-165715
	327289	5867481	Plus	49286-49536
	327296	5867482	Plus	7627-8166
	327237	5867544	Minus	59702-59813
	327145	5867548	Minus	40482-40551
60	327333	5902477	Minus	141448-141609
	327335	5902477	Minus	142879-143124
	327343	6017017	Minus	12288-12395
	327350	6248563	Minus	41890-41985
	327358	6552411	Minus	3802-3950
65	327380	6552411	Minus	6255-6422
	327409	5867750	Minus	62949-63011
	327424	5867751	Plus	160442-160598
	327430	5867764	Plus	1320-1403
	327470	5867772	Plus	150910-150973

	327460	6004455	Plus	175245-175343
	327498	6017023	Minus	42178-42283
	327509	6117815	Minus	54882-55053
	327510	6117815	Minus	56824-56944
5	327512	6117815	Plus	176256-176325
	327535	6525279	Plus	19105-19175
	330163	6042042	Minus	20321-20385
	330171	6648220	Plus	110889-111575
10	327579	5867824	Minus	37229-38335
	327672	5867843	Minus	69649-69740
	327629	5867872	Plus	49692-49811
	327640	5867890	Plus	9448-9566
	327649	5867899	Plus	205871-205927
	327612	6525283	Plus	2747-2824
15	327718	6525284	Plus	86123-86188
	327801	5867824	Plus	23239-23348
	327762	5867961	Minus	50303-50439
	327763	5867961	Plus	228347-229476
	327776	5867964	Minus	164308-164486
20	327822	5867968	Minus	168886-169633
	327823	5867968	Minus	170359-170433
	327807	5867968	Plus	33745-33811
	327845	6531962	Plus	193402-193549
	330228	6013527	Minus	3719-3787
25	330190	6165182	Plus	36103-36243
	328122	5868031	Plus	158474-158656
	328132	5868038	Minus	126737-126839
	328159	5868065	Minus	52957-53182
	328168	5868071	Plus	60321-60479
30	328175	5868073	Plus	208-271
	328217	5868096	Minus	3742-4362
	327885	5868130	Plus	61503-62205
	327866	5868131	Minus	2893-3048
	327870	5868131	Plus	53558-53757
35	327879	5868142	Minus	77722-77793
	327902	5868158	Minus	133339-133467
	327918	5868165	Plus	547530-547591
	327934	5868184	Plus	41830-42036
40	327959	5868210	Minus	48497-48682
	327976	5868212	Minus	348301-349409
	328020	5902482	Minus	556386-556652
	328042	5902482	Minus	1985085-1986626
	328008	5902482	Plus	296663-297151
45	330301	2905862	Minus	4420-5781
	330299	2905881	Minus	1020-1362
	328274	5868219	Minus	31244-31439
	328585	5868224	Plus	148738-148967
	328591	5868227	Minus	237647-237726
50	328668	5868254	Minus	10888-10984
	328677	5868256	Minus	58708-58950
	328687	5868262	Plus	624479-624585
	328708	5868270	Plus	165501-165614
	328711	5868271	Minus	97797-97890
55	328730	5868289	Plus	8068-8214
	328732	5868289	Plus	37437-37550
	328734	5868289	Plus	50559-50747
	328752	5868298	Minus	114911-115087
	328755	5868301	Minus	145959-146446
60	328761	5868302	Minus	239308-239412
	328775	5868309	Plus	12845-12820
	328784	5868309	Minus	74523-74604
	328787	5868309	Plus	135772-135963
	328809	5868327	Plus	91792-91849
	328829	5868337	Plus	36309-36830
65	328830	5868352	Plus	160563-160631
	328311	5868371	Minus	170560-170826
	328318	5868373	Plus	414945-415620
	328323	5868373	Minus	1080089-1080235
	328348	5868383	Minus	260272-260379

	328377	5868390	Plus	16947-17023
	328436	5868417	Plus	203760-203904
	328504	5868471	Plus	47064-47217
	328506	5868471	Plus	60716-60830
5	328522	5868477	Plus	1972307-1972452
	328525	5868482	Plus	12387-14313
	328541	5868486	Plus	130956-131050
	328662	6004473	Plus	1184773-1184855
	328663	6004473	Plus	1185279-1186634
10	328803	6004475	Minus	291716-291948
	328304	6004478	Minus	3894-3952
	328927	5868500	Minus	428829-428893
	328936	5868500	Minus	1352202-1352259
	328939	6004481	Minus	131139-131320
15	328941	6456765	Minus	9817-9885
	328948	6456765	Plus	28227-28413
	328968	6456775	Plus	117442-118283
	330316	6007576	Minus	119761-119931
	330350	3056622	Minus	26413-26820
20	330351	3056622	Minus	27522-27614
	330348	4544475	Minus	19855-19962
	329034	5868561	Minus	32819-32939
	329046	5868569	Plus	18971-19030
	329053	5868574	Plus	426453-426541
25	329186	5868711	Minus	13108-13225
	329237	5868729	Plus	133238-133339
	329276	5868762	Minus	222629-222709
	329333	5868806	Plus	392866-392748
	329376	5868859	Plus	52356-52694
30	329384	5868869	Minus	116524-116662
	329140	6017060	Plus	290842-290905
	329317	6381976	Plus	614823-615208
	329319	6381976	Plus	721390-721470
	329129	6588026	Plus	144569-144712
35	329373	6682537	Minus	38950-39301
	329412	6682553	Minus	68948-69041
	329424	5868879	Plus	362196-362344
	329446	5868886	Plus	84776-84899
	329449	5868886	Plus	97697-97771

TABLE 14: shows genes, including expression sequence tags, down-regulated in prostate tumor tissue compared to normal prostate tissue as analyzed using Affymetrix/Eos Hu02 GeneChip array. Shown are the ratios of "average" normal prostate to "average" prostate cancer tissues.

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Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigeneID: Unigene number
 Unigene Title: Unigene gene title
 R1: Background subtracted normal prostate : prostate tumor tissue

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Pkey	ExAccn	UnigeneID	Unigene Title	R1
331328	AA281133	Hs.88808	ESTs	18.53
320875	D60641	Hs.131821	ESTs	14.55
300994	AI251936	Hs.146298	ESTs	12.17
323461	AA418762	Hs.190044	ESTs	10.55
301015	AA947682	Hs.217173	ESTs; Weakly similar to Chain A; Cdc42hs-Gdp Complex [H.sapiens]	10.17
318419	AA543098	Hs.13848	ESTs; Highly similar to mitogen-induced [M.musculus]	9.2
323486	C05278	Hs.166800	ESTs; Moderately similar to [PYRUVATE DEHYDROGENASE(LIPOAMIDE)] KINASE ISOZYME 4 PRECURSOR [H.sapiens]	8.87
324882	AW419080	Hs.250645	ESTs	8
330569	U57796	Hs.57679	zinc finger protein 192	7.88
330126			CH.21_p2 gl[6093735	7.8
316265	AA737400	Hs.142230	ESTs	7.7
323045	AA148950	Hs.188836	ESTs	7.64
320668	R58399	Hs.146217	ESTs	7.4
330769	AA465192	Hs.16514	ESTs	7.15
312614	AI766732	Hs.201194	ESTs	7
314790	AW341754	Hs.189305	ESTs	6.83
309979	AW452118	Hs.257533	EST	6.74
314236	AA743396	Hs.189023	ESTs	6.49
329192			CH.X_hs gl[5868716	6.1
324307	AA627642	Hs.4994	transducer of ERBB2; 2 (TOB2)	5.99
303685	AW500106		EST cluster (not in UniGene) with exon hit	5.82
314921	AW452382	Hs.257564	ESTs	5.8
315840	AA679001	Hs.192221	ESTs	5.68
332776	AA034364	Hs.256551	ESTs; Weakly similar to [!!! ALU CLASS B WARNING ENTRY !!!] [H.sapiens]	5.43
313533	AW298141	Hs.157975	ESTs	5.4
303494	F30712		EST cluster (not in UniGene) with exon hit	5.35
317490	AI627358	Hs.148367	ESTs	5.31
332546	D84454	Hs.21899	solute carrier family 35 (UDP-galactose transporter); member 2	5.25
334719			CH22_FGENES.421_S0	5.25
300679	AA813958	Hs.207727	ESTs; Moderately similar to KIAA0071 [H.sapiens]	5.22
311811	AI625304	Hs.190312	ESTs	5.22
315310	AW511298	Hs.256067	ESTs	5.19
312871	H86747	Hs.227602	KIAA1116 protein	5.11
324715	AI739168		EST cluster (not in UniGene)	4.97
313870	AW206435	Hs.148057	ESTs	4.97
321453	N50080	Hs.117827	ESTs	4.78
316160	AW197887	Hs.253353	ESTs	4.63
313833	AA766825		EST cluster (not in UniGene)	4.58
315850	AW270550	Hs.116957	ESTs	4.53
303124	AF161350		EST cluster (not in UniGene) with exon hit	4.46
323346	AL134932	Hs.143607	ESTs	4.4
301383	AA913591	Hs.126480	ESTs	4.35
324513	AW501678	Hs.164577	ESTs	4.28
303480	AA331906		EST cluster (not in UniGene) with exon hit	4.25
323591	AA301270		EST cluster (not in UniGene)	4.22
313603	AW468119		EST cluster (not in UniGene)	4.2
317863	AI733395	Hs.129124	ESTs	4.1
312381	R42049	Hs.195473	ESTs	4.08
317514	AW451570	Hs.126850	ESTs	4.03
319750	AA821606	Hs.117956	ESTs	4.03

	322520	T55958	EST cluster (not in UniGene)	4
	314754	AW026761	Hs.134374 ESTs	4
	316088	AJ990652	Hs.208973 ESTs	4
	318473	AJ839339	Hs.146883 ESTs	3.96
5	307848	AJ364186	EST singleton (not in UniGene) with exon hit	3.85
	300730	AW448204	Hs.257125 ESTs	3.94
	303034	W60843	Hs.31570 ESTs	3.83
	324668	AJ679131	Hs.201424 ESTs	3.9
	324674	AA541323	Hs.115831 ESTs	3.88
10	300547	N53442	Hs.143443 ESTs	3.83
	316100	AW203988	Hs.213003 ESTs	3.79
	314801	AA481027	Hs.127336 ESTs; Weakly similar to ORF YGR245c [S.cerevisiae]	3.75
	320858	D59945	EST cluster (not in UniGene)	3.74
	313188	AJ039702	Hs.179573 collagen; type I; alpha 2	3.73
15	314187	AA804409	Hs.118920 ESTs	3.73
	311826	AA765470	Hs.122826 ESTs	3.7
	302358	D81150	EST cluster (not in UniGene) with exon hit	3.68
	311441	Z38720	Hs.151014 ESTs	3.66
	321914	AA011603	EST cluster (not in UniGene)	3.59
20	332218	H95082	Hs.102332 EST	3.52
	324771	AA831739	EST cluster (not in UniGene)	3.5
	323691	AA317581	EST cluster (not in UniGene)	3.49
	303525	AW516519	Hs.115130 ESTs	3.47
	309709	AW242630	EST singleton (not in UniGene) with exon hit	3.46
25	300038		AFFX control: MurlL4	3.38
	316528	AJ088192	Hs.135474 ESTs; Weakly similar to ATP-DEPENDENT RNA HELICASE A [H.sapiens]	3.36
	313029	AA731520	Hs.170504 ESTs	3.35
	304356	AJ196027	Hs.185188 glyceraldehyde-3-phosphate dehydrogenase	3.34
	314610	AJ948688	Hs.191805 ESTs	3.33
30	329815		CH.14_p2 g 5624888	3.32
	314949	AJ745387	Hs.239124 ESTs	3.31
	300598	N53574	Hs.158932 ESTs	3.3
	329218		CH.X_hs g 5868728	3.28
	315708	AW440742	Hs.155556 ESTs	3.28
35	303751	AW503637	EST cluster (not in UniGene) with exon hit	3.25
	307783	AJ347274	EST singleton (not in UniGene) with exon hit	3.25
	321414	AA324975	Hs.128993 ESTs; Weakly similar to KIAA0465 protein [H.sapiens]	3.25
	312187	AA700439	Hs.188490 ESTs	3.25
	334061		CH22_FGENES.327_14	3.23
40	338036		CH22_FGENES.678_7	3.23
	321477	H67818	Hs.222059 ESTs	3.21
	315760	AW139383	Hs.245437 ESTs	3.2
	316733	AA811713	Hs.163222 ESTs	3.2
	300855	AW235248	Hs.79828 ESTs	3.2
45	323611	AA304986	Hs.145704 ESTs	3.19
	314138	AA740616	EST cluster (not in UniGene)	3.17
	316774	AA814859	EST cluster (not in UniGene)	3.16
	308884	AJ833131	Hs.179100 ESTs	3.11
	331317	AA258222	Hs.87757 ESTs	3.1
50	317221	AJ989538	Hs.191074 ESTs	3.08
	316388	AA749062	Hs.180285 ESTs	3.08
	321040	H26953	EST cluster (not in UniGene)	3.08
	308828	AJ824829	EST singleton (not in UniGene) with exon hit	3.08
	300778	AA236233	Hs.188716 ESTs	3.07
55	316687	AW015940	Hs.232234 ESTs	3.07
	324614	AW503101	EST cluster (not in UniGene)	3.07
	316468	AW283048	Hs.255158 ESTs	3.07
	300671	AJ239708	Hs.189886 ESTs	3.06
	314301	AW297987	Hs.188181 ESTs	3.05
60	312335	AW043620	Hs.236993 ESTs	3.03
	322657	AA247755	EST cluster (not in UniGene)	3.01
	316848	AA830053	Hs.128798 ESTs	3.01
	313473	AA009660	Hs.251948 ESTs; Moderately similar to T07D3.7 [C.elegans]	2.99
	318518	T27119	EST cluster (not in UniGene)	2.98
65	313383	AJ076370	Hs.134037 ESTs	2.97
	331389	AA458637	Hs.152207 ESTs	2.96
	304257	AA053294	EST singleton (not in UniGene) with exon hit	2.95
	309917	AW340014	EST singleton (not in UniGene) with exon hit	2.95
	318661	H08035	Hs.21398 ESTs; Moderately similar to PUTATIVE GLUCOSAMINE-6-PHOSPHATE	2.95

			ISOMERASE [H.sapiens]	2.95
	321253	AI699484	EST cluster (not in UniGene)	2.93
	321193	AA149508	Hs.103288 ESTs	2.93
	332884		CH22_FGENES.28_4	2.92
5	300027			
		M11507	AFFX control: transferrin receptor	2.91
	324330	AA884766	EST cluster (not in UniGene)	2.88
	320014	AA137114	Hs.170291 ESTs	2.88
	333916		CH22_FGENES.296_5	2.88
10	318885	Z43272	EST cluster (not in UniGene)	2.87
	318148	AI040125	Hs.150521 ESTs	2.87
	323348	AA233058	Hs.191518 ESTs	2.85
	305703	AA825148	Hs.21229 F-box protein Fbw1b	2.84
	335882		CH22_FGENES.629_7	2.83
15	317672	AW205409	Hs.127748 ESTs	2.82
	323416	AI610397	Hs.159560 ESTs	2.81
	312652	AI419909	Hs.160994 ESTs	2.81
	324094	AA382603	EST cluster (not in UniGene)	2.81
	319761	R84237	EST cluster (not in UniGene)	2.8
20	317013	AA864468	Hs.135646 ESTs	2.8
	317383	AA913887	Hs.126511 ESTs	2.78
	314659	AW277121	Hs.254881 ESTs	2.78
	312479	AI950844	Hs.128738 ESTs; Weakly similar to non-lens beta gamma-crystallin like protein [H.sapiens]	2.77
	332808		CH22_FGENES.7_10	2.75
25	311824	AW293826	Hs.250610 ESTs	2.75
	321892	C06003	Hs.116456 ESTs	2.73
	316074	AW517542	Hs.208382 ESTs	2.73
	309839	AW296076	EST singleton (not in UniGene) with exon hit	2.73
	312071	AA683529	Hs.143119 ESTs	2.73
30	312684	AW294020	Hs.117721 ESTs	2.72
	332668	AA062971	Hs.181161 ESTs; Weakly similar to INHIBITOR OF APOPTOSIS PROTEIN 1 [M.musculus]	2.72
	322139	H53744	EST cluster (not in UniGene)	2.72
	304168	H77679	EST singleton (not in UniGene) with exon hit	2.72
	325602		CH.13_hs gl 5886994	2.71
35	319885	R59096	Hs.136698 ESTs	2.71
	300611	N75450	EST cluster (not in UniGene) with exon hit	2.71
	316854	AA831215	Hs.159068 ESTs; Weakly similar to predicted using Genefinder [C.elegans]	2.69
	318208	AI091458	Hs.134559 ESTs	2.68
	331623	R38715	Hs.153529 Homo sapiens clone 24540 mRNA sequence	2.68
40	324816	AI823999	Hs.162000 ESTs	2.68
	304968	AA614308	EST singleton (not in UniGene) with exon hit	2.67
	314912	AI431345	Hs.161784 ESTs	2.67
	300767	AW193466	Hs.136525 ESTs	2.67
	313483	AI057369	Hs.122536 ESTs	2.65
45	320600	AA135565	Hs.250739 ESTs	2.65
	301180	AI308989	Hs.156939 ESTs	2.65
	324825	AA704457	Hs.255738 ESTs; Moderately similar to gag [H.sapiens]	2.65
	300338	AW292417	Hs.255074 ESTs; Moderately similar to high-risk human papilloma viruses E6 oncoproteins targeted protein E6P1 alpha [H.sapiens]	2.64
50	317650	N29974	EST cluster (not in UniGene)	2.64
	339047		CH22_DA59H18.GENSCAN.28-7	2.64
	324580	AA492588	EST cluster (not in UniGene)	2.63
	321142	AI817833	Hs.209584 ESTs	2.62
	319478	R06841	EST cluster (not in UniGene)	2.62
55	300783	AI248571	Hs.186837 ESTs	2.61
	313733	AA838116	EST cluster (not in UniGene)	2.6
	326505		CH.19_hs gl 5867435	2.6
	314987	AW015506	Hs.130730 ESTs	2.6
	303114	AF090948	EST cluster (not in UniGene) with exon hit	2.59
60	318709	H24244	Hs.240763 ESTs; Weakly similar to /prediction	2.58
	312878	AI209108	Hs.143946 ESTs	2.57
	329224		CH.X_hs gl 5868728	2.56
	328018		CH.06_hs gl 5902482	2.56
	323231	AA324437	Hs.177230 ESTs	2.55
65	312887	AW157377	Hs.132910 ESTs	2.55
	315183	AW136134	Hs.220277 ESTs	2.55
	300259	AI479011	Hs.170783 ESTs	2.54
	313240	AI743261	Hs.131860 ESTs	2.54
	316697	AW293174	Hs.252627 ESTs	2.53

	313968	AI807551	Hs.189061	ESTs	2.53
	331263	AA015718		ze31a12.s1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:38574 3', mRNA sequence	2.51
5	310683	AW055233	Hs.160870	ESTs	2.5
	302566	AA085998	Hs.248572	Human PAC clone DJ404F18 from Xq23	2.5
	302697	AJ001408		EST cluster (not in UniGene) with exon hit	2.5
	308362	AI613519		EST singleton (not in UniGene) with exon hit	2.49
	322347	AF088538		EST cluster (not in UniGene)	2.49
10	316240	AA974253	Hs.120319	ESTs	2.49
	323208	AA203415	Hs.136200	ESTs	2.48
	321643	W76005	Hs.32094	ESTs	2.48
	330723	AA243617	Hs.31082	ESTs; Highly similar to db83 [R.norvegicus]	2.48
	323455	AA256675	Hs.200438	ESTs; Weakly similar to atypical PKC specific binding protein [R.norvegicus]	2.47
15	308383	AI824497		EST singleton (not in UniGene) with exon hit	2.47
	328744			CH.07_hs gi 5868290	2.47
	332344	W45574	Hs.252497	ESTs	2.47
	328121			CH.06_hs gi 5868031	2.47
	321915	AI670955	Hs.200151	ESTs	2.46
20	314954	AA521381	Hs.187728	ESTs	2.45
	302821	AA189868	Hs.173933	ESTs; Weakly similar to NUCLEAR FACTOR 1/X [H.sapiens]	2.45
	329454			CH.Y_hs gi 5868887	2.45
	336805			CH22_FGENES.420_4	2.45
25	300664	AI444628	Hs.256809	ESTs	2.44
	323362	AL135067	Hs.117182	ESTs	2.44
	300024	M10098		AFFX control: 18S ribosomal RNA	2.44
	325026	AI671168	Hs.12285	ESTs	2.43
	324510	AI148353	Hs.120849	ESTs	2.43
	313389	AI765182	Hs.119903	ESTs	2.43
30	301309	M78276	Hs.255917	ESTs	2.43
	313570	AA041455	Hs.209312	ESTs	2.43
	316504	AW135854	Hs.132458	ESTs	2.42
	319401	R01342		EST cluster (not in UniGene)	2.42
	312827	AI744361	Hs.205591	ESTs; Weakly similar to zinc finger protein Png-1 [M.musculus]	2.42
35	327871			CH.06_hs gi 5868131	2.41
	337173			CH22_FGENES.565-3	2.41
	302848	AA465635		EST cluster (not in UniGene) with exon hit	2.41
	324303	AL118754		EST cluster (not in UniGene)	2.4
	315527	AI791138	Hs.116768	ESTs	2.4
40	315979	AA830515	Hs.222917	ESTs	2.4
	331310	AA253351	Hs.44439	STAT induced STAT inhibitor-4	2.4
	321095	AA017595	Hs.32844	ESTs	2.4
	308581	AI701559		EST singleton (not in UniGene) with exon hit	2.39
	313035	N36417	Hs.144928	ESTs	2.37
45	322114	AA643791	Hs.191740	ESTs	2.37
	313871	W49823	Hs.145553	ESTs	2.37
	303211	AA099548	Hs.191436	ESTs; Highly similar to dJ1118D24.4 [H.sapiens]	2.37
	301256	AA932948		EST cluster (not in UniGene) with exon hit	2.36
	338165			CH22_EM:AC005500.GENSCAN.212-3	2.36
50	324632	AA557952		EST cluster (not in UniGene)	2.35
	318587	AA778704	Hs.168830	ESTs	2.35
	312378	R41582	Hs.109219	retinal degeneration B beta	2.35
	318525	T48448	Hs.193182	ESTs	2.35
	305181	AA663726	Hs.116922	EST	2.35
	300815	AA286678		EST cluster (not in UniGene) with exon hit	2.34
55	324063	AW292740	Hs.254815	ESTs	2.34
	315859	AA682305	Hs.133268	ESTs	2.33
	305092	AA642912		EST singleton (not in UniGene) with exon hit	2.33
	308598	AI000320		EST singleton (not in UniGene) with exon hit	2.33
60	300307	AI651016	Hs.246311	ESTs	2.33
	321348	Z49979		EST cluster (not in UniGene)	2.33
	325112	AI903770	Hs.124344	ESTs	2.32
	336679			CH22_FGENES.43-7	2.32
	321383	AJ002574		EST cluster (not in UniGene)	2.32
65	337357			CH22_FGENES.730-6	2.31
	300680	AW468066	Hs.257712	ESTs; Weakly similar to KIAA0986 protein [H.sapiens]	2.31
	327120			CH.21_hs gi 6531970	2.31
	302761	AW250553		EST cluster (not in UniGene) with exon hit	2.3
	312132	AI475490	Hs.170577	ESTs	2.3
	315639	AA827652		EST cluster (not in UniGene)	2.3

	312189	T95594	Hs.187435	ESTs	2.3
	306537	AA991705		EST singleton (not in UniGene) with exon hit	2.3
	327061			CH.21_hs g 5631965	2.3
5	315391	AA759098	Hs.192007	ESTs	2.3
	322384	AJ868646	Hs.33862	ESTs	2.29
	323206	AA203339	Hs.220750	ESTs	2.29
	318110	AJ680915	Hs.201379	ESTs	2.28
	335250			CH22_FGENES.516_11	2.28
	331696	Z38907	Hs.91662	KIAA0888 protein	2.28
10	318327	AW294013	Hs.200942	ESTs	2.28
	324980	AA969121	Hs.254296	ESTs	2.28
	318429	AJ608881	Hs.11482	ESTs; Highly similar to junctional adhesion molecule [H.sapiens]	2.28
	310601	AJ970543	Hs.182605	ESTs	2.28
	318905	Z43395		EST cluster (not in UniGene)	2.28
15	323442	AA252753	Hs.164039	ESTs	2.27
	304428	AA342250	Hs.99819	ubiquitin specific protease 18	2.27
	313352	AW282127	Hs.144758	ESTs	2.27
	316491	AA766025	Hs.238794	EST	2.27
	317751	AJ697658	Hs.202241	ESTs	2.26
20	314136	AA229781	Hs.221962	ESTs	2.26
	306665	AJ004614	Hs.130577	EST	2.26
	303946	AW474196	Hs.221604	ESTs	2.25
	313435	AA769123		EST cluster (not in UniGene)	2.25
	317679	AA988799	Hs.150289	ESTs	2.25
25	322370	AA330095		EST cluster (not in UniGene)	2.25
	306620	AJ000929		EST singleton (not in UniGene) with exon hit	2.24
	329109			CH.X_hs g 5868626	2.24
	311043	AJ871209	Hs.177128	ESTs	2.24
	300228	AJ458372	Hs.158748	ESTs; Weakly similar to synapsin Ib [M.musculus]	2.24
30	307223	AJ193698	Hs.184776	ribosomal protein L23a	2.24
	309023	AJ888045		EST singleton (not in UniGene) with exon hit	2.23
	310749	AJ493675	Hs.170332	ESTs	2.23
	316769	AJ14939	Hs.212184	ESTs	2.22
	320409	AA358185		EST cluster (not in UniGene)	2.21
35	333149			CH22_FGENES.87_8	2.21
	324951	M86125	Hs.137487	ESTs	2.21
	321939	AJ791617	Hs.145068	ESTs	2.2
	320594	AJ863952	Hs.169436	arginyltransferase 1	2.2
	320722	R67430	Hs.172787	ESTs	2.2
40	321781	D78667		EST cluster (not in UniGene)	2.2
	328903			CH.L8_hs g 5868514	2.2
	303889	T19204		EST cluster (not in UniGene) with exon hit	2.2
	325045	T08845		EST cluster (not in UniGene)	2.2
45	312828	AJ865455	Hs.211818	ESTs; Moderately similar to IIII ALU SUBFAMILY J WARNING ENTRY IIII [H.sapiens]	2.19
	335109			CH22_FGENES.494_15	2.18
	330878	AA131471	Hs.71440	ESTs	2.18
	311289	AJ971362	Hs.231945	ESTs	2.18
	304608	AA513456		EST singleton (not in UniGene) with exon hit	2.18
50	337393			CH22_FGENES.747-4	2.18
	332812			CH22_FGENES.7_14	2.18
	327665			CH.L04_hs g 5867839	2.18
	314581	AW504859	Hs.237849	ESTs	2.17
	326508			CH.L19_hs g 6682496	2.17
55	301242	AW161535	Hs.258803	ESTs	2.17
	312780	AJ765651	Hs.172900	ESTs	2.17
	315954	AW276810	Hs.254859	ESTs	2.16
	311179	AJ880843	Hs.223333	ESTs	2.16
	315320	AJ084182	Hs.186895	ESTs	2.16
	313017	AJ015203	Hs.118015	ESTs	2.16
60	312430	AW139117	Hs.117494	ESTs	2.15
	300884	AA406539	Hs.180958	ESTs	2.15
	314753	AA463262		EST cluster (not in UniGene)	2.15
	322574	AF156548		EST cluster (not in UniGene)	2.15
	321409	C03864		EST cluster (not in UniGene)	2.15
65	321205	AA002047		EST cluster (not in UniGene)	2.14
	320406	AA353895	Hs.152983	HUS1 (S. pombe) checkpoint homolog	2.14
	337648			CH22_EM:AC000097.GENSCAN.11-2	2.13
	303084	AF174008		EST cluster (not in UniGene) with exon hit	2.13
	312185	AA654772	Hs.186584	ESTs	2.13

	306813	AI066544	EST singleton (not in UniGene) with exon hit	2.13	
	314465	AA602917	Hs.156974 ESTs	2.12	
	318168	AI821782	Hs.220587 ESTs; Moderately similar to IIII ALU SUBFAMILY SC WARNING ENTRY IIII [H.sapiens]	2.12	
	315990	AI800041	Hs.190555 ESTs	2.11	
5	320712	R66887	EST cluster (not in UniGene)	2.11	
	318487	AI167877	Hs.143716 ESTs	2.11	
	317462	AW015206	Hs.178784 ESTs	2.11	
	304384	AA235482	Hs.62954 ferritin; heavy polypeptide 1	2.11	
	314544	AA399018	Hs.250835 ESTs	2.1	
10	319881	T72744	EST cluster (not in UniGene)	2.1	
	328078		CH.06_hs g 5868008	2.1	
	317354	AW090770	Hs.182271 ESTs	2.1	
	308617	AI738720	EST singleton (not in UniGene) with exon hit	2.09	
	311568	AW439969	Hs.218177 ESTs	2.09	
15	313605	AI761788	Hs.204674 ESTs	2.09	
	314289	AA848118	Hs.221216 ESTs	2.08	
	332833		CH22_FGENES.38_7	2.08	
	325498		CH.12_hs g 5866967	2.08	
	313659	AW288067	Hs.124108 ESTs	2.08	
20	324596	AW149321	Hs.105411 ESTs	2.08	
	324783	AA640770	EST cluster (not in UniGene)	2.07	
	302696	AA347452	EST cluster (not in UniGene) with exon hit	2.07	
	313418	AW450674	Hs.114696 ESTs	2.06	
	326820		CH.21_hs g 6456782	2.06	
25	327574		CH.03_hs g 5867818	2.06	
	323207	AI052785	Hs.182201 ESTs	2.06	
	303753	AW503733	Hs.170315 ESTs	2.05	
	305235	AA670480	EST singleton (not in UniGene) with exon hit	2.05	
	316055	AA693880	EST cluster (not in UniGene)	2.05	
30	317194	AW445167	Hs.126036 ESTs	2.05	
	319565	AW408683	Hs.32922 ESTs	2.05	
	335146		CH22_FGENES.499_2	2.05	
	301475	AI678183	Hs.170917 prostaglandin E receptor 3 (subtype EP3)	2.04	
	312442	AA120970	Hs.143199 ESTs	2.04	
35	322502	R62925	Hs.243665 ESTs	2.04	
	303693	AA290875	Hs.30120 ESTs	2.04	
	310179	AI215643	Hs.171381 ESTs	2.03	
	321121	W23285	EST cluster (not in UniGene)	2.03	
	331330	AA282197	Hs.89002 ESTs; Highly similar to CGI-07 protein [H.sapiens]	2.03	
40	306557	AA994530	EST singleton (not in UniGene) with exon hit	2.03	
	317865	AI298794	Hs.129130 ESTs	2.03	
	318667	AI493742	Hs.185210 ESTs	2.02	
	318042	AW294522	Hs.149991 ESTs	2.02	
	323818	AW245528	Hs.134754 ESTs	2.02	
45	331288	AA137062	Hs.103853 ESTs	2.01	
	311262	AI989942	Hs.232150 ESTs	2.01	
	335601		CH22_FGENES.581_41	2.01	
	311351	AI682303	Hs.201274 ESTs	2.01	
	312996	AA249018	EST cluster (not in UniGene)	2.01	
50	328190		CH.06_hs g 5868077	2	
	338030		CH22_EM:AC005500.GENSCAN.148-16	2	
	333940		CH22_FGENES.301_8	2	
	328227		CH.06_hs g 5868105	2	
55	331481	N27448	Hs.43944 EST	2	
	335288		CH22_FGENES.527_1	2	
	307513	AI274307	EST singleton (not in UniGene) with exon hit	2	
	323316	AL134620	EST cluster (not in UniGene)	2	
	319479	R21945	Hs.256153 ESTs	2	
	303482	AA502583	Hs.197271 ESTs	2	
60	327489		CH.02_hs g 6004459	1.99	
	323935	AW175841	Hs.182183 ESTs	1.99	
	309575	AW168096	Hs.195188 glyceraldehyde-3-phosphate dehydrogenase	1.99	
	337043		CH22_FGENES.439-19	1.98	
	312897	AI828174	Hs.227049 ESTs	1.98	
65	307881	AI370434	EST singleton (not in UniGene) with exon hit	1.98	
	328656		CH.07_hs g 6004473	1.98	
	314569	AA813784	Hs.123001 ESTs	1.98	
	332783	W45302	Hs.87889 helicase-mol	1.98	
	315259	AA701499	Hs.148115 ESTs	1.98	

	313171	N67879	Hs.157695	ESTs	1.97
	318060	AI241421	Hs.132238	ESTs	1.97
	332256	N66393	Hs.102754	ESTs	1.97
	312110	AI962180	Hs.226803	ESTs	1.97
5	335864		CH22_FGENES.629_9		1.97
	320389	W00545	Hs.171785	ESTs	1.97
	314065	AA868267	Hs.85524	ESTs	1.96
	323088	H15474	Hs.12214	Homo sapiens clone 23716 mRNA sequence	1.96
	323919	AA862973	Hs.220704	ESTs	1.96
10	310750	AI373163	Hs.170333	ESTs	1.96
	309435	AW090537		EST singleton (not in UniGene) with exon hit	1.96
	300129	AW028820		EST cluster (not in UniGene) with exon hit	1.96
	320130	AI820675	Hs.203804	ESTs	1.95
	323787	AW373446	Hs.169885	ESTs; Weakly similar to cDNA EST EMBL:T02216 comes from this gene [C.elegans]	1.95
15	338112		CH22_EM:AC005500.GENSCAN.185-24		1.95
	313625	AW468402	Hs.254020	ESTs	1.95
	325240		CH.10_hs gij5866848		1.95
	331833	AA412102	Hs.250911	interleukin 13 receptor; alpha 1	1.95
20	332252	N63882	za218.s1 Soares fetal liver spleen 1NFS Homo sapiens cDNA clone IMAGE:293225 3', mRNA sequence		1.95
	300279	AW237425	Hs.253817	ESTs	1.95
	326023		CH.17_hs gij5867245		1.95
	321609	H86021	Hs.198800	ESTs; Weakly similar to hMmTRA1b [H.sapiens]	1.94
	324183	AA402453	Hs.113011	ESTs	1.94
25	336276		CH22_FGENES.762_5		1.94
	334913		CH22_FGENES.458_3		1.94
	325417		CH.12_hs gij5866925		1.94
	318489	AW043590	Hs.225023	ESTs	1.94
	318455	AI148763		EST cluster (not in UniGene)	1.94
30	306890	AI092235		EST singleton (not in UniGene) with exon hit	1.94
	315073	AW452948	Hs.257631	ESTs	1.94
	321289	R84687	Hs.226306	ESTs	1.94
	308521	AI689808		EST singleton (not in UniGene) with exon hit	1.93
	306382	AA968967		EST singleton (not in UniGene) with exon hit	1.93
35	331320	AA262999	Hs.42788	ESTs	1.93
	324279	AA501412	Hs.191888	ESTs; Weakly similar to Pro-Pol-dUTPase polypeptide [M.musculus]	1.93
	309577	AW168753		EST singleton (not in UniGene) with exon hit	1.93
	327014		CH.21_hs gij5867664		1.93
	303488	AW025860		EST cluster (not in UniGene) with exon hit	1.93
40	306561	AA995223	Hs.129559	EST	1.92
	330684	AA019806	Hs.108447	spinocerebellar ataxia 7 (olivopontocerebellar atrophy with retinal degeneration)	1.92
	313083	N50545	Hs.158200	ESTs	1.92
	327752		CH.05_hs gij5867949		1.92
	318674	AA285490		EST cluster (not in UniGene)	1.92
45	301287	AW297762	Hs.255690	ESTs	1.91
	332092	AA608787	Hs.112590	ESTs	1.91
	323509	ALD36947		EST cluster (not in UniGene)	1.91
	321452	AA317554		EST cluster (not in UniGene)	1.91
	311483	AI765013	Hs.209128	ESTs	1.91
50	300978	AI246374	Hs.185861	ESTs	1.91
	323715	AA322155		EST cluster (not in UniGene)	1.91
	313800	AW286132	Hs.166674	ESTs	1.91
	332029	AA489697	Hs.145053	ESTs	1.91
	304013	AW518573	Hs.156110	immunoglobulin kappa variable 1D-8	1.91
55	322019	AA354549	Hs.41181	Homo sapiens mRNA; cDNA DKFZp727C191 (from clone DKFZp727C191)	1.91
	334150		CH22_FGENES.339_1		1.9
	310094	AW450967	Hs.235240	ESTs	1.9
	316218	AW207642	Hs.174021	ESTs	1.9
	324774	AI031771	Hs.132588	ESTs	1.9
60	326507		CH.19_hs gij5867435		1.9
	314570	AA405696		EST cluster (not in UniGene)	1.9
	336268		CH22_FGENES.758_2		1.9
	315278	AI985544	Hs.116429	ESTs	1.9
	325824		CH.15_hs gij5867048		1.9
65	316277	AA737780	Hs.213392	ESTs	1.9
	323181	AA418593	Hs.143621	ESTs	1.9
	301438	AA961643	Hs.127716	ESTs	1.89
	307050	AI147341	Hs.148734	EST	1.89
	306830	AI075803		EST singleton (not in UniGene) with exon hit	1.89

	302426	AL049325	Hs.225884	DKFZP547G0910 protein	1.89
	320127	H72615	Hs.17268	ESTs	1.89
	337738			CH22_EM:AC000097.GENSCAN.100-2	1.89
5	331319	AA262755	Hs.194264	ESTs	1.88
	310767	AJ377505	Hs.158835	ESTs	1.88
	314880	AJ732169	Hs.105429	ESTs	1.88
	312539	AJ004377	Hs.200360	ESTs	1.88
	309674	AW205604	Hs.168034	ESTs; Weakly similar to !!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!! [H.sapiens]	1.88
	314621	AJ827478	Hs.187670	ESTs	1.88
10	319495	AJ972148	Hs.192756	ESTs	1.88
	313472	AA007374		EST cluster (not in UniGene)	1.88
	302705	U09060		EST cluster (not in UniGene) with exon hit	1.88
	329511			CH.10_p2 gi 3983514	1.88
	317140	AJ699412	Hs.201925	ESTs	1.87
15	302598	AJ815985	Hs.129683	ubiquitin-conjugating enzyme E2D 1 (homologous to yeast UBC4/5)	1.87
	301153	AA725670	Hs.120485	ESTs; Weakly similar to serine/threonine kinase with SH3 domain; leucine zipper domain and proline rich domain [H.sapiens]	1.87
	332222	N28271	Hs.176618	ESTs	1.87
20	330703	AA055475	Hs.104143	clathrin; light polypeptide (Lca)	1.87
	318470	AJ159863	Hs.143713	ESTs	1.87
	314014	AW291847	Hs.121715	ESTs; Weakly similar to HP protein [H.sapiens]	1.87
	300370	AJ827817		EST cluster (not in UniGene) with exon hit	1.86
	312329	R84768	Hs.13339	Homo sapiens clone 25032 mRNA sequence	1.86
	325567			CH.12_hs gi 6682462	1.86
25	310237	AJ884313	Hs.158908	ESTs	1.86
	318872	R13085		EST cluster (not in UniGene)	1.86
	303431	AA317915		EST cluster (not in UniGene) with exon hit	1.86
	338427			CH22_EM:AC005500.GENSCAN.349-1	1.86
30	300452	AJ352293	Hs.191098	ESTs	1.85
	321279	H85330	Hs.146060	ESTs	1.85
	301690	F05865	Hs.249180	ubiquitin-conjugating enzyme E2E 2 (homologous to yeast UBC4/5)	1.85
	307932	AJ230822		EST singleton (not in UniGene) with exon hit	1.85
	318292	AJ679968	Hs.150603	ESTs	1.85
	310254	AJ239811	Hs.157491	ESTs	1.85
35	311790	AW016437	Hs.233462	ESTs	1.84
	314248	AA278347	Hs.126078	ESTs	1.84
	335588			CH22_FGENES.581_25	1.84
	339209			CH22_FF113D11.GENSCAN.6-4	1.84
40	307854	AJ419692		EST singleton (not in UniGene) with exon hit	1.84
	302549	AF055138	Hs.248162	tegorin alpha	1.84
	321629	H87213	Hs.158092	ESTs	1.84
	301239	AA807558		EST cluster (not in UniGene) with exon hit	1.84
	332434	N75542	Hs.75356	transcription factor 4	1.84
	327182			CH.01_hs gi 5867445	1.83
45	310214	AJ220072	Hs.165893	ESTs	1.83
	320516	R33857	Hs.181479	ESTs; Weakly similar to E-SELECTIN PRECURSOR [H.sapiens]	1.83
	324231	W60827		EST cluster (not in UniGene)	1.83
	336616			CH22_FGENES.613_5	1.83
	328799			CH.07_hs gi 5868316	1.83
50	324661	AW504161		EST cluster (not in UniGene)	1.83
	313190	AA766707	Hs.153039	ESTs	1.83
	301979	L28168	Hs.121495	potassium voltage-gated channel; Isk-related family; member 1	1.82
	302099	AL021397	Hs.137576	ribosomal protein L34 pseudogene 1	1.82
	320187	T99948		EST cluster (not in UniGene)	1.82
55	320791	R78808	Hs.93961	ESTs; Weakly similar to !!!!! ALU CLASS A WARNING ENTRY !!!!! [H.sapiens]	1.82
	305733	AA829535	Hs.84298	CD74 antigen (invariant polypept of MHC; class II antigen-associated)	1.82
	308280	AJ589349	Hs.160920	ribosomal protein S9	1.81
	321533	W78877	Hs.40111	ESTs	1.81
60	312846	AJ915122	Hs.204087	ESTs; Weakly similar to F33D11.9b [C.elegans]	1.81
	319474	H90265	Hs.100638	ESTs	1.81
	329519			CH.10_p2 gi 3983510	1.81
	324685	AA220982		EST cluster (not in UniGene)	1.81
	320697	N62937	Hs.139181	ESTs	1.81
	329246			CH.X_hs gi 5868732	1.81
65	332000	AA481271	Hs.193945	ESTs	1.81
	310811	AA20990	Hs.161303	ESTs	1.81
	325866			CH.16_hs gi 5867076	1.81
	322064	Z78343		EST cluster (not in UniGene)	1.8
	333712			CH22_FGENES.251_1	1.8

	313457	AA576052	Hs.193223	ESTs	1.8
	321591	H85687	Hs.117927	ESTs	1.8
	330260		CH.05_p2 g 6671884		1.8
5	311080	AI856320	Hs.197711	ESTs	1.8
	329522		CH.10_p2 g 3983507		1.8
	322889	AA081824	Hs.211417	ESTs	1.8
	300175	AI275011	Hs.204877	ESTs	1.8
	330976	H20560	Hs.244624	ESTs	1.8
10	300208	AI341180	Hs.196115	ESTs; Weakly similar to FIBRILLIN 1 PRECURSOR [H.sapiens]	1.79
	319635	R17531		EST cluster (not in UniGene)	1.79
	313454	AA730673	Hs.188634	ESTs	1.79
	303093	AI400310	Hs.148958	ESTs	1.79
	309815	AW292760		EST singleton (not in UniGene) with exon hit	1.79
	326508		CH.19_hs g 5867435		1.79
15	319845	AA649011	Hs.187902	ESTs	1.79
	300290	AI623739	Hs.186387	ESTs	1.79
	312180	AI248285	Hs.118348	ESTs	1.79
	313058	D81015	Hs.125382	ESTs	1.79
20	330120		CH.19_p2 g 6671884		1.78
	328412		CH.07_hs g 5868405		1.78
	302345	NM_000565		EST cluster (not in UniGene) with exon hit	1.78
	308100	AI475949		EST singleton (not in UniGene) with exon hit	1.78
	311386	AW205705	Hs.207514	ESTs	1.78
	330282		CH.05_p2 g 6671910		1.78
25	318856	Z43011	Hs.21169	ESTs	1.78
	312488	AA845630	Hs.117904	ESTs	1.78
	325450		CH.12_hs g 5868941		1.78
	321206	H54178	Hs.226469	ESTs	1.78
	330977	H20826	Hs.31783	ESTs	1.78
30	303487	AA333666		EST cluster (not in UniGene) with exon hit	1.77
	310398	AI264671	Hs.164168	ESTs	1.77
	313230	AI540166	Hs.129563	ESTs	1.77
	317747	AI683782	Hs.126245	ESTs	1.77
	303381	AL038841	Hs.163313	ESTs; Weakly similar to III ALU SUBFAMILY SB WARNING ENTRY III [H.sapiens]	1.77
35	336123		CH22_FGENES.701_8		1.77
	300185	AI286182	Hs.208484	ESTs	1.77
	316002	AW451733	Hs.118824	ESTs	1.77
	319850	AA001811	Hs.83722	ESTs	1.77
40	329941		CH.16_p2 g 6165199		1.77
	328329		CH.07_hs g 5868375		1.77
	322934	AI493054	Hs.158968	ESTs	1.77
	325902		CH.16_hs g 5867101		1.76
	322239	W01813	Hs.12109	WD40 protein C1a01	1.76
45	303530	AI274851	Hs.258744	ESTs	1.76
	300980	AI025527	Hs.222097	ESTs	1.76
	331909	AA437300	Hs.178210	ESTs	1.76
	321553	H92449	Hs.118408	ESTs	1.76
	301618	T52760		EST cluster (not in UniGene) with exon hit	1.76
50	319592	AA627356	Hs.163315	ESTs	1.76
	318511	T26528	Hs.227175	ESTs; Weakly similar to III ALU SUBFAMILY SQ WARNING ENTRY III [H.sapiens]	1.76
	327183		CH.01_hs g 5867442		1.76
	313516	AA029058	Hs.135145	ESTs	1.76
	318644	AI752482		EST cluster (not in UniGene)	1.76
55	321632	AA419617		EST cluster (not in UniGene)	1.76
	324657	AW451142	Hs.255628	ESTs	1.76
	300437	AW449374	Hs.257149	ESTs	1.75
	319775	AA504429	Hs.6211	methyl-CpG binding domain protein 1	1.75
	314775	AI149880	Hs.188809	ESTs	1.75
	337460		CH22_FGENES.780-5		1.75
60	309849	AW287444		EST singleton (not in UniGene) with exon hit	1.75
	301471	AA995014	Hs.129544	ESTs; Weakly similar to ORF YLL027w [S.cerevisiae]	1.75
	312739	AI318426	Hs.155925	ESTs	1.75
	319895	H15355	Hs.60887	ESTs	1.75
	326495		CH.19_hs g 5867423		1.75
65	337497		CH22_FGENES.801-4		1.75
	322633	AA004534	Hs.153981	ESTs	1.75
	332177	F10812	Hs.101433	ESTs	1.75
	326930		CH.21_hs g 6456782		1.75
	316893	AA837332		EST cluster (not in UniGene)	1.75

	324826	AA704806	Hs.143842	ESTs	1.75
	311269	AI656924	Hs.174257	ESTs	1.75
	309375	AW075342		EST singleton (not in UniGene) with exon hit	1.75
5	314171	AI821895	Hs.193481	ESTs	1.75
	311684	AI890741	Hs.252809	ESTs	1.75
	334387			CH22_FGENES.380_1	1.75
	312195	AI300101	Hs.252222	ESTs	1.75
	315707	AI418055	Hs.161160	ESTs	1.74
	324349	AW501470		EST cluster (not in UniGene)	1.74
10	300724	AI762829	Hs.206134	ESTs; Weakly similar to similar to reverse transcriptase [C.elegans]	1.74
	308906	AW339340		EST singleton (not in UniGene) with exon hit	1.74
	303714	AW501338		EST cluster (not in UniGene) with exon hit	1.74
	318704	Z24981		EST cluster (not in UniGene)	1.74
	303027	AF111178		EST cluster (not in UniGene) with exon hit	1.74
15	322601	W82824		EST cluster (not in UniGene)	1.74
	318382	H93109	Hs.33665	ESTs	1.74
	315858	AA737345		EST cluster (not in UniGene)	1.74
	332243	N55484	Hs.220540	ESTs; Highly similar to ARYL HYDROCARBON RECEPTOR NUCLEAR TRANSLOCATOR [H.sapiens]	1.74
20	330951	H02566	Hs.191268	Homo sapiens mRNA; cDNA DKFZp434N174 (from clone DKFZp434N174)	1.74
	324044	AL045752	Hs.211519	ESTs	1.73
	320630	AA199847		EST cluster (not in UniGene)	1.73
	327288			CH.01_hs gi 5867481	1.73
	314986	AI201367	Hs.142860	ESTs	1.73
25	319078	H17255	Hs.144515	ESTs	1.73
	326278			CH.17_hs gi 5867269	1.73
	302552	H49782		EST cluster (not in UniGene) with exon hit	1.73
	322322	AF088431		EST cluster (not in UniGene)	1.73
	327075			CH.21_hs gi 5831865	1.73
30	317392	AI797588	Hs.145459	ESTs	1.73
	300810	AI076890	Hs.186848	ESTs	1.73
	315978	AA830893	Hs.119769	ESTs	1.73
	323903	AA773580	Hs.193598	ESTs	1.73
	330803	AA004699	Hs.150580	putative translation initiation factor	1.73
35	309845	AW296802	Hs.255580	EST	1.73
	314983	AI689817	Hs.200934	ESTs	1.73
	311710	F08774	Hs.175971	ESTs	1.73
	315315	AI984592	Hs.15088	ESTs	1.73
	300378	AA883580	Hs.235873	ESTs; Weakly similar to K11C4.2 [C.elegans]	1.73
40	316141	AW303457		EST cluster (not in UniGene)	1.72
	318826	T71739	Hs.75442	albumin	1.72
	312961	AI033922	Hs.122517	ESTs	1.72
	334379			CH22_FGENES.379_11	1.72
	305854	AA862733		EST singleton (not in UniGene) with exon hit	1.72
45	313031	N34927	Hs.186566	ESTs	1.72
	328728			CH.14_p2 gi 8065785	1.72
	312090	N57892	Hs.118064	ESTs	1.72
	323341	AL134875	Hs.192386	ESTs	1.72
	302077	AA310580	Hs.132899	Homo sapiens chromosome 11; BAC CIT-HSP-311e8 (BC269730) containing the hFEN1 gene	1.71
50	310768	AI971438	Hs.158824	ESTs	1.71
	311450	AI809985	Hs.203340	ESTs	1.71
	311792	AW238064	Hs.253909	ESTs	1.71
	321500	H71999		EST cluster (not in UniGene)	1.71
55	311948	T78781	Hs.241569	ESTs; Moderately smtr to IIII ALU SUBFAMILY SQ WARNING ENTRY IIII [H.sapiens]	1.71
	302270	R56151		EST cluster (not in UniGene) with exon hit	1.71
	329089			CH.X_hs gi 5868614	1.71
	322331	AF088487		EST cluster (not in UniGene)	1.71
	318235	AI080361	Hs.134217	ESTs	1.71
60	304561	AA489782		EST singleton (not in UniGene) with exon hit	1.71
	312681	AI028149	Hs.193124	pyruvate dehydrogenase kinase; isoenzyme 3	1.71
	310250	AA78829	Hs.158465	ESTs	1.71
	338178			CH22_EM:AC005500.GENSCAN.219-6	1.71
	338910			CH22_DJ32110.GENSCAN.11-2	1.71
65	321225	AL080073	Hs.251414	Homo sapiens mRNA; cDNA DKFZp564B1462 (from clone DKFZp564B1462)	1.7
	322289	AA534550	Hs.539	ribosomal protein S29	1.7
	319802	AI701489	Hs.202501	ESTs	1.7
	314022	AA452420	Hs.248678	ESTs	1.7
	314937	AA515602	Hs.152330	ESTs	1.7

5	300580	AA761322	Hs.220538	ESTs	1.7
	304398	AA262785		EST singleton (not in UniGene) with exon hit	1.7
	313421	AW339515	Hs.163700	ESTs	1.7
	309763	AW270182		EST singleton (not in UniGene) with exon hit	1.7
	322092	AF085833		EST cluster (not in UniGene)	1.7
10	315603	AA764768	Hs.121158	ESTs	1.7
	325031	T08597		EST cluster (not in UniGene)	1.7
	327157			CHL01_hs g 5868841	1.7
	314809	AI741461	Hs.161904	ESTs	1.7
	320361	H67220	Hs.146408	nitrilase 1	1.69
15	324721	AW402302	Hs.43618	ESTs	1.69
	328624			CHL07_hs g 5868246	1.69
	303344	AA255977	Hs.250646	ESTs; Highly similar to ubiquitin-conjugating enzyme [M.musculus]	1.69
	328960			CHL08_hs g 6456775	1.69
	315702	AA657501	Hs.146315	ESTs	1.69
20	302385	AJ224172	Hs.204096	lipophilin B (uteroglobin family member); prostatein-like	1.68
	319699	R14537		EST cluster (not in UniGene)	1.68
	309506	AW137700		EST singleton (not in UniGene) with exon hit	1.68
	330417	D84424	Hs.57697	hyaluronan synthase 1	1.68
	315286	AA876905	Hs.125286	ESTs	1.68
25	328538			CHL07_hs g 5868485	1.68
	323923	AA354146		EST cluster (not in UniGene)	1.68
	320303	AL079289	Hs.137154	Homo sapiens mRNA full length insert cDNA clone EUROIMAGE 35971	1.68
	302967	AJ927068	Hs.110853	ESTs; Weakly similar to R10D12.12 [C.elegans]	1.68
	310695	AI472124	Hs.157757	ESTs	1.68
30	307512	AI273815	Hs.242463	keratin 8	1.68
	338508			CH22_EM:AC005500.GENSCAN.390-10	1.68
	331722	AA195405	Hs.110347	Homo sapiens mRNA for alpha integrin binding protein 80; partial	1.68
	301431	R05385		EST cluster (not in UniGene) with exon hit	1.68
	318853	Z42977	Hs.21062	ESTs	1.68
35	323032	AW244073	Hs.145946	ESTs	1.68
	317538	AW137772	Hs.185980	ESTs	1.68
	325780			CHL14_hs g 6381853	1.67
	321739	AL080280		EST cluster (not in UniGene)	1.67
	319808	T58960		EST cluster (not in UniGene)	1.67
40	313443	AA249037		EST cluster (not in UniGene)	1.67
	331368	AA424754	Hs.43149	ESTs	1.67
	316443	AI797592	Hs.207407	ESTs	1.67
	322878	AA081820		EST cluster (not in UniGene)	1.67
	330320			CHL08_p2 g 5932415	1.67
45	329081			CHLX_hs g 5868602	1.67
	334026			CH22_FGENES.318_3	1.67
	317791	AI801500	Hs.128457	ESTs	1.67
	322235	AF086106		EST cluster (not in UniGene)	1.66
	331148	R73816	Hs.17385	ESTs	1.66
50	325452			CHL12_hs g 5866941	1.66
	315108	AW452184	Hs.232100	ESTs	1.66
	326014			CHL16_hs g 5867160	1.66
	307130	AI185234		EST singleton (not in UniGene) with exon hit	1.66
	300943	AA524545	Hs.224630	ESTs	1.66
55	319402	W21298		EST cluster (not in UniGene)	1.66
	310889	AI457948	Hs.170437	ESTs; Weakly similar to hyperpolarization-activated; cyclic nucleotide-gated channel 2 [H.sapiens]	1.66
	323371	AL135118		EST cluster (not in UniGene)	1.66
	335568			CH22_FGENES.581_4	1.66
	320654	AW263086	Hs.118112	ESTs	1.66
60	338983			CH22_DA59H18.GENSCAN.3-1	1.65
	330002			CHL16_p2 g 6623863	1.65
	315343	AW205477	Hs.179891	ESTs	1.65
	334487			CH22_FGENES.395_9	1.65
	312169	AJ064824	Hs.193385	ESTs	1.65
65	309668	AW204480	Hs.253414	EST	1.65
	309518	AW148928	Hs.248895	EST	1.65
	307965	AI421641		EST singleton (not in UniGene) with exon hit	1.65
	316787	AW369770	Hs.130351	ESTs	1.65
	300835	AA401858	Hs.224843	ESTs	1.65
	338763			CH22_EM:AC005500.GENSCAN.517-16	1.65
	303327	AA232729	Hs.154302	ESTs	1.65
	313231	AW139993	Hs.163682	ESTs	1.65

	334073		CH22_FGENES.327_28	1.65
	319901 T77138	Hs.8765	RNA helicase-related protein	1.65
	326530		CH.19_hs g 5867441	1.65
5	301126 A1802877	Hs.210843	ESTs; Weakly similar to dJ1039/K5.2 [H.sapiens]	1.65
	314043 AA827082		EST cluster (not in UniGene)	1.65
	304387 AA236027		EST singleton (not in UniGene) with exon hit	1.65
	322932 AA099732		EST cluster (not in UniGene)	1.65
	337272		CH22_FGENES.660-1	1.64
10	332694 AA262768	Hs.243901	KIAA1067 protein	1.64
	318996 Z44266		EST cluster (not in UniGene)	1.64
	315338 AW342028	Hs.256112	ESTs	1.64
	313329 AW293704	Hs.122658	ESTs	1.64
	318088 AW295409	Hs.137945	ESTs	1.64
	313835 A1538438	Hs.159087	ESTs	1.64
15	320035 AA378974	Hs.130720	ESTs; Weakly similar to CELLULAR NUCLEIC ACID BINDING PROTEIN [H.sapiens]	1.64
	309372 AW074330		EST singleton (not in UniGene) with exon hit	1.63
	324157 AW402236		EST cluster (not in UniGene)	1.63
	323829 AA354940	Hs.145958	ESTs	1.63
	302490 AA885502	Hs.187032	ESTs	1.63
20	333942		CH22_FGENES.301_8	1.63
	327489		CH.02_hs g 5867772	1.63
	301918 AA476777		EST cluster (not in UniGene) with exon hit	1.63
	315694 A1744068	Hs.160712	ESTs	1.63
	304405 AA282572		EST singleton (not in UniGene) with exon hit	1.63
25	310624 A1341594	Hs.157522	ESTs; Moderately similar to env protein [H.sapiens]	1.63
	319250 F11623		EST cluster (not in UniGene)	1.63
	310608 A1962234	Hs.196102	ESTs	1.63
	317348 A1348076	Hs.831	3-hydroxymethyl-3-methylglutaryl-Coenzyme A lyase (hydroxymethylglutaricaciduria)	1.63
30	306513 AA989230		EST singleton (not in UniGene) with exon hit	1.63
	320807 AA086110	Hs.188536	Homo sapiens clone 24838 mRNA sequence	1.63
	303710 A1269069	Hs.250852	ESTs; Highly similar to ubiquitin hydrolyzing enzyme I [H.sapiens]	1.63
	328291		CH.07_hs g 5888363	1.63
	304236 W83278		EST singleton (not in UniGene) with exon hit	1.63
35	317683 A1791700	Hs.127893	ESTs	1.63
	311860 AW440133	Hs.189690	ESTs	1.62
	312834 A1028309	Hs.114248	ESTs	1.62
	325328		CH.11_hs g 5866875	1.62
	313663 A1953261	Hs.169813	ESTs	1.62
40	327528		CH.02_hs g 6381882	1.62
	300429 AW449679	Hs.158739	ESTs; Highly similar to XG GLYCOPROTEIN PRECURSOR [H.sapiens]	1.62
	305169 AA663131		EST singleton (not in UniGene) with exon hit	1.62
	316621 A1021998	Hs.122138	ESTs	1.62
	329868		CH.14_p2 g 6272129	1.62
45	318035 A1744130	Hs.131201	ESTs	1.62
	300492 AL031709		multiple UniGene matches	1.62
	316532 A1307229	Hs.184304	ESTs	1.62
	332048 AA498019	Hs.201591	ESTs	1.62
	307113 A1183686		EST singleton (not in UniGene) with exon hit	1.62
	319127 N49476		EST cluster (not in UniGene)	1.62
50	331155 R87650	Hs.33439	ESTs; Weakly similar to III ALU SUBFAMILY J WARNING ENTRY III [H.sapiens]	1.61
	338220		CH22_EM:AC005500.GENSCAN.248-9	1.61
	315783 AW515270	Hs.118342	ESTs	1.61
	323571 AA984133	Hs.153260	o-Cbl-interacting protein	1.61
55	312240 R28628	Hs.203669	ESTs	1.61
	304569 AA490934		EST singleton (not in UniGene) with exon hit	1.61
	313179 A1076101	Hs.131704	ESTs	1.61
	326858		CH.20_hs g 6552462	1.61
	317276 A1823847	Hs.129988	ESTs	1.61
	312572 AA350125	Hs.187499	ESTs	1.61
60	311832 AW451654	Hs.257482	ESTs	1.61
	302103 AA452310	Hs.26090	ESTs; Weakly similar to T20B12.1 [C.elegans]	1.61
	308413 A1636253	Hs.196511	EST	1.61
	310077 A1620617	Hs.148585	ESTs	1.61
65	337780		CH22_EM:AC000097.GENSCAN.121-2	1.61
	327796		CH.05_hs g 5867982	1.61
	308352 A1610791		EST singleton (not in UniGene) with exon hit	1.61
	324539 A1378032	Hs.125892	ESTs	1.61
	303232 AA437414		EST cluster (not in UniGene) with exon hit	1.61
	337884		CH22_EM:AC005500.GENSCAN.54-2	1.61

	303620	AA397548	Hs.119151	ESTs	1.61
	303481	AA336839		EST cluster (not in UniGene) with exon hit	1.61
	314481	AA548589	Hs.105848	ESTs	1.61
5	300327	AI908894	Hs.245893	ESTs	1.6
	323473	AA262442		EST cluster (not in UniGene)	1.6
	326154			CH.17_hs gi 5887170	1.6
	331920	AA446885	Hs.99087	ESTs; Moderately similar to ZINC FINGER PROTEIN 141 [H.sapiens]	1.6
	323827	AW406878		EST cluster (not in UniGene)	1.6
	322452	W56710		EST cluster (not in UniGene)	1.6
10	310597	AI739071	Hs.158515	ESTs	1.6
	307871	AI368665		EST singleton (not in UniGene) with exon hit	1.6
	322215	AF088005		EST cluster (not in UniGene)	1.6
	318420	AI139857	Hs.143837	ESTs	1.6
15	332217	H98987	Hs.102383	EST	1.6
	324937	M79230	Hs.192398	ESTs	1.6
	320543	AF052176	Hs.158529	Homo sapiens clone 24457 mRNA sequence	1.6
	300674	AW467388		EST cluster (not in UniGene) with exon hit	1.6
	315193	AI241331	Hs.131765	ESTs	1.6
20	319713	R24204		EST cluster (not in UniGene)	1.6
	301210	AI379982	Hs.158944	ESTs	1.6
	309365	AW072881		EST singleton (not in UniGene) with exon hit	1.6
	321403	AW451454	Hs.247568	adenylate kinase 3	1.6
	321908	AA376936	Hs.20998	ESTs	1.6
	303349	AA382861		EST cluster (not in UniGene) with exon hit	1.6
25	324338	AL138357	Hs.247514	ESTs	1.6
	310599	AW300144		EST cluster (not in UniGene)	1.6
	333193			CH22_FGENES.88_15	1.6
	336433			CH22_FGENES.825_12	1.6
	312097	AI352098	Hs.157169	ESTs	1.6
30	311445	AW204237	Hs.192703	ESTs; Weakly similar to IIII ALU SUBFAMILY J WARNING ENTRY IIII [H.sapiens]	1.59
	317736	AI361722	Hs.192410	ESTs	1.59
	308147	AI488991		EST singleton (not in UniGene) with exon hit	1.59
	313489	AA017492	Hs.135655	ESTs	1.59
	316289	AA802488	Hs.122952	ESTs	1.59
35	326983			CH.21_hs gi 5867657	1.59
	314781	AW205298	Hs.202372	ESTs	1.59
	328397			CH.07_hs gi 5868397	1.59
	331970	AA461084	Hs.187677	ESTs	1.59
40	321744	N91419	Hs.12028	ESTs	1.59
	310509	AI292181	Hs.150036	ESTs	1.59
	315921	AI147545	Hs.114172	ESTs	1.59
	322049	AI928242	Hs.144383	ESTs	1.59
	301161	AA731518		EST cluster (not in UniGene) with exon hit	1.59
45	300548	AI026838	Hs.114689	ESTs	1.59
	319142	F07368		EST cluster (not in UniGene)	1.59
	313526	AW152283	Hs.249243	ESTs	1.59
	305937	AA883238		EST singleton (not in UniGene) with exon hit	1.58
	330123			CH.19_p2 gi 5671869	1.58
50	327819			CH.05_hs gi 5867968	1.58
	318250	AI478814	Hs.134603	ESTs	1.58
	306760	AI034094	Hs.169476	tubulin; alpha; ubiquitous	1.58
	322358	AA220235	Hs.246836	ESTs	1.58
	317866	AI690269	Hs.201345	ESTs	1.58
55	320725	AA703319	Hs.120967	ESTs	1.58
	311332	AW282247	Hs.255052	ESTs	1.58
	334893			CH22_FGENES.452_7	1.58
	318730	AA398215		EST cluster (not in UniGene)	1.58
	315889	AW271639	Hs.221744	ESTs	1.58
60	303702	AW500748	Hs.224961	ESTs; Weakly similar to 73 kDa subunit of cleavage and polyadenylation specificity factor [H.sapiens]	1.57
	315088	AI492660	Hs.170935	ESTs	1.57
	332514	AA156499	Hs.8454	protein kinase; cAMP-dependent; regulatory; type II; alpha	1.57
	335549			CH22_FGENES.576_10	1.57
	329532			CH.10_p2 gi 3983505	1.57
65	323140	AA180467		EST cluster (not in UniGene)	1.57
	313168	AI801098	Hs.151500	ESTs	1.57
	337896			CH22_EM:AC005500.GENSCAN.56-3	1.57
	330658	AA319514	Hs.211093	ESTs	1.57
	324585	AI823969	Hs.132678	ESTs	1.57

	317151	AW298195	Hs.255735	ESTs	1.57
	308818	AI819700	Hs.208231	EST	1.57
	326547			CH.19_hs gj5867307	1.57
5	318633	H06234	Hs.24888	ESTs	1.57
	320488	R31386		EST cluster (not in UniGene)	1.57
	306929	AI124514		EST singleton (not in UniGene) with exon hit	1.57
	338083			CH22_EM:AC005500.GENSCAN.174-1	1.57
	316868	AI660898	Hs.195602	ESTs	1.57
10	310837	AI472880	Hs.170480	ESTs	1.57
	328638			CH.07_hs gj6004473	1.57
	310074	AI651039	Hs.148559	ESTs	1.56
	327058			CH.21_hs gj6531865	1.56
	320076	AI653733	Hs.204079	ESTs	1.56
	322345	AF086529		EST cluster (not in UniGene)	1.56
15	314731	AI745498	Hs.204579	ESTs	1.56
	318687	H49619	Hs.127301	ESTs	1.56
	303841	AI934484		EST cluster (not in UniGene) with exon hit	1.56
	302370	AJ009849	Hs.199297	Homo sapiens GNAS1 gene encoding NESP55	1.56
	322571	AF156271		EST cluster (not in UniGene)	1.56
20	318050	AI052093	Hs.133132	ESTs	1.56
	303388	AL039604		EST cluster (not in UniGene) with exon hit	1.56
	323758	AA833858		EST cluster (not in UniGene)	1.56
	328389			CH.07_hs gj5868388	1.56
	329415			CH.Y_hs gj5868874	1.56
25	303915	AW468839	Hs.257767	EST	1.56
	338794			CH22_EM:AC005500.GENSCAN.528-1	1.56
	303074	AA243481	Hs.127320	ESTs; Weakly similar to KIAA0346 [H.sapiens]	1.56
	318807	F08434		EST cluster (not in UniGene)	1.56
	334287			CH22_FGENES.369_17	1.56
30	311828	AW024788	Hs.233374	ESTs	1.55
	304592	AA505833	Hs.162017	EST	1.55
	300785	AA682913	Hs.247179	ESTs; Weakly similar to KIAA0319 [H.sapiens]	1.55
	304821	AA603092		EST singleton (not in UniGene) with exon hit	1.55
	324605	AW502851	Hs.249978	ESTs	1.55
35	324473	AW501183		EST cluster (not in UniGene)	1.55
	300566	H86709	Hs.21371	son of sevenless (Drosophila) homolog 1	1.55
	314165	AA761285	Hs.221281	ESTs	1.55
	302868	AA157392		EST cluster (not in UniGene) with exon hit	1.55
40	314034	AI299137	Hs.154214	ESTs	1.55
	325389			CH.12_hs gj5866921	1.55
	331849	AA417078	Hs.193787	ESTs	1.55
	320536	AA331732	Hs.137224	ESTs	1.55
	303347	AA258033		EST cluster (not in UniGene) with exon hit	1.55
45	315769	AA744875	Hs.189413	ESTs	1.55
	317031	AA973297	Hs.126101	ESTs	1.55
	300203	AI827065	Hs.224877	ESTs	1.55
	304037	T26438		EST singleton (not in UniGene) with exon hit	1.55
	322613	AW160507		EST cluster (not in UniGene)	1.54
50	317687	AW138174	Hs.130651	ESTs	1.54
	322313	AF066386		EST cluster (not in UniGene)	1.54
	323992	AW411383	Hs.169688	ESTs	1.54
	325303			CH.11_hs gj5866908	1.54
	312701	AA457663	Hs.128127	ESTs	1.54
55	304787	AA582878		EST singleton (not in UniGene) with exon hit	1.54
	305849	AA861571		EST singleton (not in UniGene) with exon hit	1.54
	314557	AA401367	Hs.128647	ESTs	1.54
	316507	AI381515	Hs.158381	ESTs	1.54
	315023	AA533505	Hs.185844	ESTs	1.54
60	314820	AA513408	Hs.152307	ESTs	1.54
	323097	Z44354	Hs.180950	guanine nucleotide binding protein (G protein); q polypeptide	1.54
	325043	W27919	Hs.32944	inositol polyphosphate-4-phosphatase; type I; 107kD	1.54
	307892	AI376088	Hs.158759	EST	1.54
	324573	AA491600	Hs.181942	ESTs	1.54
	313092	AI923673	Hs.212827	ESTs	1.54
65	324696	AA641092	Hs.257339	ESTs	1.54
	303019	AF098363		EST cluster (not in UniGene) with exon hit	1.54
	317158	AI459140	Hs.129109	ESTs	1.54
	309538	AW151833		EST singleton (not in UniGene) with exon hit	1.54
	301568	AI146423	Hs.146709	ESTs	1.53

	315674	AA851923	Hs.191850	ESTs	1.53
	321861	N79341		EST cluster (not in UniGene)	1.53
	310890	AI184510	Hs.143728	ESTs	1.53
	330036			CH.17_p2 gl 8042048	1.53
5	316907	AA843868	Hs.190567	ESTs	1.53
	312299	AA972712	Hs.174818	ESTs	1.53
	331128	R51361	Hs.23423	ESTs	1.53
	305177	AA863591		EST singleton (not in UniGene) with exon hit	1.53
10	337685			CH22_EM:AC000097.GENSCAN.77-1	1.53
	335290			CH22_FGENES.527_3	1.53
	308896	AI858667		EST singleton (not in UniGene) with exon hit	1.53
	307944	AI418248		EST singleton (not in UniGene) with exon hit	1.53
	300867	AW340374	Hs.121033	neural precursor cell expressed; developmentally down-regulated 1	1.53
	335320			CH22_FGENES.534_7	1.53
15	329841			CH.14_p2 gl 8672062	1.53
	317916	AI565071	Hs.159983	ESTs	1.53
	332901			CH22_FGENES.38_2	1.53
	305413	AA724659		EST singleton (not in UniGene) with exon hit	1.53
20	316707	AI016387	Hs.184406	ESTs	1.53
	313693	AW469180	Hs.170651	ESTs	1.53
	316101	AA922236	Hs.221037	ESTs	1.53
	320796	AF038968	Hs.184543	secretory carrier membrane protein 1	1.53
	307451	AI248615		EST singleton (not in UniGene) with exon hit	1.53
25	323648	AI578968	Hs.152080	ESTs	1.53
	331482	N27515	Hs.40298	ESTs	1.53
	318059	AI023175	Hs.167022	ESTs	1.53
	325958			CH.16_hs gl 5887142	1.53
	315736	AA664265	Hs.230213	ESTs	1.53
30	314740	AW015887	Hs.119427	ESTs	1.52
	314117	AA224368	Hs.185184	ESTs	1.52
	301848	AA313954		EST cluster (not in UniGene) with exon hit	1.52
	338752			CH22_EM:AC005500.GENSCAN.513-10	1.52
	309314	AW009312		EST singleton (not in UniGene) with exon hit	1.52
35	301445	AI208364	Hs.128233	ESTs; Weakly similar to REGULATOR OF CHROMOSOME CONDENSATION [H.sapiens]	1.52
	308501	AI685263	Hs.201150	EST	1.52
	312330	AA835305	Hs.121574	ESTs	1.52
	318040	AI018150	Hs.148781	ESTs	1.52
40	336205			CH22_FGENES.719_10	1.52
	325701			CH.14_hs gl 5867028	1.52
	315009	AW189460	Hs.208358	ESTs	1.52
	303121	AW407585	Hs.27769	ESTs; Weakly similar to mCAC [M.musculus]	1.52
	309271	AI986221		EST singleton (not in UniGene) with exon hit	1.52
	328385			CH.07_hs gl 5868395	1.52
45	307700	AI318545		EST singleton (not in UniGene) with exon hit	1.52
	314591	AW103292	Hs.245328	ESTs	1.52
	304484	AA432067	Hs.258373	ESTs	1.52
	304382	AA232873		EST singleton (not in UniGene) with exon hit	1.52
	304232	W52674		EST singleton (not in UniGene) with exon hit	1.52
50	309853	AW298169	Hs.57553	tousled-like kinase 2	1.52
	312504	AW207346	Hs.143202	ESTs	1.52
	313134	N63406	Hs.258697	ESTs	1.52
	330391	AF015950	Hs.115258	telomerase reverse transcriptase	1.52
	314342	AI873048	Hs.258775	ESTs	1.51
55	305977	AA887283		EST singleton (not in UniGene) with exon hit	1.51
	301165	N85789	Hs.224155	ESTs; Weakly similar to PTERIN-4-ALPHA-CARBINOLAMINE DEHYDRATASE [H.sapiens]	1.51
	300613	AI932294	Hs.249604	ESTs; Weakly similar to B-CELL LYMPHOMA 6 PROTEIN [H.sapiens]	1.51
60	324124	AI554212	Hs.185684	ESTs; Weakly similar to SERINE/THREONINE-PROTEIN KINASE NRK2 [H.sapiens]	1.51
	308037	AI458207	Hs.174181	ESTs	1.51
	323909	AL043148	Hs.188257	ESTs	1.51
	315484	AW139500	Hs.116135	ESTs	1.51
	306700	AI022058		EST singleton (not in UniGene) with exon hit	1.51
	337978			CH22_EM:AC005500.GENSCAN.107-1	1.51
65	306855	AI083982		EST singleton (not in UniGene) with exon hit	1.51
	311045	AI569399	Hs.174748	ESTs	1.51
	315010	AA531082	Hs.240049	ESTs	1.51
	310205	AW025248	Hs.202445	ESTs	1.51
	310759	AW135924	Hs.224883	ESTs	1.51

	310954	AW449044	Hs.171298	ESTs	1.51
	312019	T77048	Hs.188750	ESTs	1.51
	334773			CH22_FGENES.430_5	1.51
5	332043	AA490831	Hs.125058	ESTs	1.51
	322850	AA286219		EST cluster (not in UniGene)	1.51
	337820			CH22_EM:AC005500.GENSCAN.67-3	1.51
	328993			CH.09_hs gi 5868538	1.51
	309245	AI972447		EST singleton (not in UniGene) with exon hit	1.51
10	312172	AI222168	Hs.191168	ESTs	1.51
	304039	T47349		EST singleton (not in UniGene) with exon hit	1.5
	301329	AI149653	Hs.190498	ESTs	1.5
	313378	AI949248	Hs.200381	ESTs	1.5
	324248	AW504918		EST cluster (not in UniGene)	1.5
15	308771	AI809301		EST singleton (not in UniGene) with exon hit	1.5
	334935			CH22_FGENES.484_3	1.5
	319764	AA019827		EST cluster (not in UniGene)	1.5
	318519	T27135		EST cluster (not in UniGene)	1.5
	332807			CH22_FGENES.7_9	1.5
	322310	AF086376		EST cluster (not in UniGene)	1.5
20	324557	AA489166	Hs.156933	ESTs	1.5
	332118	AA809585	Hs.162689	EST	1.5
	319539	RI9027		EST cluster (not in UniGene)	1.5
	313149	AW291092	Hs.201058	ESTs	1.5
	329722			CH.14_p2 gi 6065785	1.5
25	323514	AA861209		EST cluster (not in UniGene)	1.5
	308078	AI472621		EST singleton (not in UniGene) with exon hit	1.5
	337955			CH22_EM:AC005500.GENSCAN.100-10	1.5
	335905			CH22_FGENES.635_13	1.5

TABLE 14A shows the accession numbers for those primekeys lacking unigeneID's for Table 14. For each probeset we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

10	Pkey: CAT number: Accession:	Unique Eos probeset identifier number Gene cluster number Genbank accession numbers	
15	Pkey	CAT number	Accession
20	322064	234514_1	BE261397 Z78343 BE176419 AA383657 N90640 AA334052 AW955761 BE536232 AA374087 AA584776
	321409	197898_1	N71838 AA282003 T54072 AA761419 H92966 AB31371 AI095435 AI690247 R99331 AW964110 AA975590 AA346128
			H94198 C03864
	322092	46678_1	AF085833 R69689 AW341677 AA923375 BE327566 AW630415 R69601 AW615339
	321452	212379_2	AW962489 H64300 AA329527
	313603	199797_1	AA284333 AW468119 AA284334 AA810992
	320856	38098_1	AB040928 T94673 AI289313 AI536039 Z44366 BE141499 D60116 D61488 D59945 AA419503 R28090 R72988 H03255
25			AI189112 AI912312 AW511018 AI401349 AW470144 C14624 AI335797 Z40300 AI014456 D60269 D60115 T16722 AI370673
			D60270
	322139	46806_1	H53744 AF075088 H53797
	321500	552826_1	BE004271 AI248023 AI022157 H71899
	313733	441212_1	AA766346 AA809877 AA836116 AW469598 AW977404
30	322215	47002_1	AF088005 N51816 N51731
	322235	47070_1	AF086106 AI193589 AW665594 N71795 AA722627 AW665373 AI300251
	321632	286374_1	AW812795 AA419617 H87827 AW299775 AW382168 AW382133 BE171659 AW392392 BE171641 AA541393
	313633	120893_1	AA766825 AA811180 AA085906 AI762946 AW977820
	322310	47376_1	AF088376 W77804 W72689 AA837735
35	322313	47386_1	AF086386 W77947 W72708
	322322	47434_1	AF086431 AA88756 AI557237
	322331	47467_1	AF086467 W81444 W81445
	322345	47537_1	W95298 AF086529 AI912190 AW294159 AI458747 W94782
	322347	47545_1	AF086538 W85969 AI831911 W95835
40	322370	187612_1	AA330095 W25112 AA249401
	321739	43998_1	AL080280 T73124 H02689 AL080281
	321781	1511778_1	D78687 D78871 C18258
	314570	280469_1	AA904776 AA405696 AA405962
	300129	635249_1	AW028820 AI219068
45	322452	497108_2	AI147202 W56755 W56710
	321881	1651920_1	N79341 N99082 N47551
	323140	159551_1	AA180487 AA449184 AA464831 AA505048
	322520	38916_1	T55958 T57205 AF147346
	321914	85114_1	AA011603 N58604 N58611
50	322571	22297_1	NM_016102 AF156271 AA781868 AW152318 AW770403 AA909463 AA482996 AA758672
	322574	39412_1	AF156548 AA639787 AI675267 AI825497 AI823355
	314753	311451_1	AA463262 AA463615 AW160405 AW407583
	300370	3910_2	AW136181 AA581939 AK001221 AA694538 AA424043 AI016272 AA098960 AA884473 AI356180 BE391633 AA437086
			AI277866 AA098827 AA982680 BE172624 AA424101 AA320776 AW962967 N77431 AW858960 AW858897 T85649
			AA357743 AI827817 AI905672
55	322601	577912_1	AI082395 W92924 BE048524 AW005302 AI084474 AI369330 AI827710 AW135508 AW288694
	322613	34330_1	AW160507 NM_013367 AF191338 AA384939 AI445790 AA730309 BE397003 BE267753 AI979163 N50386 AW583671
			AW583608 BE074468 BE074479 BE074471 AW976283 AA604393 AW162122 W73648 AI823475 N75898 W73713
			AW470099 AW513238 AW025055 AW613115 AI923379 W58081 AW664525 AW196795 AI143619 AI565152 AA025406
			AA505846 AI685494 AA829964 N59156 N59163 R15442 AA826919 AI610221 AI200120 AA603279 AW150822 AI189513
			AI807122 AI016368 AI335868 AW583389 AI193892 AI956157 AI828879 AW591589 AW583446 AI855406 AW148396
			AI340255 AI867942 AA748525 AA876991 Z38516 AI874002 AI869474 N63100 AA429094 AA082443
			AW105663 AA693880 AW517398 AI768507 BE220851 AW978538 AA831489
			BE218300 BE327455 AL134620 R36741 R17999
			AL031709 AI248061 AA807658 AI240444
60	316055	409389_1	
	323316	981458_1	
	300492	25768_1	
65			

316141	423880_2	AW303457 AA972713 AA724265
323371	117336_2	N45114 N51465 BE087338 AI083551 AL135118 BE395609
307700	30923_11	BE280998 BE254670 BE294951 BE564979 AW405364 AA069256 AA129837 AI559687 BE281405 AW410850 BE041153
5		AI254811 AW301340 AI813335 AW301411 AI609469 AI611607 AI611616 AI377823 AI335509 AI613544 BE043165 AI371663
		AI340452 AI612066 AW072890 AI254558 AI349884 AI370095 AI613383 AI611946 AI613353 AI307414 AI318229 AI612685
		AW305327 AW268924 AI370063 AI349292 BE049068 AI369098 AW274099 AI344845 AW075187 AI053401 AI345220
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	329728 c14_p2	
	306890	AI082235
	308100	AI475949
	308147	AI498991
	306929	AI124514
55	308352	AI610791
	308383	AI624497
	308521	AI689808
	308561	AI701559
	308617	AI738720
60	308771	AI809301
	308828	AI824829
	308896	AI858667
	303019 41850_1	AF098363 AF098365
	303084 44211_1	AF174008 AF174027 AF174106
65	305092 AA642912	
	305169	AA663131
	305177	AA663591
	305235	AA670480
	305413	AA724659

	305849	AA861571
	305854	AA862733
	307113	AI183688
	307130	AI185234
5	305937	AA883238
	305877	AA887293
	307451	AI248615
	307513	AI274307
	307848	AI364188
10	307871	AI388665
	307881	AI370434
	307832	AI230822
	307844	AI418248
	307854	AI418692
15	307865	AI421641
	309245	AI972447
	309271	AI986221
	309365	AW072861
	309372	AW074330
20	309435	AW090537
	309506	AW137700
	309536	AW151833
	309709	AW242630
25	325417 c12_hs	
	325450 c12_hs	
	325452 c12_hs	
	309815	AW292760
	309839	AW296076
	309849	AW297444
30	309906	AW339340
	302705 31765_1	U09060 U09061
	304037	T26438
	304039	T47349
	304236	W83278
35	304257	AA053294
	304382	AA232873
	304405	AA282572
	304561	AA489792
	304569	AA490934
40	304767	AA582678
	304821	AA603092
	327819 c_5_hs	
	304968	AA614308
	306382	AA68967
45	331263 47479_1	AW780192 AA015718 W02571
	332252 1663967_1	N63882 T91174

TABLE 14B shows the genomic positioning for those primekeys lacking unigene ID's and accession numbers in Table 14. For each predicted exon, we have listed the genomic sequence source used for prediction. Nucleotide locations of each predicted exon are also listed.

10 Pkey: Unique number corresponding to an Eos probeset
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers
 Strand: Indicates DNA strand from which exons were predicted.
 Nt_position: Indicates nucleotide positions of predicted exons.

	Pkey	Ref	Strand	Nt_position
15	332807	Dunham, I. et.al.	Plus	297686-297808
	332808	Dunham, I. et.al.	Plus	298277-298360
	332812	Dunham, I. et.al.	Plus	309688-310561
	332901	Dunham, I. et.al.	Plus	1841954-1842090
20	333149	Dunham, I. et.al.	Plus	3574317-3574413
	333916	Dunham, I. et.al.	Plus	8288994-8299169
	334026	Dunham, I. et.al.	Plus	9196549-9196681
	334061	Dunham, I. et.al.	Plus	9686941-9687077
	334073	Dunham, I. et.al.	Plus	9792201-9792374
25	334150	Dunham, I. et.al.	Plus	10529221-10529854
	334379	Dunham, I. et.al.	Plus	13908356-13908467
	334719	Dunham, I. et.al.	Plus	15778859-15779028
	334773	Dunham, I. et.al.	Plus	16235169-16235328
	334893	Dunham, I. et.al.	Plus	19302753-19302881
30	334935	Dunham, I. et.al.	Plus	20108247-20108373
	335146	Dunham, I. et.al.	Plus	21491282-21491457
	335320	Dunham, I. et.al.	Plus	22542132-22542246
	335568	Dunham, I. et.al.	Plus	24935021-24935655
	335586	Dunham, I. et.al.	Plus	24990333-24990497
35	335601	Dunham, I. et.al.	Plus	25044923-25045157
	336038	Dunham, I. et.al.	Plus	28019788-28019877
	336123	Dunham, I. et.al.	Plus	30051089-30051186
	336268	Dunham, I. et.al.	Plus	31897555-31898040
40	337173	Dunham, I. et.al.	Plus	23624127-23624224
	337460	Dunham, I. et.al.	Plus	32536159-32536395
	337685	Dunham, I. et.al.	Plus	3547161-3547245
	337738	Dunham, I. et.al.	Plus	3850500-3850643
	337780	Dunham, I. et.al.	Plus	4113783-4113990
	337965	Dunham, I. et.al.	Plus	7034267-7034392
45	337976	Dunham, I. et.al.	Plus	7186011-7186119
	338030	Dunham, I. et.al.	Plus	8072708-8072827
	338112	Dunham, I. et.al.	Plus	10391398-10391600
	338165	Dunham, I. et.al.	Plus	12205719-12205875
50	338178	Dunham, I. et.al.	Plus	12800037-12800181
	338427	Dunham, I. et.al.	Plus	19685043-19685354
	338506	Dunham, I. et.al.	Plus	21221871-21221853
	338784	Dunham, I. et.al.	Plus	27114697-27114763
	338910	Dunham, I. et.al.	Plus	28795375-28795551
	339047	Dunham, I. et.al.	Plus	30760783-30760968
55	332864	Dunham, I. et.al.	Minus	1390386-1390298
	332933	Dunham, I. et.al.	Minus	2035790-2035681
	333193	Dunham, I. et.al.	Minus	3832993-3832494
	333712	Dunham, I. et.al.	Minus	7286177-7286073
	333940	Dunham, I. et.al.	Minus	8523830-8523671
60	333942	Dunham, I. et.al.	Minus	8552629-8552330
	334287	Dunham, I. et.al.	Minus	13294116-13293871
	334387	Dunham, I. et.al.	Minus	13946021-13945781
	334487	Dunham, I. et.al.	Minus	14432191-14432132
	334913	Dunham, I. et.al.	Minus	19463909-19463815
65	335109	Dunham, I. et.al.	Minus	21325782-21325687
	335250	Dunham, I. et.al.	Minus	21852922-21852828

	335288	Dunham, I. et al.	Minus	22304275-22303770
	335290	Dunham, I. et al.	Minus	22309950-22309891
	335549	Dunham, I. et al.	Minus	24666203-24666128
5	335862	Dunham, I. et al.	Minus	26690300-26690125
	335884	Dunham, I. et al.	Minus	26694537-26694382
	335905	Dunham, I. et al.	Minus	26988888-26988719
	336205	Dunham, I. et al.	Minus	30477458-30477311
	336276	Dunham, I. et al.	Minus	32093320-32093181
10	336433	Dunham, I. et al.	Minus	34067540-34067425
	336605	Dunham, I. et al.	Minus	15616509-15616358
	336616	Dunham, I. et al.	Minus	26021027-26020848
	336679	Dunham, I. et al.	Minus	2035780-2035681
	337043	Dunham, I. et al.	Minus	17407330-17407251
	337272	Dunham, I. et al.	Minus	28241476-28241307
15	337357	Dunham, I. et al.	Minus	30906179-30906109
	337393	Dunham, I. et al.	Minus	31471747-31471569
	337497	Dunham, I. et al.	Minus	33371317-33371258
	337646	Dunham, I. et al.	Minus	2648689-2648632
20	337920	Dunham, I. et al.	Minus	6051648-6051510
	338083	Dunham, I. et al.	Minus	9318438-9318301
	338220	Dunham, I. et al.	Minus	14166440-14166104
	338752	Dunham, I. et al.	Minus	26421374-26421135
	338763	Dunham, I. et al.	Minus	26628148-26628009
	338993	Dunham, I. et al.	Minus	29908865-29908702
25	339209	Dunham, I. et al.	Minus	32492953-32492593
	325240	5866848	Minus	32301-32650
	329532	3983505	Plus	42937-43014
	329522	3983507	Minus	35265-35458
30	329519	3983510	Plus	18407-18597
	329511	3983514	Plus	20965-21325
	325326	5866875	Plus	47726-48024
	325303	5866908	Minus	73556-73630
	325389	5866921	Plus	239672-239759
35	325417	5866925	Minus	110635-110745
	325450	5866941	Minus	435379-435552
	325452	5866941	Minus	704103-704202
	325498	5866967	Plus	173372-173930
	325587	6682462	Plus	126724-126967
40	325602	5866994	Plus	79122-79251
	325701	5867028	Minus	72836-73046
	325780	6381953	Plus	63634-63873
	329722	6065785	Minus	112713-112992
	329728	6065785	Minus	207544-207741
45	329666	6272129	Plus	98307-98446
	329815	6624888	Minus	68431-68720
	329841	6672062	Minus	40181-40331
	325824	5867048	Minus	42450-42833
	325868	5867076	Minus	94358-94628
50	325902	5867101	Minus	127729-127842
	325958	5867142	Plus	53437-53550
	326014	5867160	Minus	10358-10447
	329941	6165199	Minus	34319-34411
	330002	6623983	Plus	48097-48158
55	326154	5867170	Minus	7103-7179
	326023	5867245	Plus	171789-171898
	326278	5867269	Plus	75250-75903
	330036	6042048	Plus	117120-117216
	326547	5867307	Minus	623877-623870
60	326495	5867423	Plus	11843-11930
	326507	5867435	Minus	13038-13111
	326505	5867435	Minus	8818-8949
	326506	5867435	Minus	8368-8509
	326530	5867441	Minus	303000-303122
65	326508	6682496	Plus	78904-79112
	330120	6671864	Minus	127553-127658
	330123	6671869	Minus	35311-35406
	326858	6552462	Minus	69337-69670
	326983	5867657	Minus	16023-16581
	327014	5867664	Plus	1017830-1017788

	326930	6456782	Plus	606950-607705
	326920	6456782	Minus	42425-42519
	327058	6531965	Plus	2384268-2384835
	327061	6531965	Minus	3486389-3486673
5	327075	6531965	Plus	4041318-4041431
	327120	6531970	Minus	6-1088
	330126	6093735	Plus	82458-82623
	327157	5866841	Minus	4408-4748
	327183	5867442	Plus	84317-84531
10	327182	5867445	Minus	194652-194764
	327288	5867481	Plus	48583-48773
	327469	5867772	Plus	145549-145708
	327489	6004459	Minus	57796-58015
	327526	6381882	Minus	97010-97123
15	327574	5867818	Plus	68767-69128
	327665	5867839	Plus	141738-141900
	327752	5867949	Plus	93721-94421
	327819	5867968	Minus	92202-92717
	327798	5867982	Plus	85287-85405
20	330260	6671884	Plus	45203-45269
	330282	6671910	Plus	3982-4114
	328078	5868008	Plus	72807-72865
	328121	5868031	Plus	153782-153850
	328190	5868077	Plus	21082-21165
25	328227	5868105	Minus	21082-21242
	327871	5868131	Minus	88889-89221
	328018	5902482	Minus	542547-543133
	328624	5868246	Minus	120666-120838
	328744	5868290	Plus	138639-138722
30	328799	5868316	Minus	80771-80923
	328291	5868363	Minus	144244-144434
	328329	5868375	Plus	191709-192239
	328369	5868388	Plus	75371-75583
	328385	5868395	Plus	369952-370155
35	328397	5868397	Plus	344867-345063
	328412	5868405	Plus	86427-86519
	328538	5868485	Plus	3814-4243
	328658	6004473	Plus	782616-782729
	328638	6004473	Plus	294618-294903
40	328903	5868514	Plus	23625-24468
	328960	6456775	Plus	38547-38837
	330320	5932415	Minus	54458-54697
	328993	5868538	Plus	49160-50084
	329081	5868602	Plus	93368-93510
45	329089	5868614	Plus	25805-26923
	329109	5868626	Plus	102168-102273
	329182	5868716	Plus	168936-167020
	328218	5868726	Minus	71408-71707
	329224	5868728	Plus	27422-27664
50	329246	5868732	Minus	250541-250782
	329415	5868874	Plus	1011438-1011818
	329454	5868887	Plus	51342-51593

TABLE 15: 169 GENES WITH SEQUENCE INFORMATION DEPICTED IN TABLE 16

Table 15 depicts UnigeneID, UnigeneTitle, Primekey, Predicted Cellular Localization, and Exemplar Accession for all of the sequences in Table 16. The information in Table 15 is linked by EosCode to Table 16.

5	Pkey:	Unique Eos probeset identifier number				
	ExAccn:	Exemplar Accession number, Genbank accession number				
	UnigeneID:	Unigene number				
	Unigene Title:	Unigene gene title				
	EosCode:	Internal Eos name				
10	Localization:	Predicted cellular localization of gene product				
15	Pkey	ExAccn	UnigeneID	Unigene Title	EosCode	Localization
20	100394	D84276	Hs.66052	CD38 antigen (p45)	PBC1	plasma membrane
	100452	D87742	Hs.241552	KIAA0268 protein	PAB7	not determined
	101249	L33881	Hs.1904	protein kinase C, iota	OAA1	cytoplasmic
	101485	M24738		selectin E (endothelial adhesion molecule	ACC5	plasma membrane
	101514	M28214	Hs.123072	RAB3B, member RAS oncogene family	PFJ2	cytoplasmic
25	101851	M94250	Hs.82045	midkine (neurite growth-promoting factor	LBH9	secreted
	102398	U42359		gbHuman N33 protein form 1 (N33) gene,	PDG3	
	102522	U53347	Hs.183556	solute carrier family 1 (neutral amino a	PFJ4	plasma membrane
	102689	U71207	Hs.29279	eyes absent (Drosophila) homolog 2	LEM9	cytoplasmic
	103119	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta	LBG2	plasma membrane
30	103709	AA037316	Hs.13804	hypothetical protein dJ462023.2	PDO6	
	104080	AA402871	Hs.57771	kallikrein 11	PBA8	secreted
	104144	AA447439	Hs.183380	hypothetical protein FLJ13590	PDM3	
	104691	AA011176	Hs.37744	Homo sapiens beta-1 adrenergic receptor	PAV1	plasma membrane
	105370	AA236476	Hs.22791	transmembrane protein with EGF-like and	PDM9	plasma membrane
35	106149	AA424881	Hs.256301	hypothetical protein MGC13170	PDO8	
	106579	AA456135	Hs.23023	ESTs	PAA4	plasma membrane
	107102	AA609723	Hs.30652	KIAA1344 protein	PAA3	not determined
	107217	D51095		DKFZP588E1621 protein	PDG8	
	108153	AA054237	Hs.40808	ESTs	PBF1	plasma membrane
40	109014	AA156780	Hs.262036	ESTs, Weakly similar to Z223_HUMAN ZINC	PDG7	
	109112	AA169379	Hs.257924	hypothetical protein FLJ13782	BCU4	not determined
	109890	H04649	Hs.20843	Homo sapiens cDNA FLJ11245 fis, clone PL	PDG4	
	110151	H18838	Hs.31608	hypothetical protein FLJ20041	PAV9	plasma membrane
	112971	T17185	Hs.83883	transmembrane, prostate androgen induced	CHA1	not determined
45	113021	T23859	Hs.129836	KIAA1028 protein	PDO3	
	114908	AA236545	Hs.54973	cadherin-like protein VR20	PFJ6	plasma membrane
	114985	AA250737	Hs.72472	ESTs	BCY2	mitochondrial
	116393	AA599463		hypothetical protein MGC2648	PDV3	secreted
	116416	AA609219	Hs.39982	ESTs	OAB6	
50	117698	N41002	Hs.45107	ESTs	PDT9	ER
	117984	N51919	Hs.106778	ATPase, Ca++ transporting, type 2C, memb	PAJ5	not determined
	118985	N94303	Hs.55028	ESTs, Weakly similar to I54374 gene NF2	PDM8	
	118018	N95796	Hs.278685	Homo sapiens prostasin mRNA, complete cds		-PAB2 plasma membrane
	119126	R45175	Hs.117183	ESTs	PBF8	
55	120992	AA398246	Hs.97594	KIAA1210 protein	PDG5	
	121710	AA418011		prostate androgen-regulated transcript 1	PDV5	
	121913	AA428062		ESTs; protease inhibitor 15 (PI15)	BCU7	vesicular
	122041	AA431407	Hs.98732	Homo sapiens Chromosome 16 BAC clone CIT		PAZ1 not determined
	122593	AA453310	Hs.128749	alpha-methylacyl-CoA racemase	PDO1	
60	123209	AA489711	Hs.203270	ESTs, Weakly similar to ALU1_HUMAN ALU S		PAA2 plasma membrane
	124526	N62096	Hs.283185	ESTs, Weakly similar to JC7328 amino acid	PAV4	plasma membrane
	126399	AA128075		transmembrane, prostate androgen induced	PDY4	
	126845	A167942	Hs.81635	six transmembrane epithelial antigen of	PAA5	plasma membrane
	126966	R38438	Hs.182575	solute carrier family 15 (H+/peptide tra	PDO5	plasma membrane
65	127537	AA569531	Hs.162859	ESTs	PAA8	not determined
	128790	AA291725	Hs.105700	secreted frizzled-related protein 4	8CX2	secreted
	129109	AA491295	Hs.108708	calcium/calmodulin-dependent protein kin	PFJ7	
	129184	W26769	Hs.109201	CGI-86 protein	PAV6	vesicular
	129389	AA621604		spondin 2, extracellular matrix protein	CJAS	not determined

	129404	AA172056	ESTs	PAB4	
	129534	R73640	Hs.11260 hypothetical protein FLJ11264	PAJ3	secreted
	130760	AA128997	Hs.18953 phosphodiesterase 8A	PEE8	nuclear
	131425	AA219134	Hs.26691 ESTs	PBA7	
5	132884	AA031360	ESTs	PAA7	plasma membrane
	132887	AA032221	Hs.61635 six transmembrane epithelial antigen of	PM17	plasma membrane
	133179	U81599	Hs.68731 homeo box B13	PFJ5	nuclear
	133330	U42360	Hs.71119 Putative prostate cancer tumor suppressor	PDM1	plasma membrane
	133520	X74331	Hs.74519 primase, polypeptide 2A (58kD)	PDM2	
10	133724	U07919	Hs.75746 aldehyde dehydrogenase 1 family, member		PDT1 mitochondrial
	133724	U07919	Hs.75746 aldehyde dehydrogenase 1 family, member		PDT1 mitochondrial
	133944	AA045870	Hs.7780 Homo sapiens mRNA; cDNA DKFZp564A072 (fr		PAB9 cytoplasmic
	134110	U41060	Hs.79138 LJV-1 protein, estrogen regulated	BCR4	plasma membrane
	301805	AJ800004	Hs.142848 hypothetical protein	PEU4	nuclear
15	302005	AJ869868	Hs.123119 MAD (mothers against decapentaplegic, DrPB)6		cytoplasmic
	302881	AA508353	Hs.105314 relaxin 1 (H1)	PBH3	secreted
	303506	AA340605	Hs.105887 ESTs, Weakly similar to Homolog of rat Z	PEG4	
	303699	D30891	Hs.19525 hypothetical protein FLJ22784	PBM4	not determined
	303753	AW503733	Hs.8414 KIAA1488 protein	PBY3	not determined
20	308050	AJ460004	Hs.31608 hypothetical protein FLJ20041	PEU5	plasma membrane
	310382	AJ734009	Hs.127699 KIAA1603 protein	PCQ8	
	310431	AJ420227	Hs.149358 ESTs, Weakly similar to A46010 X-linked	PBH1	plasma membrane
	310573	AW292180	Hs.156142 ESTs	PEN3	plasma membrane
	310598	AJ338013	Hs.140546 ESTs	PCW3	
25	310816	AJ973051	Hs.224965 ESTs	PET5	
	311598	AJ682088	Hs.79375 holocarboxylase synthetase (biotin-prop	PBH8	
	313676	AA861697	Hs.120591 ESTs	PBY2	
	314121	AJ732100	Hs.187619 ESTs	PBY1	
	314691	AW207206	Hs.136319 ESTs	BFF8	not determined
30	314785	AJ538228	Hs.32976 guanine nucleotide binding protein 4	CB07	cytoplasmic
	314907	AJ672225	Hs.222886 ESTs, Weakly similar to TRHY_HUMAN TRICH		PBM2 not determined
	315051	AW282425	ESTs	PBM9	
	315052	AA876910	Hs.134427 ESTs	PBJ7	plasma membrane
	316442	AA760894	Hs.153023 ESTs	PBJ9	
35	317548	AJ854187	Hs.195704 ESTs	PBQ6	
	317869	AW295184	Hs.129142 deoxyribonuclease II beta	PBQ7	
	318524	AW291511	Hs.159068 hypothetical protein FLJ10188	PBJ1	cytoplasmic
	319191	AF071538	prostate epithelium-specific Ets transcr	PEN1	
	319763	AA460775	Hs.6295 ESTs, Weakly similar to T17248 hypotheti	PEO7	
40	320324	AF071202	Hs.139338 ATP-binding cassette, sub-family C (CFTR	PBH5	plasma membrane
	320561	NIM_006953	Hs.159330 uroplakin 3	PEL9	plasma membrane
	320796	AF038968	Hs.31218 secretory carrier membrane protein 1	PBY4	not determined
	321441	AW297633	Hs.118498 Homo sapiens LUCA-15 protein mRNA, splic		PBY8 not determined
	322303	W07459	Hs.157601 ESTs	CBF9	secreted
45	322782	AA056060	Hs.202577 Homo sapiens cDNA FLJ12166 fis, clone MA		PBQ1 not determined
	322818	AW043782	Hs.293618 ESTs	PCQ7	plasma membrane
	323228	AF055019	Hs.21906 Homo sapiens clone 24670 mRNA sequence		PC12 not determined
	323287	AA639902	Hs.104215 ESTs, Moderately similar to SPCN_HUMAN S		PBJ5
	324295	AJ146688	Hs.143691 ESTs	PBQ9	not determined
50	324430	AA484018	Hs.184598 Homo sapiens cDNA: FLJ23241 fis, clone C		PBY6 not determined
	324603	AW016378	Hs.292834 ESTs	PBM3	
	324617	AA508552	Hs.195839 ESTs, Weakly similar to I38022 hypotheti	PBH4	cytoplasmic
	324626	AJ685484	gb:tt88f04.x1 NCL_CGAP_P28 Homo sapiens	PCW8	
	324658	AJ694767	Hs.129179 Homo sapiens cDNA FLJ13581 fis, clone PL		PBJ4 plasma membrane
55	324718	AJ557019	Hs.116487 small nuclear protein PRAC	CBK1	nuclear
	330211			PBJ2	not determined
	330546	U31382	Hs.299867 guanine nucleotide binding protein 4	PEW4	cytoplasmic
	330762	AA449677	Hs.15251 hypothetical protein	PBM1	not determined
	330780	T48536	Hs.122764 TMPRSS2, transmembrane protease, serine		PEL3 plasma membrane
60	330892	AA149579	Hs.91202 ESTs	PBQ4	plasma membrane
	331099	R36671	Hs.14848 Homo sapiens mRNA; cDNA DKFZp564D016 (fr		PCQ1 cytoplasmic
	331490	N32912	Hs.291039 ESTs	PC14	nuclear
	331889	AA431407	Hs.98802 ESTs, Moderately similar to T14342 NSD1	PBH7	not determined
	332247	N58172	gb:za21f09.s1 Soares fetal liver spleen	PBQ5	nuclear
65	332398	AA340504	gb:hw31a09.x1 NCL_CGAP_KJd11 Homo sapien		PBJ8 not determined
	332697	T94885	transgelin 2	PBQ8	secreted
	332798			PBH2	nuclear
	334447			PBY9	not determined
	338255			PBY7	not determined

	401424				PFG2	mitochondrial
	407122	H20276	Hs.31742	ESTs	PEW7	
	408430	S78876	Hs.44926	dipeptidylpeptidase IV (CD26, adenosine	PEZ3	plasma membrane
5	408826	AF216077	Hs.48376	Homo sapiens clone HB-2 mRNA sequence	PEY1	
	409282	AK000631	Hs.52256	hypothetical protein FLJ20624	PFG1	nuclear
	409361	NM_005982	Hs.54416	sine oculis homeobox (Drosophila) homolog	PEW3	nuclear
	411096	U80034	Hs.68583	mitochondrial intermediate peptidase	PEZ9	mitochondrial
	413125	BE244589	Hs.75207	glyoxalase I	PFJ3	cytoplasmic
10	413623	AA825721	Hs.246973	ESTs	OBH6	
	414422	AA147224	Hs.337232	Homeo box A13	PFC6	
	415263	AA948033	Hs.130853	ESTs	PEZ5	
	417153	X57010	Hs.81343	*collagen, type II, alpha 1 (primary ost	PFJ1	secreted
	418601	AA279490	Hs.86368	calmegin	PFA1	ER
15	418848	AJ820961	Hs.193465	ESTs	PEY4	
	418882	NM_004996	Hs.89433	ATP-binding cassette, sub-family C (CFTR	OBH2	
	419839	U24577	Hs.93304	*phospholipase A2, group VII (platelet-a	PFH9	secreted
	421887	AW161450	Hs.109201	CGI-86 protein	PFH2	plasma membrane
	422083	NM_001141	Hs.111256	*arachidonate 15-lipoxygenase, second ty	PFH5	cytoplasmic
20	424565	AW102723	Hs.75295	guanylate cyclase 1, soluble, alpha 3	PFA3	
	425071	NM_013989	Hs.154424	*deiodinase, iodothyronine, type II"	PFH6	secreted
	425710	AF030880		solute carrier family, member 4	PFD4	plasma membrane
	427958	AA418000	Hs.98280	potassium intermediate/small conductance	PFH1	plasma membrane
	428819	AL135623	Hs.193914	KIAA0575 gene product	PFD8	nuclear
25	429900	AA460421	Hs.30875	ESTs	PEZ7	
	429918	AW873988	Hs.119383	ESTs	PEY5	
	430228	BE245562	Hs.2551	adrenergic, beta-2-, receptor, surface	PEZ4	plasma membrane
	431217	NM_013427	Hs.250830	Rho GTPase activating protein 6	PFG6	nuclear
	431716	D89053	Hs.268012	fatty-acid-Coenzyme A ligase, long-chain	PEZ1	
30	431892	NM_002742	Hs.2891	protein kinase C, mu	PFH4	cytoplasmic
	432189	AA527841		gbmh30c04.s1 NCI_CGAP_Pr3 Homo sapiens	PFA2	
	432244	AI669973	Hs.200574	ESTs	PEW8	
	432437	W07088	Hs.293685	ESTs	PFG3	
	432966	AA650114	Hs.325198	ESTs	PEY3	
35	439176	AI448444	Hs.190394	ESTs, Weakly similar to B28096 line-1 pr	PEW5	
	440260	AI972867	Hs.7130	copine IV	PEW6	
	440901	AA909358	Hs.128612	ESTs	PFC8	
	445424	AB028945		cortactin SH3 domain-binding protein	PEZ6	
	446320	AF126245	Hs.14791	*acyl-Coenzyme A dehydrogenase family, m	PFH7	
40	447210	AF035269		phosphatidylserine-specific phospholipas	PFH8	
	449156	AF103907	Hs.171353	prostate cancer antigen 3, non-coding DD	PEZ8	
	449625	NM_014253		odx (odd Oz/ten-m, Drosophila) homolog 1	PEZ2	plasma membrane
	449650	AF055575	Hs.23838	calcium channel, voltage-dependent, L ty	PFD2	plasma membrane
	451939	U80456	Hs.27311	single-minded (Drosophila) homolog 2	PFJ8	
45	451982	F13036	Hs.27373	Homo sapiens mRNA; cDNA DKFZp564O1763 (f	PFG9	plasma membrane
	452039	AI922988		ESTs	PFD8	
	452340	NM_002202	Hs.505	ISL1 transcription factor, LIM/homeodoma	PFG4	nuclear
	452784	BE463857	Hs.151258	hypothetical protein FLJ21062	PFC5	cytoplasmic
	452946	X95425	Hs.31092	EphA5	PFH3	plasma membrane

TABLE 15A shows the accession numbers for those primekeys lacking a unigeneID in Table 15. For each probeset we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

Pkey:	Unique Eos probeset Identifier number
CAT number:	Gene cluster number
Accession:	Genbank accession numbers

Pkey	CAT number	Accession
116393	131543_1	AI972402 AI634409 AI523716 AI799749 W44518 AI424438 AI688513 AI971048 AI686324 AW013854 AA588483 AA528111 AI627428 AI582200 AI669296 AI826926 AI620526 AI669858 AI972458 AI924500 AA512903 W44517 AA335363 AW238997 BE300165 BE250665 AA284195 AA523420 W52834 AI471970 AI952824 AW003820 AW009463 AA669796 AA114968 AI653342 AA115038 AI342150 AI082100 AI968211 W51894 AI804005 AI201420 AI123210 AI738405 AI674964 AI870341 AW027500 AI493316 AI333193 AI139353 AA599463 AI656163 AI804200 AI365321 AI990213 AI657011 AA650025 AI968810 AI341978 AA599839 AW592602 AA644289 AI468578 AI565265 AI565228 BE221535 AW973052
101485	18113_1	AA296520 AL021940 M30640 NM_000450 M24736 M61894 AL047443 H39560 AI694691 AA916787 AI214786 AA939085 AI150616 AA412553 AA412545 AI051015 T27654 AA694430
126399	17331_1	AA088767 AF224278 AA128075 AL035541 AA027826 AI781441 AI972096 AW071693 AI742327 AI377498 AI804815 AI640802 AI885001 AI921394 AA595115 N71820 AI921217 AW007283 AI467828 AI369306 AA917446 AI493588 AA088701 AA126889 AI936228 AIW204238 AI039567 AI925027 BE138909 AW452945 AW135998 AA310984 AA027880 AW073519 AI537597 AA953976 AI521341 AW273569 AW050740 AA536113 AA559064 AI474392 AW135709 AA535181 AW572859 AA570597 AI905484 AI677810 AI587642 AW875102 AA424310 AA482527 N64182 AA658276 AW889117 AA486591 AW889172 AI381890 AI381891 AI673419 AI990950 AA487031 AI272934 AI150585 AA229168 AW316722 AI142707 BE222396 AA814168 AA122028 AW338227 AA632457 AI968728 AW369662 AA512956 AA541675 AA451748 AI250993 BE146418 AA122025
132964	94346_1	AI362575 AI805082 AW263421 AI432462 AA135870 AA031360 AA031604 AA298475 AA298464
129389	21074_1	NM_012445 AB027468 BE407510 BE047605 AA047125 AW084003 AA149494 AA149490 AA292528 AA570505 AA528186 AW008250 AW007762 AI341557 AI798668 AI972710 AI377866 AI962810 AI084783 AI458032 AI190971 AW148913 AA372354 AW970032 AIW007428 AA650188 AI123203 AI122890 AI280975 W73595 W73495 AI863238 AA374109 AA603988 AW149089 AW957523 AI307748 AI921087 AI384663 F24537 AI380460 AI367500 AI189309 AI814701 AI766821 AW572108 AA037024 AW072576 AA578293 AI288103 AA235464 AW450642 AA574230 AW294024 AI589228 AI580733 AW512227 AA877009 AI660255 AW188587 AA558228 AI572782 AA658397 AI274628 AI888359 AA864573 AI264439 AA821604 AW515493 AW243333 Z39737 AI567038 AA573997
129404	156454_1	AA573559 AW238431 AI652870 AI684973 AA034505 AA047126
107217	9836_1	AI267700 AI720344 AA191244 AI023543 AI469633 AA172056 AW958465 AA172238 AW953397 AA355086 AL080235 AA031750 D81382 AI480231 AI095947 AI560953 BE010721 AI870290 AA374945 AA125792 D51527 D51556 AI685541 D51559 AW117288 AA195741 AI675138 AW593439 AI201885 T30590 AW952100 D51095 AA523884 W70043 AA987586 AI421515 AI205532 AA127069 AI337387 D51595 AI453785 AW075677 AW088359 C14287 C14284
121710	19266_1	AF163474 NM_016590 AF163475 AI781105 AI770098 AA410580 AA411616 AI590343 AI739050 AL050198 AI862645 AA419104 AA513809 AA333032 AI816915 AW139625 AA640889 AI311391 AI627693 AW135514 AA419011 AI269149 AI245259 AI970008 AI970017 AW139445 AA569503 AI761072 AI766179 AI759995 AI300776 AI870129 AW150770 AA226501 AA226220
121913	291015_1	AI249368 AI742316 AA428062 AA442089 AI864189 BE349478 AI803475 AI584049 BE552085 AI088609 AI264197 AI888144 AI129474 AI307145 BE181300 AW058403 AI696838 AW748598 AA442196 AI216428
102398	entrez_U42359U42359	
315051	347217_1	AW292425 BE487167 AI702953 BE550961 BE222309 AI299348 AI693336 AA541708
324626	338411_1	AI685464 AW971336 AA513587 AA525142
319191	16065_1	NM_012391 AF071538 AB031549 AI885592 AI745528 AA682204 AW130657 AA682164 AW971121 AI668916 AA513274 AI991223 AI979170 AW288436 AA639821 AI859010 AW513942 AI687669 AA662521 AA548598 AI345056 AI305374 BE043418 AI432858 AI334840 AI379796 AI492693 AI307915 BE042082 AI307834 AI307858 AI309488 BE042210 AI435670 AI371605 AI862491 AI284563 AI306872 AI255044 AI254601 AI251238 AI473073 AI473042 AI432760 AI435684 AI336826 AI289365 AI369096 AI862274 AI334871 AI349863 AI250405 AI377617 AI309885 AI313017 AI862291 AI311938 AI378718 AI305722 AI306769 AI308888 AI334565 AI862296 AI344230 AI435685 AI344087 AI378696 AI311209 AI435775 AI310611 AI311154 AI432289 AI431561 AI432681 AI432867 AI335288 AI492796 AI432769 AI310289 AI432273 AI379820 AI275319 AI435753 AI609441 AI432787 AI369100 AI311420 AI349974 AI247157 AI334677 AI270910 AI224320 AI305608 AI334489 AI377152 AI350012 AI370088 AI335053 AI306781 AI306750 AI334849 AI334874 AI340380 AI307876 AI305974 AI305972 AI311521 AI334872 AI862509 AI311498 AI335051 AI289684 AI310859 AI311862 AI862483 AI492775 AI307906 AI492708 AI289693 AI340373 AI307910 AI311359 AI435653 AI334865 AI311492 AI492809 AI492690 AI431576 AI862268 AI311879 AI308435 AI492782 AI862512 AI275321 AI431568 AI431564 AI307885 AI307826 AI435692 AI435778 AI310182 AI308894 AI492707 AI492713 AI308560 AI307829 AI343234 AI580598 AW472786 AI340918 AI310243 AI309368 AI307820 AI289665

5 AI306777 AW086318 AW086282 AW086378 AI310027 AI275293 AI369082 AI340900 AI306749 AI371558 AW086287 BE043803
AI306793 AI306272 AI287948 AI270917 AI284816 AI336813 AI284546 AI308044 AI275290 AI270872 AI306795 AI289687 AI223570
AI305303 AI289677 AI287742 AI275284 AI306812 AI336701 AI371554 AI378719 AI344888 AI223631 AI335141 AI343222 AI284568
AI305357 AI275270 AI345932 AI335459 AI307925 AI311502 AI344238 AI343182 AI308508 AI305988 AI270790 AI379782 AI305647
AI305410 AI432251 AI436517 AI343227 AI305534 AI340387 AI271043 AI305499 AI271048 AI305962 AI289465 AI305378 AI289725
AI310848 AI305848 AI289362 AI252964 AI307049 AI310831 AI306893 AI306796 AI224659 AI305969 AI349855 AI306164 AI306948
AI284676 AI309155 AI343202 AI432785 AI306815 AI369081 AI270885 AI289699 AI435704 AI309647 AI305716 AI311281 AI287927
AI472695 AI340423 AI270958 AI307069 AI305364 AI270807 AI275306 AI311890 AI275263 AI432750 AI289371 AI432861 AI255113
AI305709 AI473008 AI311168 AI309711 AI377164 AI271201 AI289560 AI309710 AI306195 AI311201 AI287741 AI271066 AI432876
AI275281 AI379785 AI472972 AI311867 AI306826 AI305465 AI270782 AI473019 AI305340 AI270922 AI305985 AI305482 AI254144
AI270969 AI473012 AI305390 AI275278 AI223644 AI289692 AI250318 AI305372 AI289691 AI250521 AI306283 AI306814 AI307933
AI473160 AI432903 AI223720 AI254979 AI334862 AI306926 AI289541 AI432248 AI435722 AI435698 AI432859 AI310683 AI473175
AI335144 AI289467 AI436489 AI306828 AI473033 AI305763 AI307868 AI307882 AI348959 AI435736 AI432857 AI432896 AI435735
AI432283 AI473086 AI432883 AI473081 AI432825 AI307840 AI473164 AI432885 AI473166 AI472982 AI435734 AI473060 AI473171
AI432279 AI432882 AI334670 AI436512 AI432827 AI432852 AI473051 AI473077 AI435697 AI271509 AI482781 AI472883 AI473018
AI432897 AI473043 AI432871 AI436536 AI473157 AI439715 AI432777 AI473016 AI473158 AI340369 AI307941 AI432773 AI377148
AI432791 AI270950 AI305342 AI284604 AI306269 AI284811 AI270811 AI289347 AI334869 AI334852 AI311759 AI250382 AI309520
AI289550 AI305721 AI340870 AI270901 AI308575 AI307804 AI340715 AI270941 AI309808 AI246867 AI473014 AI307039 AI289360
AI473069 AI492788 AI344013 AI305878 AI436510 AI340742 AI473028 AI307891 BE041871 BE041268 BE042340 BE041948
BE041783 AI306173 AI201948 AI926972 AI275769

20 338255 CH22_6856FG_LINK_EM:AC00
330211 c_5_p2
332798 CH22_14FG_6_5_LINK_C4G1.G
334447 CH22_1746FG_387_7_LINK_EM

25 332247 372969_1
332398 20265_1
AA689097 AA513815 AA026798 AA676526 AA704429 AA704289 AW118292 AA579216 N58172
AW579842 BE156562 BE156690 BE156489 BE081033 AK001559 BE149402 M85387 AW367811 AW367798 R17370 AI089847
AA382932 R58449 H18732 AA371231 AW62899 AA713530 AW892946 R53463 H11063 AW068542 Z40761 BE176212 BE176155
W23952 W92188 AW374883 AA303497 AW954769 AA036808 BE168063 AW382073 AW382085 AL041475 H80748 AI078181
BE463983 AI805213 AI761264 W94885 N94502 AI623772 AI419532 AI810302 AI634190 AW002516 AW150777 AI352312 AI367474
AW204807 AI675502 AI337026 AW134715 BE328451 AI123157 AI560020 AI300745 AI608631 AI248873 AI424284 AW051635
H18646 AI245045 AA507111 AI840510 AI925594 AA115747 AA143035 AA151108

30 332697 13899_1
X51405 NM_001873 T11322 AL118886 BE328175 AW136009 BE467445 AW470313 AA774852 BE504139 AW501046 AA082782
AW389231 AA370044 R36841 AA371457 C04813 R25791 R25556 AW895854 AW903819 AW895671 AW895677 BE159723
AW895684 AW895597 AW895585 AW895685 AW888518 AI903724 F06081 F08503 AL119462 AW895730 AW888516 R26511
R26489 AA334126 AA327626 N85713 AW895998 AA223822 F05468 AA370749 W05590 M78202 AA371073 AW498607 R15017
T16991 AAD01282 AAD01138 AA551566 AA330159 AI922855 AA383512 AA029603 D82246 D82171 T94833 H56545 AA348060
AA178888 R86764 AW451817 AA385766 AA452818 AI690057 AA888822 BE549928 AA150901 W57992 AW898925 C05281
AA932042 AA370980 AW962877 W04741 AA369982 AW385948 AA922466 N75882 AI422070 AI361256 AI680224 D57122 T94885
R53266 R46713 T19071 AW796277 AA325333 F04719 F02334 AA358146 AA626597 AA358304 AW028089 AL119570 D57290
D58273 D57786 N48555 AI361869 AA329457 D57225 AW024046 AA992606 AW022118 AW021538 AA935845 H89870 H56546
AW961218 AA453239 AW837541 N45521 BE218029 AA318877 AA327740 AW861809 T92139 D53216 D52365 D53363 D53312
D53116 AI547267 AA678835 AW026552 AW026418 AW190507 AI927710 AW244108 D50848 AW054991 AW021063 AW022511
AA493436 AI365636 BE464751 AW149384 AA102442 AW771368 AI818251 AI126368 D51049 AI421542 AI559467 AW079779
AW021048 AW023969 AW044214 AI458264 AA027274 AI620254 AW028917 BE218511 AA326242 N67561 AI971273 AA878328
D57131 AA770662 AI309299 AI796767 AA613338 W58076 AI566287 AI445573 AI880260 AA001919 AW339259 AI492610 AI492811
R97692 AI301425 AA722603 D58361 AI350323 AA973926 AI431263 AA516126 AA865467 AI925177 N39443 AA001943 AI299371
AI082412 AA685090 AA583433 H89871 AA977231 AI362219 AI056096 AI270446 N67524 N22103 AW614224 AA744054 AW243622
AI613188 AI929173 AI350243 AI362138 AA744004 AA176661 D56787 AI955625 AI393109 AI094769 AI479728 AI423107 AI955617
AI034038 AI582186 AW284534 AI418961 AA570761 AI943538 AA650341 AA992503 AA770004 AL039668 AI862675 AW190335
AA610274 AW418627 BE467472 D56786 T28749 AI217610 AI359556 T23523 AL040189 AA846222 AA651636 D51280 AI888986
AI521167 AI340177 AW612815 AI625285 AA621607 AA177059 AA229768 AA829788 AI749682 AW190631 N75299 AA230089
AI915632 BE089542 AA890020 AA528397 AA985390 BE503860 AA570812 AW339396 AI979986 AI203725 AI282379 AA670375
AA461513 F01728 AW243599 C00856 N75587 R95995 AA150932 R95961 AA648060 AA933800 AA927073 AA101126 AA864180
T93568 BE167472

55 425710 25529_1
432189 342819_1
445424 6391_1
AF030880 NM_000441 AC002467 AA385554 H23053 AW891838 AI139968 AA653057 AI695233
AA527941 AI810808 AI820190 AA635268
AB028945 T77648 F13328 AL157605 Z46212 AA304736 F11855 T66098 T30174 AW954164 AW176301 AW748243 AA456428
AI369958 AA938565 AW959613 Z42008 AA994778 AI683909 F11019 F10926 AI769597 AI752550 T65015 AI884314 AA643854
Z41838 AW020147 AI038822 AW571822 AA299781 AA894828 AF131790 BE005411 AI902476 AW082695 AA464384 R42750
AW902301 AA464273 R05837 Z38294 H41098 AI134507 M86079
AF035269 AF035268 NM_015900 T96213 U37591 AA156832 AA299371 AI084325 H95977 AI765967 BE221465 AA156726 AI989563
AW024539 AI436791 AI849451 AA843093 AI452756 AA824232 AI306687 T96131 AW207447 AW243556 AW957032 AI084332
H95978 U30998

60 447210 7119_1
AF035269 AF035268 NM_015900 T96213 U37591 AA156832 AA299371 AI084325 H95977 AI765967 BE221465 AA156726 AI989563
AW024539 AI436791 AI849451 AA843093 AI452756 AA824232 AI306687 T96131 AW207447 AW243556 AW957032 AI084332
H95978 U30998

65 449625 8113_1
NM_014253 AF100772 BE088769 AL022718 BE161779 AW863569 BE161840 AL039060 BE168542 AW296554 AA323193 AA235370
AW779760 N48674 AI375997 R45432 D59344 AI203107 F07491 R35380 R25094 AI913631 AI498402 T61382 AI016320 N45528
T61415 AA331486
AI922988 H05475 AA021608 AW169947 AA913750 Z41614 AW800012

TABLE 15B shows the genomic positioning for those primekeys lacking unigene ID's and accession numbers in Table 15. For each predicted exon, we have listed the genomic sequence source used for prediction. Nucleotide locations of each predicted exon are also listed.

5

10 Pkey: Unique number corresponding to an Eos probeset
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
 Strand: Indicates DNA strand from which exons were predicted.
 Nt_position: Indicates nucleotide positions of predicted exons.

15

Pkey	Ref	Strand	Nt_position
334447	Dunham, I. et al.	Plus	14308764-14308824
332798	Dunham, I. et al.	Minus	232147-231974
338255	Dunham, I. et al.	Minus	15242294-15242231
330211	6013592	Plus	59158-59215
401424	8176894	Plus	24223-24428

20

TABLE 11 AND SEQUENCE LISTING

		SEQ ID NO:1 BCU4 DNA SEQUENCE	
Nucleic Acid Accession #: NM_024915			
Coding sequence: 13-1890 (underlined sequences correspond to start and stop codons)			
		1 11 21 31 41 51	
5		ATTGGATCAA ACATGTCACA AGAGTCGGAC AATAATAAAA GACTAGTGGC CTTAGTGCCC	60
10		ATGCCAGATG ACCCTCCATT CAATACCCGA AGAGCTCTACA CCAGTGAGGA TGAAGCTGG	120
		AAGTCATACT TGGAGAATCC CCTGACAGCA GCCACCAAGG CCATGATGAT CATTAAATGGT	180
		GATGAGGACA GTGCTGCTGC CCTGGGCTG CTCTATGACT ACTACAAGGT TCCTCGAGAC	240
		AAGAGGCTGC TGCTGTAAAG CAAAGCAAGT GACAGCCAAG AAGACCAGGA GAAAAGAAAC	300
15		TGCCTTGGCA CCAGTGAAGC CCAGAGTAAT TTGAGTGGAG GAGAAAAACG AGTGCAAGTC	360
		CTAAAGACTG TTCCAGTGAA CCTTTCCTA AATCAAGATC ACCTGGAGAA TTCCAAGCGG	420
		GAACAGTACA GCATCAGCTT CCCCAGAGAG TCTGCCATCA TCCCGGTGTC GGGAAATCAG	480
		GTGGTGAAAG CTGAAGATTT CACACCAATT TTCAATGGCC CACTGTGCA CTATCCCGG	540
		GGAGATGGGG AAGAGCAACG AGTGGTTATC TTGAACAGA CTCAGTATGA CGTGCCCTCG	600
20		CTGGCCACCC ACAGCCCTA TCTCAAAGAC GACCAGCCCA GCATCCCGA CAGCACATAC	660
		AGCGAGAGCT TCAAGGACCG AGCCACAGAG AAATTTCCGA GTGCTTCAGT TGGGGCTGAG	720
		GAGTACATGT ATGATCAGAC ATCAAGTGGC ACATTTCAAT ACACCTTGA AGCCACCAAA	780
		TCTCTCGTC AGAAGCAGGG GGAGGGGCC ATGACCTACC TCAACAAAGG ACAGTTCTAT	840
		GCCATAACAC TCAGCGAGAC CGGAGACAAC AAATGCTTCC GACACCCAT CAGCAAAAGTC	900
25		AGGAGTGTGG TGATGGTGGT CTTCACTGAA GACAAAAACA GAGATGAACA GCTCAAAATAC	960
		TGGAATACT GGCAGTCTCG GCAGCATACG GCGAAGCAGA GGGTCTTGA CATTGCCGAT	1020
		TACAAAGGAA GCTTTAATAC GATTGGAAC ATTGAAGAGA TTGCATATAA TGCTGTTTCC	1080
		TTTACCTGGG AGTGGAATGA AGAGGCAAG ATTTTCATCA CCGTGAATTG CTTGAGCACA	1140
		GATTTCCTCT CCCAAAAAGG GGTGAAAGGA CTTCCTTTGA TGATTGAGT TGACACATAC	1200
30		AGTTATAACA ATCGTAGCAA TAAACCCATT CATAGAGCTT ATTGCCAGAT CAAGGTCTTC	1260
		TGTGACAAAG GACGAGAAAG AAAAAATCCG GATGAAGAGC AGAAGCAGAA CAGGAAAGAA	1320
		GGGAAAGGCC AGGCTCCCA AACTCAATGC AACAGCTCT CTGATGGGAA GTTGGCTGCC	1380
		ATACTTTAC AGAAGCAAG TGACATCAC TACTTCAAAA CCATGCTGA TCTCACTCA	1440
		CAGCCAGTTC TCTTCATACC TGATGTTTAC TTGCAAAACC TGCAGAGGAC CGGACAGGTG	1500
35		TATTACAACA CGGATGATGA ACGAGAAGGT GGCAGTGTCC TTGTTAAACG GATGTTCCCG	1560
		CCCATGGAAAG AGGAGTTTGG TCCGCTGCT TCAAAGCAGA TGAAGAAGA AGGGACAAG	1620
		CGAGTGCTCT TGATCGTAG GAAGGAGACT GACGATGTGT TCGATGCATT GATGTTGAAG	1680
		TCTCCACAG GATGGGCTG GATGGAAGCG ATATCTGAGA AATATGGGCT GCGCTGGAG	1740
		AAGATAGCAA AGCTTTACAA GAAAAAGCAA AAAGGCATCT TGGTGAACAT GGATGACAAC	1800
40		ATCATCGAGC ACTACTCGAA CGAGGACACC TTATCTCTCA ACATGGAGAG CATGGTGGAG	1860
		GGCTTCAAGG TCAAGCTCAT GGAAATCTAG CCTGGGTTT GGCATCCGCT TTGGCTGGAG	1920
		CTCTCAGTGC GTTCTCTCT GAGAGAGACA GAAGCCCCAG CCCCAGAAC TGGAGACCCA	1980
		TCTCCCATCT TCACAACATG CTGTTACAAG ACCGTGCTGG GGAGTGGGGC AAGGGACAGG	2040
		CCCCACAGTC GGTGTGCTTG GCCATCCAC TGGCACTAC CAGGAGCCG AAGCCTGAGC	2100
45		CCCTCAGGAA GGTGCTCTAG GCTGTGGA TTCTATTTA TTGCCACCT TTTCTGGAG	2160
		CCCAGGTCCA GGCCGCCAG GACTCTGCAG GTCACTGCTA GCTCCAGATG AGACCGTCCA	2220
		GGGTTCCTCC TTCAAGAGAA ACATCTATCC CGAACAGCCT AAAAAATCC CATCCCTCT	2280
		TCTCACCCCT TCCATATCTA TATCTCCGA GTGGCTGCAC AAAATGAGCT ACGTCTGGT	2340
		GCAGTAGTTA TAGGTGGGGC AAGAGGTGGA TGCCACTTT CTGGTCAGAC ACCTTTAGGT	2400
50		TGCTGTGGGG AAGGCTGTCT TGCTAAATAC CTCAGGGTT CCCAGCAAGT GGCCACCAGG	2460
		CTTTGTCAAG GAAGCATTC AGTCACCGTG TAATTAGTAA CACAGAAAGT CTGCTGTCT	2520
		GCAITGTACA TAGTGTATT AATATTGTA TAATATATT TACCTGTGGT ATGTGGGCAT	2580
		GTTTACTGCC ACTGGCTAG AGGAGACACA GACCTGGAGA CCGTTTAAAT GGGGGTTTT	2640
		GCTCTGTGC CTGTTTCAAG GACTTGCAGG GCTAGGTAGA GGGCTTTGG GATGTTAAGG	2700
55		TGACTGCAGC TGATGCAAG ATGGACTCT CAATGGGCAT ACCTGGGGC TCGTTCCTG	2760
		TCCCCAGAGG AAGCCCCCTC TCTTCTCCA TGGGCATGAC TCTCTTCA GGCACCAAG	2820
		TTTATCTCAC AATGATGTGT TTTGCTGAC TTTCCTTTG CGCTGTCTG TGGGAAAGGT	2880
		CATCTGTCT GAGACCCAG CTCCTCTCC AGCTTTGCT GCGGGCATGG CTTGAGCTTT	2940
		CTGGAGAGCC TCTGCAGGGG GTTTCATC AGGGCCCTGT GGCTGGGTCT GCTGCAGAGC	3000
60		TCCTTGGCTA TCAGGAGAA CTCTGACACT GTACTGTGCC TCOCAGTTA CAAACACGCC	3060
		CTTCATCTCA AGTGGCCCTT TAAAAGGCC CTCTGCATGT GAGAGCTGT AACAGCTCAG	3120
		CTCTGAGTGC GCAGACTGGG GCTTCTCTCT GGGCCACCAG ATGGAAAGGG GGTATTGTTT	3180
		GCCTCACTCC TGGATGCTGC GTTTAAGGA AGTGAGTGAG AAAGAATGTG CCAAGATAAC	3240
		TGGCTCTGT GAAACACGCC TCAGGAGGGA AACTGGGAGA GAGAAGCTGT GGTCTCTGCT	3300
65		TACATGCCCT GGGAGCTGGA AGAGAAAAAC ACTCCCTAA ACAATCGCAA AATGATGAAC	3360
		CATCATGGGC CACTGTCTCT TTTGAGGGGA CAGGTTTAGG GGTTTGCCTT CGCCCTTGTG	3420
		GGCTGAAGCA CTAGCTTTTT GGTAGCTAGA CACATCTCTG ACCCAAAAGT TCTCTACAAA	3480
		GGCCAGATT TGTTTGTAAA GCACCTTGGC TCTTACCTGG AGGCCGCTC TCTAAGGGCT	3540
		TCTGTGCTC CCACTCTATC TGTCCCTGAG ATGCAGAGCA GGATGGAGGG TCTGCTCTTA	3600
		GCTCAGCTGT TCTCTCTGA GGTTCGGAG GAATTGAATT GAATGGGACA GAGGGCAGGT	3660
70		GCTGTGGCCA AGAAGATCTC CGAGCAGCAG TGACGGGGCA CCTGCTGTG TGTCTCTGG	3720
		GCAATGTAAC CCTTCTGTGG GGCACAAAGG TTGCATCGTG GATCCAGCTG TGCTCCAGTC	3780
		TGTCCCTCC TCCTCCACTC TGACTGCCAC GCGCCGAGCC AGCAGCTTGG GGACCTCCA	3840
		GGGTACTAAT GGGGCTCTGT TCTGAGATGG ACAAATTCAG TGTGGGAAAT ACATGTTGTA	3900
		CTATGCACCT CCACTGCTCC TAGGGTTAGG AATAGTTTCA AACATGATTG GCAGACATAA	3960
75		CAACGGCAAA TACTCGGACT GGGGCATAGG ACTCCAGAGT AGGAAAAAGA CAAAGATTT	4020
		GGCAGCTGA CACAGGCAAC CTACCCCTCT CTCTCAGGC TCCTTATGAA ACTGTTGTTT	4080
		TGCCAGTCT GGCCTAAGGC AGAAGATGAA TTGAAGATGC TGTGATGTT TCCTAAGTCC	4140
		TTGAGCAATC ATGGTGGTGA CAATTGCCAC AAGGGATATG AGGCAGTGC CACCAAGGG	4200

5 TGGTGCCAAAG TGCCACATCC CTTCGGATCC ATTCOCCTCT GTATCCTCGG AGCACCCAG 4260
 TTGCGCTTG ATGTGTCGC TGTGTATGTT AGCTGAACCT TGATGAGCAA AATTCCTGA 4320
 GCGAAACACT CCAAGAGAT AGGAAAACCT GCGGCTCTT CTTTITGTC CCTTAATCAA 4380
 ACTCAAATAA GCTTAAAAAA AATCCATGGA AGATCATGGA CATGTGAAAT GAGCATTTT 4440
 10 TTCTTTTCTT TTTTITTTT TTTTITTAAC AAAGTCGAA CTGAACAGAA CAAGACTTTT 4500
 TCCTCATACA TCTCCAAATT GTTAAACCT ACTTTATGAG TGTITGTTA GAAATTCGGA 4560
 CCAACAGAAA AATGCACTCA GATGTCATCT TGGAAATGGT TCTTAAAGA GTAAGGCATG 4620
 TCCTGCCCCA GAAACTTAGG AAGCATGAAA TAAATCAAAT GTTATTTTC CTCTTATTT 4680
 AAAATCATGC TAATGCAACA GAAATAGAGG GTTGTGCCA AATGCTATGA ACGGCCCTT 4740
 CTAAAGACA AGCAAGGAG ATTGATATAT GTACAATTG CTCTCATGTT TTT

SEQ ID NO:2 BCU4 Protein sequence:
 Protein Accession #: NP_079191.1

15 1 11 21 31 41 51
 MSQESDNKR LVALVMPSPD PPNTRRAYT SEDEAWKSYL ENPLTAATKA MMINGDEDS 60
 20 AAALQLLYDY YKVPDRKRL SVSKASDSQE DQEKRNCLGT SEAQSNLSGG ENRVQVLKTV 120
 PVNLSLNQDH LENSREQYS ISFESSAI PVSGITVKA EDFIPVFMAP PVHYPRGDGE 180
 BQRVVFEBQ QYDVPSLATH SAYLKDDQRS TPDSTYSEF KDAATEKFRS ASVGAEBYMY 240
 DQTSSTFQY TLEATKSLRQ KQEGPMTYL NKGQFYAIL SETGDNKCFR HPISKVRSVV 300
 MVVSEDKNR DEQLKYWKYV HSRQHTAKR VLDIADYKES FNTIGNIEI AYNVSFTWD 360
 25 VNEAKIFT VCLSTDPSS QKGVKGLPLM IQIDTYSYNN RSNKPIHRAY CQIKVPCDKG 420
 AERKIRDEEQ KQNRKNGKQ ASQTQCNSSS DGKLAAPLQ KKSDFYFKT MPDLHSQPVL 480
 FIPDVHFANL QRTGQVYNT DDEREGGSVL VKRMFRPMEE EFGPVPSKQM KEEGTRVLL 540
 YVRKETDDVF DALMLKSPV MGLMEASEK YGLPVEKIAK LYKSKKGIL VNMDDNIEH 600
 YSNEDTFLN MESMVEGFKV TLMEI

SEQ ID NO:3 BCU7 DNA SEQUENCE VARIANT 1:

Nucleic Acid Accession #: AA428062
 Coding sequence: 1-777 (entire sequence represents open reading frame)

35 1 11 21 31 41 51
 ATGATAGCAA TCTCTGCCGT CAGCAGTGCA CTCTGTCTCT CCTTCTCTG TGAAGCAAGT 60
 40 ACCGTGCTCC TACTCAATTC CACTGACTCA TCCCGGCCAA CCAATAATT CACTGATATT 120
 GAAGCAGCTC TGAAGCACA ATTAGATTCA GCGGATATCC CCAAGCCAG GCGGAAGCGC 180
 TACATTTCGC AGAATGACAT GATCGCCATT CTGATTATC ATAATCAAGT TCGGGGCAAA 240
 GTGTCCAC CCGCAGCAAA TATGGAATAT ATGGTTTGGG ATGAAAATCT TGCAAAATCG 300
 GCAGAGGCTT GGGCGGCTAC TTGCATTGG GACCATGGAC CTCTCTACTT ACTGAGATT 360
 45 TTGGGCCAAA ATCTATCTGT ACGCACTGGA AGATATCGCT CTATTCTCCA GTTGCTCAG 420
 CCATGGTATG ATGAAGTGA AGATTATGCT TTTCCATATC CCCAGGATG CAACCCGAGA 480
 TGTCTATGA GATGTTTGG TCCCATGTGC ACACATTATA GGCAGATGGT TTGGGCCACT 540
 TCCAAATCGA TAGGATGCGC AATTTCATGCT TGCCAAAACA TGAATGTTTG GGGATCTGTG 600
 TGCGACGCTG CAGTTTACTT GGTATGCAAC TATGCCCAA AGGGCAATTG GATTGGAGAA 660
 50 GCACCATATA AAGTAGGGGT ACCATGTTCA TCTGTCTCTC CAGTTATGG GGGATCTTGT 720
 ACTGACAATC TGTGTTTTC AGGAGTTACG TCAAACTACC TGTACTGGTT TAAATAA

SEQ ID NO:4 BCU7 DNA SEQUENCE VARIANT 2:

Nucleic Acid Accession #: AA428062
 Coding sequence: 1-777 (entire sequence represents open reading frame)

55 1 11 21 31 41 51
 60 ATGATAGCAA TCTCTGCCGT CAGCAGTGCA CTCTGTCTCT CCTTCTCTG TGAAGCAAGT 60
 ACCGTGCTCC TACTCAATTC CACTGACTCA TCCCGGCCAA CCAATAATT CACTGATATT 120
 GAAGCAGCTC TGAAGCACA ATTAGATTCA GCGGATATCC CCAAGCCAG GCGGAAGCGC 180
 TACATTTCGC AGAATGACAT GATCGCCATT CTGATTATC ATAATCAAGT TCGGGGCAAA 240
 65 GTGTCCAC CCGCAGCAAA TATGGAATAT ATGGTTTGGG ATGAAAATCT TGCAAAATCG 300
 GCAGAGGCTT GGGCGGCTAC TTGCATTGG GACCATGGAC CTCTCTACTT ACTGAGATT 360
 TTGGGCCAAA ATCTATCTGT ACGCACTGGA AGATATCGCT CTATTCTCCA GTTGCTCAG 420
 CCATGGTATG ATGAAGTGA AGATTATGCT TTTCCATATC CCCAGGATG CAACCCGAGA 480
 TGTCTATGA GATGTTTGG TCCCATGTGC ACACATTATA GGCAGATGGT TTGGGCCACT 540
 70 TCCAAATCGA TAGGATGCGC AATTTCATCT TGCCAAAACA TGAATGTTTG GGGATCTGTG 600
 TGCGACGCTG CAGTTTACTT GGTATGCAAC TATGCCCAA AGGGCAATTG GATTGGAGAA 660
 GCACCATATA AAGTAGGGGT ACCATGTTCA TCTGTCTCTC CAGTTATGG GGGATCTTGT 720
 ACTGACAATC TGTGTTTTC AGGAGTTACG TCAAACTACC TGTACTGGTT TAAATAA

SEQ ID NO:5 BCU7 Protein sequence Variant 1:

Protein Accession #: none

75 1 11 21 31 41 51
 MIALSAVSEA LLFSLICEAS TVVLLNSTDS SPPTNNFTDI EAALKAQLDS ADIFKARRKR 60

YISQNDMIAI LDYHNQVRGK VPPPAANMEY MVWDENLAKS AEAKAATCIW DHGSPSYLLRF 120
 LGQNLVSRIG RYRSILQLVK FWYDEVKDYA FPFQDCNPR CPMRCFPGMC THYTMVWAT 180
 SNRIGCAIHT CQNMNVGMSV WRRAYVLVCN YAPKGNWIGE APYKGVVPCS SCPPSYGGSC 240
 TDNLCPFGVT SNLYLWPK

SEQ ID NO:6 BC17 Protein sequence Variant 2:
 Protein Accession #: none

1 11 21 31 41 51
 MIAISAVSSA LLPSLLCEAS TVVLLNSTDS SPPTNFTDI EAALKAQLDS ADIPKARRKR 60
 YISQNDMIAI LDYHNQVRGK VPPPAANMEY MVWDENLAKS AEAKAATCIW DHGSPSYLLRF 120
 LGQNLVSRIG RYRSILQLVK FWYDEVKDYA FPFQDCNPR CPMRCFPGMC THYTMVWAT 180
 SNRIGCAIHT CQNMNVGMSV WRRAYVLVCN YAPKGNWIGE APYKGVVPCS SCPPSYGGSC 240
 TDNLCPFGVT SNLYLWPK

SEQ ID NO:7 BCX2 DNA SEQUENCE

Nucleic Acid Accession #: NM_003014

Coding sequence: 238-1278 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 GGCGGGTTCG CGCGCCGAAG GCTGAGAGCT GCGCGTCTC GTGCGCTGTG TGCCAGACGG 60
 CGGAGCTCCG CGCGCCGACC CGCGGCCCC GCTTGTCTG CGACTGGAGT TTGGGGGAAG 120
 AAATCTCTCT GCGCCCCAGA AGATTCTTC CTGCGCGAAG GGACAGCGAA AGATGAGGGT 180
 GGCAGGAAGA GAAGGCGCTT TCTGTCTGCC GGGGTCCGAG CGCGAGAGGG CAGTGCCATG 240
 TTCTCTCTCA TCTAGTGGC GCTGTGCTG TGGCTGCACC TGGCGCTGGG CGTGCGCGGC 300
 GCGCGCTGCG AGGCGGTGGG CATCCCTATG TGCCGCGACA TGCCCTGGAA CATCACGCGG 360
 ATGCCAAACC ACGTCACCA CAGCAGCAG GAGAACGCCA TCTGGCCAT CGAGCAGTAC 420
 GAGGAGCTGG TGGACGTGAA CTGCAGCGCC GTGCTGCGCT TCTTCTCTG TGCCATGTAC 480
 GCGGCCATTG GCACCTTGGG GTTCTGTCAC GACCTATCA AGCGGTGCAA GTCCGTGTGC 540
 CAACGCGCGC CGGCGGCGAC CGAGCCCTC ATGAAGATGT ACAACACAG CTGGCCCGAA 600
 AGCTGGGCTT GCGACGAGCT GCGTGTCTAT GACCGTGGCG TGTGCAATTC GCGTGAAGCC 660
 ATGTGACGGG ACCTCCGGA GATGTGTAAG TGGATAGACA TCACACCAGA CATGATGTA 720
 CAGGAAAGGC CTCTGTATGT TGACTGTAAA CGCCTAAGCC CGATCGGTG CAAGTGTAAG 780
 AAGGTGAAGC CAACCTTGGC AACGTATCTC AGCAAAACT ACAGCTATGT TATTCATGCC 840
 AAAATAAAGG CTGTGCGAG GAGTGGCTGC AATGAGGTCA CAACGGTGGT GGATGTAAAA 900
 GAGATCTTCA AGTCTCTATC ACCCATCCCT CGAAGCTCAAG TCCCGCTCAT TACAAATCT 960
 TCTTGCCAGT GTCCACATC CCGCCCAT CAAGATGTT TCATCATGTG TTACGAGTGG 1020
 CGTTCAAGGA TGATGCTTCT TGAATAATGC TTAGTTGAAA AATGGAGAGA TCAGCTTAGT 1080
 AAAAGATCCA TACAGTGGGA AGAGAGGCTG CAGGAACAGC GGAGAACAGT TCAGGACAAG 1140
 AAGAAACAGG CGGCGGCGAC CAGTGTAGT AATCCGCCCA AACCAAGGG AAAGCTCTCT 1200
 GCTCCAAAC CAGCCAGTCC CAAGAAGAAC ATTAAGCTCA GAGTGGCCA GAAGAGAACA 1260
 AAACCGAAAA GAGTGTGAGC TAACTAGTTT CCAAGCGGA GACTCCGAC TTCTTACAG 1320
 GATGAGGCTG GGCATTGCTT GGCACAGCT ATGTAAGGCC ATGTGCCCT TGCCCTAACA 1380
 ACTCACTGCA GTGCTCTTCA TAGACACATC TTGCAGCATT TTCTTAAAG CTATGCTTCA 1440
 GTTTTCTT GTAAAGCCAT ACAAGCCATA GTGGTAGGTT TGCCCTTGG TACAGAAAGT 1500
 GAGTTAAAGC TGTGTGAAAA GGCTTATTGC ATTGCATTCA GAGTAACCTG TGTGCATCT 1560
 CTAGAAGAGT AGGGAATAA ATGCTTGTTA CAATTCGACC TAATATGTGC ATTGTAAAA 1620
 AAATGCCATA TTCAAAACA AACAGTAAT TTTTATACAG TAGTTTAT TACCTTTGA 1680
 TATCTGTGTG TCAATGTGA GTGATGTTT AAAATGTGAT GAAAAATATA TGTTTTAA 1740
 AAGGAACAGT AGTGAATGA ATGTTAAAG ATCTTTATGT GTTTATGGTC TGCAGAAGGA 1800
 TTTTGTGAT GAAAGGGGAT TTTTGAAGA ATTAGAGAAG TAGCATATGG AAAATTATA 1860
 TGTGTTTTT TACCAATGAC TTCAGTTCT GTTTTAGCT AGAACTTAA AAACAAAAAT 1920
 AATAATAAG AAAATAAAT AAAAAGGAGA GGCAGACAAT GTCTGGATT CTGTTTTTG 1980
 GTTACCTGAT TTCCATGATC ATGATGCTT TGTCAACAC CCTCTAAGC AGCACCAGAA 2040
 ACAGTGAGTT TGTCTGTAAC ATTAGGAGTT AGGTACTAAT TAGTTGGCTA ATGCTCAAGT 2100
 ATTTTATACC CACAAGAGAG GTATGTCACT CATCTTACTT CCAGGACAT CCACCTGAG 2160
 AATAATTGA CAAGCTTAAA AATGGCCTTC ATGTGAGTGC CAAATTTGT TTTCTTCAT 2220
 TTAATATTT TCTTGGCTA AATACATGTG AGAGGAGTTA AATATAAATG TACAGAGAGG 2280
 AAAGTTGAGT TCACCTCTG AAATGAGAAT TACTTGACAG TTGGGATACT TTAATCAGAA 2340
 AAAAAGAACT TATTGACG ATTTATCAA CAAATTCAT AATTGTGGAC AATTGGAGGC 2400
 ATTTATTTA AAAACAATT TATTGGCCT TTGCTAACA CAGTAAGCAT GTATTTTATA 2460
 AGGCATTCAA TAAATGCACA AGCCCAAGG GAAATAAAT CCTATCTAAT CCTACTCTC 2520
 ACTACAGAG GTTAATCACT ATTAGTATT TTGGCATATTA TTCTCAGGT GTTTGCTTAT 2580
 GCACCTATAA AATGATTTGA ACAAATAAAA CTAGGAACCT GTATACATGT GTTTCATAAC 2640
 CTGCTCTCT TGTCTGGCC TTTATTGAGA TAAGTTTTC TGTCAAGAAA GCAGAAAOCA 2700
 TCTCATTTCT AACAGCTGTG TTATATCCA TAGTATGCAT TACTCAACAA ACTGTTGTGC 2760
 TATTGGATAC TTAGTGGTT TCTTACTGA CAATACTGAA TAAACATCTC ACCGGAATTC

SEQ ID NO:8 BCX2 Protein sequence:
 Protein Accession #: NP_003005.1

1 11 21 31 41 51
 MFLSILVALC LWLHLALGVR GAPCEAVRIP MCRHMPWNIT RMPNHLHHST QENAILAEQ 60

5 YEELVDVNCs AVLRFFFCAM YAPICTLEFL HDPIKPKSV CQRARDDCEP LMKMYNHSWP 120
 ESLACDELFP YDRGVCSPE AIVTDLPEDV KWIDITPDMV VQERPLDVC KRLSPDRCKC 180
 KKVKPTLATY LSKNYSYVIH AKIKAVQBSG CNEVTTVVVDV KEIFKSSSI PRITQVFLITN 240
 SSOQCPHLP HQDVLIMCYE WSRMMILEN CLVEKWRDQL SKRSIQWEER LQEQRRIVQD 300
 KKKTAGRTSR SNPPKPKGKP PAKPASPKK NIKTRSAQKR TNPKRV

SEQ ID NO:9 CBK1 DNA SEQUENCE

10 Nucleic Acid Accession #: NM_032391
 Coding sequence: 129-302 (underlined sequences correspond to start and stop codons)

15 1 11 21 31 41 51
 GTCTTCTCTC TCCTAGCCTA AGGCGTGCAA ACAGAGGCGC ACTGGGAGGC TGAAACCTTT 60
 AGGCCGATGC TTGCTTGCAA GGTGAGGCAA GCTGGATTCT GGTCCGCCAC TTGCGAGAGA 120
 GACACCGGAT GTGTGCGGCC CATTTCTCAG ATCAAGGACC GGCCCATCTT ACTACCTCCA 180
 AGAGTCTCTT TCTCTCTAAT AAGAAAACAT CTACTTTGAA ACATCTACTG GGCAGAGCCA 240
 GGAGTGATGG CTCAGCCTGT AATTCTGGAA TTTCGGGAGG CCGAGGCAGG AAGATTCCTT 300
 GAGCAGAGA GTTCCAGACC AGCCTGGGCA ATGTAGCAAG ACGCTGTCTC TATTATATACA 360
 ATAAATTTT TTTAAAAAAG G

25 SEQ ID NO:10 CBK1 Protein sequence:
 Protein Accession #: NP_115767

30 1 11 21 31 41 51
 MLCAHFSDDQ PAHLTTSKSA FLSNKKTSTL KHLLEGTRSD GSACNSGISG GRGRKIP

SEQ ID NO:11 CHA1 DNA SEQUENCE

35 Nucleic Acid Accession #: NM_020182
 Coding sequence: 98-854 (underlined sequences correspond to start and stop codons)

40 1 11 21 31 41 51
 TCCTTGGGTT CGGGTGAAG CGCCTGGGGG TTCGTGGCCA TGATCCCCGA GCTGCTGGAG 60
 AACTGAAGGC GGACAGTCTC CTGCGAAACC AGGCAATGGC GGAGCTGGAG TTGTGTCAGA 120
 TCATCATCAT CGTGGTGGTG ATGATGGTGA TGGTGGTGGT GATCAGGTGC CTGCTGAGCC 180
 ACTACAAGCT GTCTGCACGG TCCTTCATCA GCCGGCACAG CCAGGGGCGG AGGAGAGAAG 240
 ATGCCCTGTC CTCAGAAAGA TGCCCTGTGC CCTCGGAGAG CACAGTGTCG GGCACAGGAA 300
 TCOCAGAGCC GCAGGTCTAC GCCCGGCTC GGCCCAACGA CCGCTGGGCC GTGCCGCCCT 360
 TCGCCAGCGG GGAGCGCTTC CACCGCTTCC AGCCCACTCA TCCGTACCTG CAGCACGAGA 420
 TCGACCTGCC ACCCAACATC TCGCTGTGAG ACGGGGAGGA GCGCCACACC TACCAGGGCC 480
 CTGCAACCTC CCAGCTTCGG GACCCGAGC AGCAGCTGGA ACTGAACCGG GAGTCGGTGC 540
 CGCACAACCC AAACAGAAC ATCTTCGACA GTGACCTGAT GGATAGTGCC AGGCTGGGCG 600
 GCCCTGGCC CCCCAGCAGT AACTCGGCA TCAGCGCCAC GTGTACGGC AGCGGCGGGC 660
 GCATGAGGGG GCGCGCGGCC ACCTACAGCG AGGTATCGG CCACTACCGG GGTCTCTCCT 720
 TCCAGACCA GCAGAGCAGT GGGCCGCCCT CCTTCGTGGA GGGGACCCGG CTCACACCA 780
 CACACATCGC GCGCCTAGAG AGCGCAGCCA TCTGGAGCAA AGAGAAGGAT AAACAGAAAG 840
 GACACCTCTC CTAGGGTCCC CAGGGGGGCC GGGCTGGGCG TCGTAGGTG AAAAGGCAGA 900
 ACACCTCGCG CTCTTTAGAA GAGGAGTGAG AGGAAGGCGG GGGGCGCAGC AACGCATCGT 960
 GTGCCCTCC CCGCCCACT CCTGTGTAT AAATATTTAC ATGTGATGTC TGGTCTGAAT 1020
 GCACAGCTA AGAGAGCTTG CAAAAAAGA AAAAAAAGG AAAAAAAGA ACCACGTTTC 1080
 TTTGTGAGC TGTGTCTTGA AGGCAAAAGA AAAAAAATT CTACAGTAAA AAAAAAAGA 1140
 A

60 SEQ ID NO:12 CHA1 Protein sequence:
 Protein Accession #: NP_064567

65 1 11 21 31 41 51
 NAELEPVQII IIVVMMVMV VVITCLLSHY KLSARSPISR HSQRRRREDA LSSEGCLWPS 60
 ESTVSGNIP EPQVYAPRP TDLAVPPFA QRERFIRPQP TYFYLQHEID LPPTISLSDG 120
 EEPPPYQGPC TLQLDPEQO LELNRESVRA PPRRTIFDSD LMSARLGGP CPFSSNSGIS 180
 ATCYSGGRM EGPPPTYSEV IGHYPGSSFO HQSSGPPSL LEGTRLRHTH IAPLESAAIW 240
 SKEKDKQKH PL

SEQ ID NO:13 CIA5 DNA SEQUENCE

75 Nucleic Acid Accession #: NM_012445
 Coding sequence: 278-1271 (underlined sequences correspond to start and stop codons)

80 1 11 21 31 41 51
 305

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GCACGAGGGA AGAGGGTGAT CCGACCCGGG GAAGGTGCGT GGGCAGGGCG AGTTGGGAAA 60
GGGGCAGCCC CCGCCGCCCC CGCAGCCOCT TCTCCTCCTT TCTCCACAGT CCTATCTGCC 120
TCTGCTGGA GGGCAGGCCG TGCAGCATCG AAGACAGGAG GAATGAGAGC CTCATTTGGC 180
GGCCCGGGGG GCGCGGCTCG GGCTTAAATA GGAGCTCCGG GCTCTGGCTG GGACCCGACC 240
GCTGCCGGCC CCGCTCCGGC TGCTCCTGCC GGTGTATGGA AAACCCAGC CCGGCCGGCG 300
CCCTGGGCAA GGCCTCTGCG GCTCTCCTCC TGGCCACTCT CCGCGCCGCC GGCAGGCTCT 360
TTGGGGGAGA GTCCATCTGT TCCGCCAGAG CCGCGGCCAA ATACAGCATC ACCTTCACGG 420
GCAAGTGGAG CCAGACGGCC TTCCCAAGC AGTACCCOCT GTTCCGCCCC CCTGCGCAST 480
GGTCTTCGCT GCTGGGGGCC GGCATAGCT CCGACTACAG CATGTGGAGG AAGAACCAGT 540
ACGTGAGTAA CCGGCTGGCG GACTTTGCGG AGCGCGGCGA GGCTTGGCGG CTGATGAAGG 600
AGATCGAGGC GCGCGGGGAG GCGCTGCAGA GCGTGCACGC GGTGTTTTCG GCGCCCGCGG 660
TCCCAGCGG CACCGGCGAG ACGTGGCGG AGCTGGAGGT GCAGCGCAGG CACTCGCTGG 720
TCTCCTTTGT GGTGCGCATC GTGCCAGCC CCGACTGGTT CGTGGGCGTG GACAGCCTGG 780
ACCTGTGCGA CCGGGACCGT TGGCGGGAAC AGCGCGCGCT GGACCTGTAC CCTACGAGC 840
CCGGGAGCGA CCGGCGCTTC ACCTTCTOCT CCCCACACTT CGCCACCATC CCGCAGGACA 900
CGGTGACCGA GATTAACGTCT TCTCTCCCA GGCACCCGGC CAACTCCTTC TACTACCCGC 960
GGCTGAAGAG CCTGCTCTCC ATCGCCAGGG TGACACTGGT GCGGCTGCGA CAGAGCCCCA 1020
GGGCTTCAT CCTCCGCC CCACTCTGCG CCAGCAGGGA CAATGAGATT GTAGACAGCG 1080
CCTCAGTTCC AGAAAGCCCG CTGGACTGCG AGGTCTCCCT GTGGTCTGCC TGGGGACTGT 1140
GCGGAGGCGA CTGTGGGAGG CTCGGGAGCA AGAGCAGGAC TCGCTACGTC CGGTCCAGC 1200
CCGCCAACAA CCGGAGCCCG TCGCCGAGC TCGAAGAAAG GGCTGAGTGC GTCCCTGATA 1260
ACTGCTCTA AGACAGAGC CCGCAGGCC CTGGGGCCCG CGGAGCCATG GGTGTGCGG 1320
GGCTCCTGTG CAGGCTCATG CTGCAGGCG CCGAGGCACA GGGGGTTTGG CGCTGCTCCT 1380
GACCGCGGTG AGCGCGGCC GACCATCTCT GCACTGAAGG GCGCTCTGGT GGCCGGCAGC 1440
GGCAATTGGA AACAGCCTTC TCTTTCCCA ACCTTGCTTC TTAGGGGCGC CCGTGTCCCG 1500
TCTGCTCTCA GCGCTCCTCT CTGCGAGGAT AAGTCAATCC CCAAGGCTCC AGCTACTCTA 1560
AATTATGTC TCTTATTAAG TTATTGCTGC TCCAGGAGAT TGTCTTCAT CGTCCAGGGG 1620
CCTGGCTCCC ACGTGGTTGC AGATACCTCA GACCTGGTGC TCTAGGCTGT GCTGAGCCCA 1680
CTCTCCCGAG GCGCGATCCA AGCGGGGCC ACTTGAGAG TGAATAAATG GGGCGGTTTC 1740
GGAAGCGTCA GTGTTTCCAT GTTATGGATC TCTCTCGCTT TGAATAAAGA CTATCTCTGT 1800
TGCTCAC

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35
SEQ ID NO:14 C/AS Protein sequence
Protein Accession #: NP_036577

40
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1 11 21 31 41 51
MENPSPAAL GKALCALLLA TLGAAGQPLG GESICSARAP AKYSITFTGK WSQTAPFKQY 60
PLFRFPAGWS SLLGAHSSD YSMWRKQYV SNGLRDFAEER GEAWALMKEI EAAGEALQSV 120
HAVFSAFAPV SLTGQTSAEL EVQRHSLVS FVVRIVPSFD WFGVVDLSDL CDGDRWREQA 180
ALDLIPYDAG TDSGTFSSP NFATIPQDTV TETTSSSPSH PANSFYFRL KALPPIARVT 240
LVRLQSFRA FIPPAFVLPV RDNHIVDSAS VPETPLDCEV SLWSSWGLCG GHCGRLOTKS 300
RTRYRVQPA NNGSPCPELE EBACVPIINC V

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SEQ ID NO:15 LBH9 DNA SEQUENCE

50
Nucleic Acid Accession #: NM_002391
Coding sequence: 26-457 (underlined sequences correspond to start and stop codons)

55
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65

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1 11 21 31 41 51
CGGGCGAAGC AGCGCGGSCA GCGAGATGCA GCACCGAGGC TTCTCCTCTC TCACCTCCTT 60
CGCCCTGCTG GCGCTCACCT CCGCGGTGCG CAATAAGAGAAA GATAAGGTGA AGAAGGGCGG 120
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GCCCTGCAAC TGAAGAAGG AGTTGGAGC CGACTGCAAG TACAAGTTTG AGAACTGGGG 300
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CAATGCTCAG TGCCAGGAGA CCAATCCGGT CACCAAGGCC TGCAACCCCA AGAACCAAGC 420
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CACCAGTGCC TTCTGTCTGC TCGTTAGCTT TAATCAATCA TGCCCTGCCT TGTCCCTCTC 600
ACTCCCCAGC CCCACCCCTA AGTGCCCAAA GTGGGGAGGG ACAAGGGATT CTGGGAAGCT 660
TGAGCCTCCC CCAAGCAAT GTGAGTCCA GAGCCCGCTT TTGTTCTTCC CCACAATTCC 720
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TAATAT

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70
SEQ ID NO:16 LBH9 Protein sequence
Protein Accession #: NP_002382

75

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1 11 21 31 41 51
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CGAQTQRLRC RVFCNKKKEF GADCKYKFN WGACDGGTGT KVRQGTLLKA RYNAQCQETI 120
RVTKPCTPKT KAKAKAKKK GKD

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SEQ ID NO:17 LEM9 DNA SEQUENCE

Nucleic Acid Accession #: NM_005244

Coding sequence: 1-1617 (underlined sequences correspond to start and stop codons)

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1 11 21 31 41 51

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AAGTTTAACC GTGCTGACGC TGCTGTGTGG ACTCTGAGTG ACAGACRAGG CATCACCAAA 120
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CAGCCTTCCA CAGCCATGGC AGCCTACGGC CAGACGCACT ACAGTGCGGG GATCCAGCAG 240
GCTACCCCTT ATACAGCTTA CCCACCTCCA GCACAAGCCT ATGGAATCCC TTCTACAGC 300
ATCAAGACAG AAGACAGCTT GAACCAATCC CTGGCCAGA GTGGATTCCT CAGCTATGGC 360
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AATGGCCAAG ATCTAAGCAG ATACAACCTC TCCGCTGACG GCTTCCACAG TTCCGCCCCA 1080
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SEQ ID NO:18 LEM9 Protein sequence:

Protein Accession #: NP_005235

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45
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1 11 21 31 41 51

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QFSTAMAAAG QIYASAGIQQ ATPYTAAYPP AQAYGIPSYIS IKTEDSLNHS PQSGFLSYG 120
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SYNPPYVPAE SICPSPLSTS TVVLQEAASHN VPNQSSBSLA GEYNTHNGPS TPAKEGDTDR 240
PRASDGLKL GRSKRSSDPS PAGDNEIERV FVMDLDETII IFHSLLTGTF ASRYGKDTTT 300
SVRIGLMMEE MIFNLADTHL PFNDLEDCEQ IHVDDVSSDD NQQLSTYNP SADGFHSSAP 360
GANLCLGSGV HGGVDNRMLK AFYRKRKVKEM YNTYKNNVGG LIGTFKREIW LQLRAELEAL 420
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SEQ ID NO:19 OAA1 DNA SEQUENCE

Nucleic Acid Accession #: NM_002740

Coding sequence: 178-1968 (underlined sequences correspond to start and stop codons)

55
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65
70
75
80

1 11 21 31 41 51

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TGGGGACTTG GACGCCAAGG ATATAAGTGC ATCAACTGCA AACTCTTGGT TCATAAGAAG 720
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20 SEQ ID NO:20 QAA1 Protein sequence:
 Protein Accession #: NP_002731

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 25 MSHTVAGGGS GDHSHQVRVK AYYRGDIMIT HPEPSISPEG LCNEVRDMCS FDNBQLPTMK 60
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 30 GLQDFDLRLH IGRGSYAKVL LVRLKKTDR IYAMKVVKEL VNDEEDIDWV QTEKHVFEQA 300
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 35 DNFDQSQFTN PVQLTPDDDD IVRKIDQSEF EGFEYINPLL MSAEECV

40 Nucleic Acid Accession #: L05628
 Coding sequence: 197-4792 (undefined sequences correspond to start and stop codons)

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50 SEQ ID NO:22 QH2 Protein sequence
 Protein Accession #: AAB46618

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 80 ARALLKTKI LVLDEATAAV DLETDLIQS TIRTQPEDCT VLTIAHRLAT IHDYTRVIVL 1500
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SEQ ID NO:23 PAA2 DNA SEQUENCE

5 Nucleic Acid Accession #: NM_013309
Coding sequence: 1-1280 (underlined sequences correspond to start and stop codons)

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30 TTTGGCATGT ATAGATGTAC TATTCACTTC CAGAGTTACA GGCAAGAAGT GGACAGAACT 1260
TGTGCAAAAT GTCAAGATTC TAGTCCCTGA

SEQ ID NO:24 PAA2 Protein sequence:

35 Protein Accession #: NP_037441

1 11 21 31 41 51
| | | | |
40 MAGSGAWKRL KSLMRKDDAP LFLNDTSAPD FSDEAGDEGL SRFNKLRVVV ADDGSEAPER 60
PVNGAHPITQ ADDDSLDDQ LPLTNSQLSL KVDSCDNCSK QREILKQKV KARLTIAAVL 120
YLLFMIHELIV GGYIANSIAI MTDALMLTD LSAILITLTA LMLSSKSPTK RPTFGPHRLE 180
VLSAMISVLL VYIIMGFLLY EAVQRTIHMN YEINGDIMLI TAAVGVAVNV IMGFLINQSG 240
HRHSHSHSLP SNSPTRGSGC ERNHEGQDSL VRAAPVHALG DLVQSVGLI AAYIRFEPK 300
45 YKIADPICTY VFSLVAPFT FRIIMDTVVI ILEGPVSHLN VDYIKALMK IEDVYSVEDL 360
NIWSLTSGKS TALVHIQLIP GSSSKWEEVQ SKANHLLIAT FGMRYCTIQL QSYRQVEDRT 420
CANCSSSSP

SEQ ID NO:25 PAA3 DNA SEQUENCE

50 Nucleic Acid Accession #: AB037765
Coding sequence: 375-2788 (underlined sequences correspond to start and stop codons)

55 1 11 21 31 41 51
| | | | |
60 GCGGAGTCGG TGCGCGCTGC AGGCTGGGAG GGAGAAATGC TACGCCCTTG CAGGTTGGCG 60
AAGTGGTTCC AGGCTACCCG GCTAGTCTGG CACGGCCCGG TCTTCGCTCT CCTCTCCGT 120
CGCGTGGCGG CGGGAACGTG TGCGCGCGCG GCCTCGGGAA CGGCCACGGT CCGCGCCGCG 180
AGGTCCCGGG CAGATAACAT AGATCATCAG TAGAAAACCT CTTGAAGTTG TTCAAGAAAA 240
65 ATTTGAAAGT AGCAAAATAG AAAATAAAGA ATTAAACAGCA GATACAGAGG ACAGCATGGA 300
AGTGTGTGCT TAGGAAACAG AACACAGCAG TGAAAAAACA GACAAAATCC GCTCAGATAC 360
AACTGCAGCT GATAATGTTT TCCGGCTTCA ATGTCTTTAG AGTTGGGATC TCTTTTGTCA 420
TAATGTGCAT TTTTACATG CCAACAGTAA ACTCTTTACC AGAAGTGTAG CCTCAGAAAT 480
ATTTTAGTAC ATTGCAACCA GGTCTTGAAG AACTGAATGA GGCTGTTAGA CCTCTGCAGG 540
ACTATGGAAT TTCAGTTGCC AAGGTTAATT GTGTCAAAGA AGAAATATCA AGATACTGTG 600
GAAAAGAAAA GGATTTGATG AAAGCATATT TATTCAAGGG CAACATATTG CTCAGAGAAT 660
TCCTACTGTA CACCTTGTTT GATGTGAATG CCATTGTCCG CCATGTCTCT TTTGCTCTTC 720
70 TTTTATAGTA AGTGAATATG ATTACCAACC TGAAGACCT TCAGAACATA GAAAATGCTC 780
TGAAAGGAAA AGCAAAATAT ATATTCTCAT ATGTAAGAGC CATTGGGAATA CCAGAGCACA 840
GAGCAGTCAAT GGAAGCCGGT TTTGTGTATG GGACTACATA CCAATTGTCT TTAACACAG 900
AAATTGCCCT TTTGGAAGT ATTGGCTCTG AGGATGTGGA ATATGCACAT CTCTACTTTT 960
TTCATTGTAA ACTAGTCTTG GACTTGACCC AGCAATGTAG AAGAACACTA ATGGAACAGC 1020
CATGTACTAC ACTGACATAT CACCTGTTTA TTAAGACAAAT GAAAGCACCT CTGTTGACTG 1080
AAGTGTCTGA AGATCCTCAA CAAGTTTCAA CTGTCCATCT CCAACTGGGC TTACCACTGG 1140
75 TTTTATGTT TACGCAACAG GCTACTTATG AAGCTGATAG AAGAACTGCA GAATGGGTTG 1200
CTTGGCGTCT TCTGGGAAAA GCAGGAGTTC TACTCTTGTT AAGGGACTCT TTGGAAGTGA 1260
ACATTCTTCA AGATGCTAAT GTGGTCTTCA AAAGAGCAGA AGAGGGAGTT CCACTGGAAT 1320
TTTTGTATTT ACATGATGTT GATTTAATAA TATCTCATGT GGAATAAAT ATGCACATTG 1380
AGGAATATCA AGAAGATGAA GACAATGACA TGAAGGTGCC AGATATAGAT GTTCAGGATG 1440
80 ATGAAGTGGC AGAACTGTTT TTCAGAGATA GGAAGAGAAA ATTACCTTTG GAACTTACAG 1500

5 TGGAACTAAC AGAAGAAACA TTTAATGCAA CAGTGATGGC TTCTGACAGC ATAGTACTCT 1560
 TCTATGCTGG TTGGCAAGCA GTATCCATGG CATTTTTCGA ATCTATATTT GATGTGGCAG 1620
 TTAAGCTGAA AGGCACATCT ACTATGCTTC TTACTAGAAT AAAGTGTGCA GATTGGTCTG 1680
 ATGATGTGAC TAAGCAAAAT GTTACTGAAT TTCTATCAT AAAGATGTAC AAGAAAGGCG 1740
 AGAACCAGT ATCTATGCT GGAATGTTAG GAACCAAGA TCTCTAATA TTTATCCAGC 1800
 TCAACAGGAT TTCAATATCA GTGAATATA CATCGATCCA AGAAGCAGAA GAATATTTAA 1860
 GTGGGGAATT ATATAAGAC CTCACTTGT ATTCTAGTGT GTCAGTATG GACTATTTA 1920
 GTCCAACCAT GAAACACGCA AAAGAAGATT TTAGTGAAGC AGGAACACTAC CTAAAGGAT 1980
 10 ATGTTATTCAC TGAATTTTAT TCTGAAGAAG ATGTTTTCCT ACTGTCAACC AAATATGCTG 2040
 CAGCTCTTCC AGCCCTGCTG CTGCGCAGAC ACACAGAAGG CAAATAGAG AGCATCCAC 2100
 TAGCTAGCAC ACATGCACAA GACATAGTTC AAATAATAAC AGATGCACATA CTGGAATGT 2160
 TTCCGGAAAT CACTGTGGAA AATCTTCCCA GTTATTTTCAG ACTTCAGAAA CCATTTATGA 2220
 TTTTGTTCAG TGATGGCACT GTAAATCCCT AATATAAAAA AGCAATATG ACACCTGGTAA 2280
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 15 GGAGAGATGA TAAGCAACAA TATTTTGATC CTCTGCTTCC CCTTCTCTT CTGTGTTTGG 2400
 TGAATCTGCA TTCAGGTGGC CAGTATTTTG CATTTCTTCC AGACCAGGCT ATAATTGAAG 2460
 AAAACCTTGT ATGTGCTGGT AAGAAATTAG AAGCAGGACT AGAAATCAT ATCAAAATTT 2520
 TACCTGCTCA AGAATGGAAA CCTCTCTTTC CAGCTTATGA TTTTCTAAGT ATGATAGATG 2580
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 20 AGAGATATGA TAAGCAACAA CATGAAGATA AATCGGCACT CAGAAAGAA CCGATTGAAA 2700
 CTCTGAGATG AAAGCATTGG AATAGAAGTA ATTGGTTTAA AGAAGCAGAA AAATCATTTA 2760
 GACGTGATAA AGAGTAGGA TGCTCAAAAG TGAATTAATT TTATAGGGCT GTGGTTTCCA 2820
 AAATTTTTTT GGCAATGATG ACTTAATTTA TTTCTTAAA GAATAATATT AATCATTTTC 2880
 AAGTTTGCAG ACTAGTGCCA TCCAATAGAA TTATAATATA AGTCACATAT TTTATTTAAA 2940
 25 ATTTTCTAGT AACTACATTA AACAAAGTAA AAGTGAGCAG GGCAAAATTA TTTTGATATT 3000
 ACTTTTCAAC CAGTAGTATA CCAAAATAG CGAAATATAG AAATTTATTA TGAGATATTT 3060
 TACATCTTGT TTTGTACCAA GTCTTCTAAA TGCAGTACAT ATTTTATACT TACTGCATTT 3120
 CTTACTTCCG AGTAGCCATA TTTCAAGTGT TCAITGGCCAC ATGTGGCCTG TGACTACTGT 3180
 ATTGGACAGT TCAGTACTAG ACAAAACTA GCATAATTA CTTAGTTCTA GCCATGATTT 3240
 30 CTATTTGGAT TAATAATTAA CTCTAATCAC AGTTAACTCC ACAGTGCAAT CATGCAGCTG 3300
 ACAGTTATAT TTGTTTATTT GGAGTCATGA TATTAATATC AGCGTTTGTG AACCTCAGGG 3360
 GATATTTAGC AATTGTGCGG AGACATTTT GATGTCATGA CTAGGCGCAGT TATTGCATT 3420
 TAGTGAGTAG AGGCCATGGA TOCTGCTAAA TAACCTGCAT TGGACAGCGC CCCACAACAA 3480
 AGAATTATCC TGCCCGAAAT GGTAGTCGTG CCAAGGCTGA GTAACTTGT GTTAAAGTAA 3540
 35 ACCTGTGGCA GACTAGGTTT CCAGAAATTC CTGGTTCTG TCACGTATCA TGTTTGAAA 3600
 AATTTTGGCT ATTAAGATA TGTATTAGAT GGTCTTATCC TGATTATTAC CTGGATACAA 3660
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 GATATTTATA TTTTAAGTGA GTCTTAAAC CTCTCTTAT TTCTACAGT TATATGGCTA 3780
 AATTTCAAGT TGAACAGGGA TTCAGCATTC TGCCATCTCC TCATGGAAG AGAGGCTCCC 3840
 40 TCATCTGAAG COTCTCTGAA ATCTACCCCT GCAAGCTTCA GACAAATCAG TTGATCTCCC 3900
 TGAGCCACAC GGCCTCATTC TGTGAGGAG GGAAGATTA GCCAAAGAT TAATTTTCAT 3960
 TCCAAATCAC TTAGCTGTTA GACTGATCTG TTTGTAGCAG TTGTTTGTCT CATTTTGTCT 4020
 CTGTCCATTT TTTGAGACAT TTGTTGAGAA TATCTATTT GGTGCTCTAC TGTATTTTC 4080
 TTTTATATAT TACTTGATA TCTGTCTT TAAATTTTCT TCACATATGG TTTGCTGAT 4140
 45 ACAACTGATT TTATAACTG AAATTTAAGG AATCTAACAG CTAAACTCA GTAAGTGCAT 4200
 MTATTTCTCT ATACATAGA CCGTGTGCTA CTCTCAGCAC CCTCTCTCA ATTTTTCCT 4260
 CTGTAGCATG TGATGCTGCA TTAACATCAT TTTCATTTGC TTTTATTTCT AATATGGGAA 4320
 CAATGAGAGT GAATCTTAAA TATAGGTGT AGTAATAAAA CATCATTAGC CTAATTTATA 4380
 50 GAAATATCTA ATTAAGTACC AGCAGATAGA AACATGAAAT TGCTTAGTCA TTGTACCTTT 4440
 GTCAGCAATT TTGACAGTCA TTAATGTTTG TCATAATTTT AAATAAAGTG TCTGGGTTTC 4500
 AGAATACCTT CAAAAAATA AAAAAA

SEQ ID NO:26 PAA3 Protein sequence
 Protein Accession #: BAA82582

55 1 11 21 31 41 51
 MFSGFNVRV GISFVIMCIP YMPTVNSLPE LSPQKYPSTL QPGLZELNEA VRPLQDYGIS 60
 VAKVNCVKEE ISRYCGKERD LMKAYLPKGN ILLREPTDT LFDVNAIVAH VLFALLPSEV 120
 60 KYITNLEDLQ NIENALRGKA NIIPSYVRAI GIPEHRAVME AGFVYGTITYQ FVLITTEIAL 180
 ESIGSDVEY AHLYPFCKL VLDLTQOCRR TLMEQPLTTL NIHLPIKTMK AFLITEVAED 240
 PQQVSTVHLQ LGLPLVPIVS QQATYEADRR TAEMVAMRLI GKAGVLLLR DSLEVNIPQD 300
 ANVVPKRAEB GVFPVELVLH DVDLIISHEV NNMHIEHQE DEEDNMEGPD IDVQDEVAE 360
 TVFRDRKRKL PLELTVELTE ETPNATVMAS DSIVLPYAGW QAVSMAPLQS YIDVAVKLKG 420
 65 TSTMLLRIN CADWSDVCTK QNVTEFPIIK MYKGENPVS YAGMLGTEKL LKFIQLNRIS 480
 YFVNITSIGI AEEYLSGELY KDLILYSSVS VLGLFSPTMK TAKEDFSEAG NYLKGIVITG 540
 IYSEEDVLLL STKYAASLPA LLLARHTEGK IESTPLASTH AQDIVQIITD ALLEMPPEIT 600
 VENLPSYFRL QRPLILFSPD GTVNPQYKA ILTLVKQRYL DSFTPCMLNL KNTFVGRGIL 660
 RAYPDLPLPL PLLVLVNLHS GGQVFPAPSD QAIIEENLVL WLKLEAGLE NHITILPAQE 720
 70 WKPFLPAYDF LEMIDAATSG RGTREVPKCM KETDVQENDK EQHEDKSAVR KEPIETLRK 780
 HWNRSNWFEK AEKSFRDRKE LGCCKVN

SEQ ID NO:27 PAA5 DNA SEQUENCE

75 Nucleic Acid Accession #: NM_012449
 Coding sequence: 66-1085 (underlined sequences correspond to start and stop codons)
 80 1 11 21 31 41 51
 CCGAGACTCA CGGTCAAGCT AAGCGGAAGA GTGGGTGGCT GAAGCCATAC TATTTTATAG 60
 AATTAATGGA AAGCAGAAAA GACATCACAA ACCAAGAAGA ACTTTGAAA ATGAAGCCTA 120

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GGAGAAATTT AGAAGAAGAC GATTATTTCG ATAAGGACAC GGGAGAGACC AGCATGCTAA 180
AAAGACCTGT GCTTTTGCAT TTGCACCAAA CAGCCCATGC TGATGAATTT GACTGCCCTT 240
CAGAACTTCA GCACACACAG GAACCTCTTC CACAGTGGCA CTGCCCAATT AAAATAGCTG 300
CTATTATAGC ATCTCTGACT TTCTCTTACA CTCTCTGAG GGAAGTAATT CACCTTTTAG 360
CAACTTCCCA TCAACAATAT TTTTATAAAA TTCCAATCCT GGTCAATCAAC AAAGCTCTGC 420
CAATGGTTTC CATCACTCTC TTGGCATTGG TTTACCTGCC AGGTGTGATA GCAGCAATTG 480
TCCAACATCA TAATGGAACC AAGTATAAGA AGTTTCCACA TTGGTTGGAT AAGTGGATGT 540
TAACAAGAAA GCAGTTTGGG CTCTCTCAGT TCTTTTTTGC TGTACTGCAT GCAATTATTA 600
GTCTGTCTTA CCCAATGAGG CGATCCTACA GATACAGT GCTAAACTGG GCATATCAAC 660
AGGTCCAACA AAATAAAGAA GATGCCGTGA TTGAGCATGA TGTTTGGAGA ATGGAGATTT 720
ATGTGTCTCT GGAATTTGTG GGATTTGGCA TACTGGCTCT GTTGGCTGTG ACATCTATTG 780
CATCTGTGAG TGACTCTTTG ACATGGAGAG AATTTCACTA TATTCAGAGC AAGCTAGGAA 840
TTGTTTCCCT TCTACTGGCG ACATACACAG CATTTGATTT TGGCTGGAAT AAGTGGATAG 900
ATATAAAACA ATTTGTATGG TATACACCTC CAACTTTTAT GATAGCTGTT TTCTTCCAA 960
TTGTTTCCCA GATATTAAAG AGCATACTAT TCCCTGCCATG CTGAGGAAAG AAGATACTGA 1020
AGATTAGACA TGGTTGGGAA GACGTACCA AATTAACAA AACTGAGATA TGTTCOCAGT 1080
TGTAAGATTA CTGTTTACAC ACATTTTGTG TCAATATTGA TATATTTTAT CACCAACATT 1140
TCAAGTTTGT ATTTGTTAAT AAAATGATTA TTCAAGGAAA AAAAAAAAAA AAAAA

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SEQ ID NO:28 PAAS Protein sequence
Protein Accession #: NP_036581

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30

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1 11 21 31 41 51
MESREDITNQ EELWKKPKRR NLEDDYLHK DTGETSMLKR PVLLHLHQTA HADEFDPCSE 60
LQHTQELFPQ WMLPKIAAI IASLTFLYTL LREVIHPLAT SHQYFYKIP ILVINKVLPM 120
VSITLALVY LPGAIAIVQ LHNGTKYKKF PHLWDEWMLT RKQFGLSFP FAVLHAIYSL 180
SYPMRSRYX KLLNWAYQQV QQNKEDAWIE HDVWRMEIYV SLGIVGLAIL ALLAVTSIPS 240
VSDSLTWREF HTYQSKLGIV SLLGTTIHAL IFAMNKWIDI KQFWYTPPT FMIAVFLPIV 300
VLIFPSILFL PCLRKILKI RHGWEDVTKI NKTEICSQL

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SEQ ID NO:29 PAAT DNA SEQUENCE

Nucleic Acid Accession #: NM_030774

Coding sequence: 1-883 (underlined sequences correspond to start and stop codons)

35
40
45
50
55
60
65
70
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80

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1 11 21 31 41 51
ATGAGTTCCT GCAACTTCAC ACATGCCACC TTTGTGCTTA TTGGTATCCC AGGATTAGAG 60
AAAGCCCAAT TCTGGGTGGG CTTCCCCCTC CTTTCCATGT ATGTAGTGGC AATGTTTGGG 120
AACTGCATCG TGGTCTTCAT CGTAAGGAGC GAACGCAGCC TGCAAGCTCC GATGTACCTC 180
TTTCTCTGCA TGCTTGACAG CATTGACCTG GCGTTATCCA CATCAACCAT GCGTAAGATC 240
CTTCCCTTTT TCTGGTTTGA TTCCCAGAGG ATTAGCTTTG AGGCCCTGCT TACCCAGATG 300
TCTTTTATTC ATGCCCTCTC AGCCATTTGA TCACCATCC TGCTGGCCAT GGCCTTTGAC 360
CGTTATGTGG CCATCTGCCA CCCACTGGGC CATGCTGCAG TGCTCAACAA TACAGTAACA 420
GCCCAGATGT GCATCTGGGC TGTGGTCCGC GGATCCCTCT TTTTCTTCCC ACTGCCCTCG 480
CTGATCAAGC GCGTGGCTTT CTGCCACTCC AATGTCTCTT CGCACTCCTA TTGTGTCCAC 540
CAGGATGTAA TGAAGTTGGC CTATGCAGAC ACTTTGCCCA ATGTGGTATA TGGTCTTACT 600
GCCATCTGCG TGGTCATGGG CGTGGACGTA ATGTTTATCT CTTTGTCTTA TTTTCTGATA 660
ATACGAACGG TTTCTCAACT GCGTTCCAAG TCAGAGCGGG CCAAGGCCCT TGGAACTGTT 720
GTGTACACCA TTTGCTGGT ACTCGCCTTC TATGTGCCAC TTATGGGCTC CTGAGTGGTA 780
CACCGCTTTG GAACACGCGT TCATCCCAAT GTGCGTGTG TCATGGGTGA CATCTACCTG 840
CTGCTGCCCT CTGTCTATCA TCCCATCATC TATGGTGCCA AAACCAACA GATCAGAACA 900
CGGGTCTGCG CTATGTTCAA GATCAGCTGT GACAAGGACT TGCAAGCTGT GGGAGGCAAG 960
TGACCCCTAA CACTACACTT CTCTTATCT TTTATGGCTT GATAACATA ATTATTCTA 1020
ACACTAGCTT ATTTCCAGTT GCCATAAGC ACATCAGTAC TTTTCTCTGG CTGGAATAGT 1080
AACTAAAGT ATGTTACATC TACCTAAAGG ACTATTATGT GGAATAATAC ATACTAATGA 1140
AGTATTACAT GATTTAAAGA CTACAATAAA ACCAAACATG CTTATAACAT TAAGAAAAAC 1200
AATAAAGATA CATGATTGAA ACCAAGTTGA AAAATAGCAT ATGCCTTGGA GGAATGTGTC 1260
TCAATTAATC AATGATTTAG TGTGTGCCCT ACTTCTCTCT TCTTTTCTCT TTCTTTTCTT 1320
TTTATTATGG TTAGCTGTCA CATACAATT TTTTCTTTT TTGAGATGGG TCTCGCTCTG 1380
TCACCAAGCT GAGTGCAGT GCGCGCATCT CGGCTCACTG CAACCTCCAC ATCCCATGTT 1440
GAAGTAATTC TTCTGCCCTA GCGTCCCGAG TAGCTGGGAC TAGAGGAACG TGCCACCATG 1500
ACTGGCTAAT TTTCTGTATT TTTTAGTAGA GACAGATTTT CACCATGTTG GCCAGGATGG 1560
TCTCGATCTC CTGACCTTGT GATCCACCCG CCTCAGCCTC CCAAGTGTGT GGGATTACAG 1620
GTGTGAACCA CTGTGCCCGG CCTGTGTACA ACTTTTAAAA TAGGGAATAT GATAGCTTCG 1680
CATGTGGTGT TGCACTATA GCGCCCACTG CCTGGAAAGC TGAGGTGGGA GAATCGCTGT 1740
AGTCCAGGAG TTTGAGGTTA CAGTGATCCA CGATCGTACC ACTACACTCC AGCCTGGGCA 1800
ACAGAGCAGG ACCCTGTCTC AAAGCATAAA ATGGAATAAC ATATCAAAATG AAACAGGGAA 1860
AATGAAGCTG ACAATTATAG GAAGCCAGGG CTGTGCACAG TCTCTACTGT TATTATGCAT 1920
TACCTGGGAA TTAGCTATAAG CCGTTAATAA TARTGCCAAT GAACATCTCA TGTGTGCTCA 1980
CAATGTCTCG GCACTATTAT AAGTGCTTCA CAGGTTTTAT GTGTCTCTCG TAACTTTATG 2040
GAGTAGGTAC CATTGTGTCT TCTTTATTAT AAGTGAGAGA AATGAAGTTT ATATTATCAA 2100
GGGACTTAA GTACACCGGC TTGTGGGCAC TGTGCCAAGA TTTAAATTA AATTTGATGG 2160
TTGAATACAG TTACTTATAG ACCATGTTAT ATTGCTTCTT GTGTAACTC TGCCATTTAT 2220
TTCTCAGCTG GTACAAATCC TCTGTCTTCT CTCGTGTACA CACTAACATC AATGGCTTTG 2280
TACTGTGTAT GAGAGATAAC CTTGCCCTAG TTGTGGGCAA CACATGCAGA ATATCCTGT 2340
TTTACAGCTG CCTTTCTGTA TCTTATGTCT TGCTTTTCTC CAGATTACAG GAGAATGTTG 2400
TTGTCTATT TTCTCTTACA TCTCCTTGAT CATGCTTCA TTTTAAATG TGCTCTGTAC 2460
CTGTCAAAAA TTTTGAATGT ACACCACATG CTATTGTCTG AACTTGAGTA TAAGATAAAA 2520
TAAAAATTTA TTTTAAATTT T

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SEQ ID NO:30 PAA7 PROTEIN SEQUENCE

Protein Accession #: NP_110401

5 1 11 21 31 41 51
 | | | | |
 MSSCNFTHAT FVLIGIPGLE KAHFWVGFFL LSMVVMVAMFG NCIUVFIVRT ERSIHAFMYL 60
 PLCLAAAILD ALSTSTMPRI LALFWFDSRE ISPEACLTQM FFIHALSAIB STILLAMAFD 120
 RYVAICHPLR HAVALNNTVT AQIGIVAVVR GSLFFFPFLPL LIKRLAPCHS NVLSHSYCVH 180
 10 QDVVKLAYAD TLFNVVYGLT AILLVMGV DV MFISLSYFLI IRTVLQLPSK SERAKAFGTC 240
 VSHIGVVLPF YVPLIGLSV VHRFGNSLEPI VRVVMGDIYL LLPPVINPII YGARTKQIRT 300
 RVLAMFKISC DKDLQAVGGK

SEQ ID NO:31 PAV6 DNA SEQUENCE

Nucleic Acid Accession #: XM_050837

Coding sequence: 1-1020 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
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 20 ATGAACCTGGG AGCTGCTGCTG GTGGCTGCTG GTGCTGTGCG CGCTGCTCCT GCTCTTGGTG 60
 CAGCTGCTGC GCTTCTCTGAG GGCTGACGGC GACCTGAAGC TACTATGGGC CGAGTGGCAG 120
 GGACGACGCC CAGAAATGGGA GCTGACTGAT ATGGTGGTGT GGGTGACTGG AGCCTCGAGT 180
 GGAATTGGTG AGGAGCTGGC TTACCACTTG TCTAACTAG GAGTTTCTCT TGTGCTGTCA 240
 25 GCCAGAGAGT TGCATGAGCT GGAAGGGTG AAAAGAGAT GCCTAGAGAA TGGCAATTTA 300
 AAAGAAAAG ATATACTTGT TTTGCCCTT GACCTGACCG ACACCTGGTTC CCATGAAGCG 360
 GCTACCAAG CTGTCTCCA GAGTTTGGT AGAATCGACA TTCTGGTCAA CAATGGTGA 420
 ATGTCCACG GTTCTCTGTG CATGGATACC AGCTTGGATG TCTACAGAAA GCTAATAGAG 480
 CTTAACTACT TAGGACGGT GTCTTGACA AAATGTGTTT TGCCTCACAT GATCGAGAG 540
 30 AAGCAAGGAA AGATTGTTAC TGTGAATAGC ATCCTGGGTA TCATATCTGT ACCTCTTTC 600
 ATTGGTACT GTCTAGCAA GCATGCTCTC CGGGGTTTTT TTAATGGCCT TCGAACAGAA 660
 CTTGCCACAT ACCCAGGTAT AATAGTTTCT AACATTGGC CAGGACCTGT GCAATCAAT 720
 ATTGTGGAGA ATTCCTAGC TGGAGAAGTC ACAAGACTA TAGGCAATAA TGGAGACAG 780
 TCCACAGA TGACAACAG TCGTTGTGTG CGGCTGATGT TAATCAGCAT GGCCTAATG 840
 35 TTGAAAGAG TTTGGATCTC AGAACCAACCT TTCTGTGTAG TAACATATT GTGGCAATAC 900
 ATGCCAACCT GGGCCTGGTG GATAACCAAC AAGATGGGGA AGAAAGGAT TGAGAACTTT 960
 AAGAGTGGTG TGATGCAGA CTCCTCTTAT TTTAAATCT TTAAGACAAA ACATGACTGA

SEQ ID NO:32 PAV6 Protein sequence

Protein Accession #: XP_050837

40 1 11 21 31 41 51
 | | | | |
 MNWELLWLL VLCAALLLV QLLRFLRADG DLTLLWAEWQ GRRPEWELTD MVVWVTGASS 60
 GIGEEAYLQL SKLGVSLLVS ARRVELERV KRRCLNENL KEDILVLPL DLTDTGSHEA 120
 45 ATKAVLQEPG RIDILVNNGG MSQRLCMDT SLDVYRLIE LNYLGTVSLT KCVLPHEMER 180
 RQKRIYTVNS ILGLISVPLS IGVCAKHAL RGFENGLRTE LATYFGLIIV NICRPFVQSN 240
 IVENSLAGEV TKFTGNNGDQ SEKMITSRCV RLMLISMAND LKEVWISBP PLLVFTYLAQY 300
 MPTWAWWTIN KMOKKRIENF KSGVDADSSY FKIFKTKHD

SEQ ID NO:33 PBA6 DNA SEQUENCE

Nucleic Acid Accession #: NM_006853

Coding sequence: 26-874 (underlined sequences correspond to start and stop codons)

55 1 11 21 31 41 51
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 AGGAATCTGC GCTCGGGTTC CGCAGATGCA GAGGTGAGG TGGCTGCGGG ACTGGAAGTC 60
 ATCGGGCAGA GGTCTCACAG CAGCCAAGGA ACCTGGGGCC CGCTCTCTCC CCTTCCAGGC 120
 CATGAGGATT CTGCAGTTAA TCTGTCTTGC TCTGGCAACA GGGCTTGTAG GGGGAGAGAC 180
 60 CAGGATCATC AAGGGGTTCG AGTGCAAGCC TCACTCCAG CCCTGGCAGG CAGCCCTGTT 240
 CGAGAAGACG CGGCTACTCT GTGGGGCGAC GCTCATCGCC CCAGATGGC TCCTGACAGC 300
 AGCCCATGCG CTCAGGCCCC GCTACATAGT TCACCTGGGG CAGCACAACC TCCAGAAGGA 360
 GGAGGGCTGT GAGCAGACC GGACAGCCAC TGAGTCTTTC CCCCACCCCG GCTTCAACAA 420
 CAGCTCCCC AACAAAGACC ACCGCAATGA CATCATGCTG GTGAGATGG CATGCCAGT 480
 65 CTCCATCACC TGGGCTGTGC GACCCCTCAC CCTCTCTCA CGCTGTGTCA CTGCTGGCAC 540
 CAGCTCGCTC ATTTCCGGCT GGGGCGACAC GTCCAGCCCC CAGTTACGCC TGCCTCACAC 600
 CTTGCGATGC GCCAATATCA CCATCATTGA GCACAGAAG TGTGAGAAGC CCTACCCCGG 660
 CAACATCACA GACACCATGG TGTGTGCCAG CGTGACAGAA GGGGGCAAGG ACTCCTGCCA 720
 GGGTACTCTC GGGGGCCCTC TGGTCTGTAA CCAGTCTCTT CAAGGCATTA TCTCCTGGGG 780
 70 CCAGGATCCG TGTGGGATCA CCGGAAAGCC TGGTGTCTAC ACGAAAGTCT GCAAAATATG 840
 GGACTGGATC CAGGAGACGA TGAAGAACAA TTAGACTGGA CCCACCCACC ACAGCCCATC 900
 ACCCTCATTT TCCACTTGGT GTTTGGTTCC TGTCACTCT GTTAATAAGA AACCTAAGC 960
 CAAGACCTTC TACGAACATT CTTTGGGCTT CCTGGACTAC AGGAGATGCT GTCACTTAAT 1020
 AATCACCCTG GGGTTCGAAA TCAATGAGAC CTGGATTCAA ATTCTGCCTT GAAATATTGT 1080
 75 GACTCTGGGA ATGACAAAC CTGGTTTGT CTCTGTGTGA TCCCCAGCCC CAAAGACAGC 1140
 TCCTGGCCAT ATATCAAGGT TTCAATAAAT ATTTGCTAAA TGAGTG

SEQ ID NO:34 PBA6 PROTEIN SEQUENCE

Protein Accession #: NP_006844

1 11 21 31 41 51
 5 MRILQLILLA LATGLVGGET RIIRKGFCEKF HSQPNQAAALF EKTRLLCGAT LIAFRWLLTA 60
 ARCLKPRYIV HLGQHNLOKE EGCEBQTRTAT ESPPHPGPN SLPAKDRND IMLVKMASPV 120
 SITWAVRPLT LSSRCVTAGT SCLISGWGST SSPQLRLPHT LRCANITILE HQKCNAYPG 180
 NITDMVCAS VQEGGKDSQ GDSGGPLVCN QSLQGIISWG QDPCAITRKP GVTYKVCCKV 240
 DWIQETKKN

10 SEQ ID NO:35 PBC1 DNA SEQUENCE

Nucleic Acid Accession #: NM_001775

Coding sequence: 70-872 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 15 CTAAAGCTCT CTGCTGCTCT AGCCTCTCTG CGGCTCTATC TTGCGCCAGC CAACCCCGGC 60
 TGGAGCCCTA TGGCCAACTG CGAGTTCAGC CCGGTGTCCG GGGACAAACC CTGCTGCCGG 120
 CTCTCTAGGA GAGCCCAACT CTGTCTTGGC GTCACTATCC TGGTCTCGAT CCTCGTCGTG 180
 GTGCTGGCGG TGGTGTCTCC GAGGTGGCGC CAGACGTGGA GCGGTCCGGG CACCACCAAG 240
 20 CGCTTCCCGG AGACCGTCTC GCGCGGATGC GTCAAGTACA CTGAAATTC TCTGAGATG 300
 AGACAGTAGT ACTGCCAAGG TGTATGGGAT GCTTCAAGG GTGCATTAT TCAAAACAT 360
 CCTTGCACAA TTACTGAAGA AGACTATCAG CCACTAATGA AGTTGGGAAC TCAGACCGTA 420
 CCTTGCACAA AGATTCTTCT TTGGAGCAGA ATAAAGATC TGGCCCATCA GTTCACACAG 480
 GTCCAGCGGG ACATGTTTAC CCTGGAGGAC ACGCTGCTAG GCTACCTTGC TGATGACCTC 540
 25 ACATGGTGTG GTGAATTCAA CACTTCCAAA ATAACTATC AATCTTGGCC AGACTGGAGA 600
 AAGGACTGCA GCAACACCC TGTTCAGTA TTCTGGAATA CCGTTTCCCG CAGGTTTGCA 660
 GAAGCTGCTC GTGATGTGTG CCAATGTGAT CTCATATGAT CCGCAGTAA AATCTTTGAC 720
 AAAACACGCA CTTTGGGGAG TGTGGAAGTC CATTAATTGC AACCAGAGAA GGTTCAGACA 780
 CTAGAGGCTC GGGTGTATCA TGGTGAAGA GAAGATTCCA GAGACTTATG CCAGGATCCC 840
 30 ACCATAAAG AGCTGGAATC GATTATAAG AAAAGGAATA TTCAATTTC CTGCAAGAAT 900
 ATCTACAGAC CTGACAGTGT TCTTCAAGT GTGAAAATC CTGAGGATTC ATCTTGACA 960
 TCTGAGATCT GAGCCAGTGT CTGTGGTTGT TTTAGCTCCT TGACTCCTTG TGGTTTATGT 1020
 CATCATACAT GACTCAGCAT ACGTGTCTGT GCAGAGCTGA AGATTTTGGG GGGTCTCTCA 1080
 35 CAATAAGGTC AATGCCAGAG ACGGAAGCCT TTTTCCCCAA AGCTTTAAAA TAACCTATAT 1140
 CATCAGCATC CCTTTATTGT GATCTATCAA TAGTCAAGAA AAATTATTGT ATAAGATTAG 1200
 AATGAAAATT GTATGTTAAG TTACTTCCTT TAG

SEQ ID NO:36 PBC1 Protein sequence

Protein Accession #: NP_001768

1 11 21 31 41 51
 40 MANCEPSPVS GDRPCRLSR RAQLCLGVSI LVLILVVVLA VVVRWRQIW SGPPTTKRFP 60
 ETVLARCVRY TEIHPERHIV DCQSVWDAFK GAFISKHPCN IYEDYQPLM KLGQTVPNC 120
 45 KILLWRIKD LAHQPTQVQR DMPTLEDILL GYLADLTWC GEFNTSKINY QSCPDRKDC 180
 SNNPVSFVK TVSRFPABEA CDVVHVMLNG SRSKIFDKNS TFGSVEVHNL QPEKVQTLA 240
 WVEHGREDS RDLCDQPTTK ELSIISKRN IQFSCNRYR FDKFLQCVN PEDSSCTSEI

50 SEQ ID NO:37 PBH1 DNA SEQUENCE

Nucleic Acid Accession #: XM_017718

Coding sequence: 1-3315 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 55 ATGTCCTTTC GGGCAGCCAG GCTCAGCATG AGGAACAGAA GGAATGACAC TCTGGACAGC 60
 ACCCGGACCC TGTACTCCAG CCGCTCTCGG AGCACAGACT TGTCTTACAG TGAAGCGGAC 120
 TTGGTGAATT TTATTCAAGC AATTTTAAAG AAACGAGAAT GTGTCTTCTT TACCAAGAT 180
 TCCAAGCCCA CGGAGAATGT GTGCAAGTGT GGCTATGCCC AGAGCCAGCA CATGGAAGGC 240
 60 ACCCAGATCA ACCAAAGTGA GAATGGAAC TACAAGAAC ACACCAAGGA ATTTCCTACC 300
 GACGCTTTG GGGATATTCA GTTTGAGACA CTGGGGAAGA AAGGGAAGTA TATACGTCGT 360
 TCTGTGACA CGGACGCGGA AATCCTTTAC GAGCTGCTGA CCCAGCACTG GCACCTGARA 420
 ACACCCAAAC TGGTCATTTC TGTGACCGGG GCGCCAAGA ACTTCGCCCT GAAGCCGCGC 480
 ATGCGCAGA TCTTCAGCCG GCTCATCTAC ATCGGCGAGT CCAAGGTGTC TTGGATTCTC 540
 65 ACGGGAGGCA CCCATTATGG CCTGATGAAG TACATCGGGG AGGTGGTGAG AGATAACACC 600
 ATCAGCAGGA GTTCAGAGGA GAATATTGTG GCCATTGGCA TAGCAGCTTG GGGCATGGTC 660
 TCCAACCGGG ACACCCCTCAT CAGGAATTGC GATGCTGAGG GCTATTTTIT AGCCAGTAC 720
 CTTATGGATG ACTTCACAAG AGATCCACTG TATATCTCGG ACAACAACA CACACATTTG 780
 CTGCTGTGTG ACAATGGCTG TCATGGACAT CCCACTGTG AAGCAAGACT CCGGAATCAG 840
 70 CTAGAGAATG ATATCTCTGA GCGCACTATT CAAGATTCCA ACTATGGTGG CAAGATCCCC 900
 ATGTGTGTGT TTGCCAAGG AGGTGGAATA GAGACTTTGA AAGCCATCAA TACCTCCATC 960
 AAAAATAAAA TTCTTGTGT GTGTGGTGA GGTCTGGGCG AGATCGCTGA TGTGATCGCT 1020
 AGCCTGTGTG AGGTGAGGA TGCCCTGACA TCTTCTGCG TCAAGGAGAA GCTGGTGGCG 1080
 TTTTACCCCG GCACGGTGTG CCGGCTGCGT GAGGAGGAGA CTGAGAGTTG GATCAAATGG 1140
 75 CTCAAAGAAA TTCTCGAATG TTCTCACTTA TTAACAGTGA TTAATAATGA AGAAGCTGGG 1200
 GATGAATATG TGAGCAATGC CATCTCCTAC GCTCTATACA AAGCCTTCAG CACCACTGAG 1260
 CAAGACAAGG ATAACTGGAA TGGCGAGCTG AAGCTTCTGC TGGAGTGGAA CCAGCTGGAG 1320
 TTAGCCAATG ATGAGATTTT CACCAATGAC CGCGATGGG AGTCTGCTGA CTTTCAAGAA 1380
 GTCATGTTTA CGGCTCTCAT AAAGGACAGA CCCAAGTTTG TCCGCTCTCT TCTGGAGAAT 1440
 80 GGCTTGAACC TACGGAAGTT TCTCACCAT GATGCTCTCA CTGAAGCTCT TCCAACCAAC 1500
 TTCAGCACGC TTGTGTACCG GAATCTGCAG ATCGCCAAGA ATTCCTATAA TGATGCCCTC 1560

5 CTCACGTTTG TCTGGAAACT GGTTCGGAAC TTCGGAAGAG GCTTCCGGAA GGAAGACAGA 1620
 AATGGCCGGG ACGAGATGGA CATAGAACTC CACGACGTGT CTCTATTAC TCGGCACCCC 1680
 CTGCAAGCTC TCTTCATCTG GCCCATCTCT CAGRATAAGA AGGAACTCTC CAAAGTCATT 1740
 TGGGAGCAGA CCAGGGGCTG CACTCTGGCA GCCCTGGGAG CCAGCAAGCT TCTGAAGACT 1800
 CTGGCCAAAG TGAGGAACGA CATCAATGCT GCTGGGGAGT CCGAGGAGCT GGCTAATGAG 1860
 TACGAGACCC GGGCTGTTGA GCTGTTCACT GAGTGTACA GCAGCGATGA AGACTTGGCA 1920
 GAACAGCTGC TGTACTATTC CTGTGAAGCT TGGGGTGGAA GCAACTGTCT GGAGCTGGCG 1980
 GTGGAGGCCA CAGACCAGCA TTTCATCGCC CAGCCTGGGG TCCAGAATTG TCTTCTAAG 2040
 CAATGGTATG GAGAGATTTT CCGAGACACC AAGAACTGGA AGATTATCTT GTGTCTGTTT 2100
 10 ATTATACCTT TGGTGGGCTG TGGCTTTGTA TCATTTAGGA AGAAACCTGT CGACAAGCAC 2160
 AAGAAGCTGC TTTGGTACTA TGTGGCGTTC TTCACCTCCC CCTTCGTGGT CTCTCTCTGG 2220
 AATGTGCTCT TCTACTCCG CTTCCTCTCT CTGTTTGCCT ACGTCTGTCT CATGGATTTC 2280
 CATTCCGTGC CACACCCCC CGAGCTGGTC CTGTACTCGC TGGTCTTTGT CCTCTCTGT 2340
 GATGAAGTGA GACAGTGGTA CGTAAATGGG GTGAATTATT TTACTGACCT GTGGAAATGT 2400
 15 ATGGACACGC TGGGGCTTTT TTACTTCATA GCAGGAATTG TATTTCGGCT CCACCTCTCT 2460
 AATAAAGCT CTTTGTATTG TGGACGAGTC ATTTTCTGTC TGGACTACAT TATTTTCACT 2520
 CTAAGATTGA TCCACATTTT TACTGTAAAG AGAAACTTAG GACCCAGAT TATAATGCTG 2580
 CAGAGGATGC TGATCGATGT GTTCTCTCT CTGTCTCTCT TTGGGTGTG GATGGTGGCC 2640
 TTTGGGCTGG CCAGGCAAGG GATCCTTAGG CAGAATGAGC AGCCTGGAG GTGGATATTC 2700
 20 CGTTCGGTCA CTACCTGGCC ATGTTCCGCC AGGTGCCAG TGACGTGGAT 2760
 GGTACCACTG ATGACTTTGC CCACTGCACC TTCACTGGGA ATGAGTCCAA GCCACTGTGT 2820
 GTGGAGCTGG ATGAGCACAA CCTGCCCCGG TTCCCGGAGT GGATCACCAT CCCCCTGGTG 2880
 TGCATCTACA TGTATATCCG CAACATCCTG CTGGTCAACC TGCTGGTCCG CATGTTTGGC 2940
 TACACCGTGG GCACCGTCCA GGAGAACAA GTACAGGTCT GGAAGTCCA GAGGTACTTC 3000
 25 CTGGTCAGG AGTACTGCAAG CCGCTCAAT ATCCCTTCC CTTTCACTGT CTTCGCTTAC 3060
 TTCTACATGG TGTGAAGAA GTGCTCAAG TGTGTCTGCA AGGAGAAAA CATGGAGTCT 3120
 TCTGTCTGCT GTTCAAAAA TGAAGACAA GAGACTCTGG CATGGAGGG TGTCAATGAG 3180
 GAAAACCTAC TTGTCAAGAT CAACACAAA GCCAACGACA CCTCAGAGGA AATGAGGCAT 3240
 30 CGATTAGAC AACTGGATAC AAAGCTTAAT GATCTCAAG GTCTTCTGAA AGAGATTGCT 3300
 AATAAATCA AATGA

SEQ ID NO:39 PBH1 Protein sequence

Protein Accession #: XP_017718

35 1 11 21 31 41 51
 MSFPAARLSH RNRRNDTLDS TRTLYSSASR STDLSYSED LVNFIQANPK KRCVFFTKD 60
 SKATENVCKC GYAQSQHMEG TQINQSEKWN YKRHTKEFPT DAFGDIQFET LGKKGYIRL 120
 40 SCDTDAEILY ELITQRMHLK TPNLVISVTO GAKNFALKPR MRKIFSRLEY IAQSKGAWIL 180
 TGGTHYGLMK YIGBVVRDNT ISRSSEENVV AIGIAAWGMV SNRDTLIRNC DAEGYFLAQY 240
 LMDDFTRDEL YILDNHPTHL LLVNGCHGH PTVEAKLRNQ LEKYISERTI QDSNYGGKIP 300
 IVCPAGQGGK ETLKAINTSI ENKIPCVVVE GSGQLADIVA SLVEVEDALT SSAVKELVR 360
 FLPRYTSRPL EESTESWLKW LKELLECSSL LVVIMKEBAG DEIVSNALSY ALYKAFSTSE 420
 45 QKDNWNGQL KLLLEWQLD LANDEIFTND RRWESADLQE VMFTALIKDR PKFVRLFLEN 480
 GLNLRFPLTH DVLTELFNSH FSTLVYRNLO IAKNSYNDAL LTFVWKLIVN FRGFRKEDR 540
 NGRDEMDIEL HDVSPITREP LQALFIWAIL QNKELSKVI WEQTRGCTLA ALGASKLLKT 600
 LAKVKNDINA AGESEELANE YETRAVELFT ECVSDEDLA EQLLVYSCEA WGSNCLBLA 660
 VERTDQHFIA QPGVQNPLSK QWYGEISRDT KWKILCLF IIPLVGCGFV SFRKKPVDEK 720
 50 KILLWYVAF FTSPPVVFPM NVVPIYAFLL LFAYVLLMDT HSPVFPPELV LYSLVVPLFC 780
 DEVRQHYVNG VNLFTLWNV MDTLGLFYFI AGIVFRLHSS NKSSLYSGRV IFCLDYIIFT 840
 LRLIHFVTS RNLFPIKILM QRLIDVFFF LFLFAVWVVA FGVARQGLR QNEQRWRWIF 900
 RSVIYEPYLA MFGQVPSDWD GTTYDFHCT PTGNESKPLC VELDEHNLPR FPEWITIPLV 960
 55 CTYHLSNLL LVNLLVAMFG YTVGTVOENN DQVWKFQRYF LVQEYCSRLN IFFVFFVFAV 1020
 FYMVVKCKFK CCKCKNMES SVCCFKNEEN ETLAWEGVMK ENYLVKINTK ANDTSEEMRH 1080
 RFRQLDTKLN DLKGLLEKIA NKIK

SEQ ID NO:39 PBH3 DNA SEQUENCE

Nucleic Acid Accession #: XM_011804

Coding sequence: 1-558 (underlined sequences correspond to start and stop codons)

60 1 11 21 31 41 51
 ATGCTCTGCG TGTCTCTGTT CCACCTGCTA GAATCTCTGT TACTACTGAA CCAATTTTCC 60
 AGAGCAGTGC CGGCCAAATG GAAGGACGAT GTTATTAAAT TATGCGGCGG CGAATTAGTT 120
 65 CCGCGGCAGA TTGCCATTGG CGGCATGAGC ACCTGGAGCA AAAGGTCTCT GAGCCAGGAA 180
 GATGCTCTCT AGACACCTAG ACCAGTGGCA GAAATTGTAC CATCTTCAT CAACAAGAT 240
 ACAGAACTA TAATTATCAT GTTGAATTC ATTGCTAATT TGCCACCGGA GCTGARGGCA 300
 GCCCTATCTG AGAGGCAACC ATCATTACCA GAGCTACAGC AGTATGTACC TGCAATTAAG 360
 70 GATTCCAATC TTAGCTTTGA AGAATTTAAG AACTTTATTC GCAATAGGCA AAGTGAAGCC 420
 GCAGACAGCA ATCCTTCAGA ATTAATAATC TTAGGCTTGG ATACTCATTC TCAAAAAAAG 480
 AGACGACCTT ACGTGGCACT GTTTGAGAAA TGTGTGCTAA TTGGTGTGAC CAAAGGTCT 540
 CTTGCTAAAT ATTGCTGA

SEQ ID NO:40 PBH3 PROTEIN SEQUENCE

Protein Accession #: NP_008842

75 1 11 21 31 41 51
 MPRLFLPHLL EFCLLLNQFS RAVAAKWKDD VIKLCGRRLV RAQIAICGMS TWSKRSLSQE 60

DAPQTRPRVA EIVPSEFINK TETIIMLEF IANLPPELKA ALSERQPSLP ELQQYVPALK 120
 DSNLSFPEFK KLIRNRQSEA ADSNPSELKY LGLDTHSQK RRPYVALFEK CCLIGCTKRS 180
 LAKYC

5

SEQ ID NO:41 PBH5 DNA SEQUENCE

Nucleic Acid Accession #: NM_005845

Coding sequence: 1-3978 (underlined sequences correspond to start and stop codons)

10 1 11 21 31 41 51
 | | | | | |
 ATGCTGCCCG TGTACCAGGA GGTGAAGCCC AACCCGCTGC AGGACGCGAA CCTCTGCTCA 60
 CGCGTGTCTC TCTGGTGCTC CAATCCCTTG TTTAAAATAG GCCATAAACG GAGATTAGAG 120
 GAAGATGATA TGTATTTCAGT GCTGCCAGAA GACCGCTCAC AGCACCTTGG AGAGGAGTTG 180
 CAAGGGTTCT GGGATAAAGA AGTTTAAAGA GCTGAGAATG ACGACAGAA GCCTTCTTTA 240
 15 ACAAGAGCAA TCATAAAGTG TTAAGTGAAT TCTTATTAG TTTTGGGAAT TTTTACGTTA 300
 ATTGAGGAAA GTGCCAAAGT AATCCAGCCC ATATTTTGGG GAAAAATTAT TAATTATTTT 360
 GAAATATTAT ATCCCATGGA TTCTGTGGCT TTGAACACAG CGTACGCCCTA TGCCACGGTG 420
 CTGACTTTTT GCACGCTCAT TTTGGCTATA CTGCATCACT TATATTTTTA TCACGTTTCA 480
 20 TGTGCTGGGA TGAGGTTACG AGTAGCCATG TGCCATATGA TTTATCGGAA GGCACCTTCG 540
 CTTAGTAACA TGGCCATGGG GAAGACAACC ACAGGCCAGA TAGTCAATCT GCTGTCCAAT 600
 GATGTGAACA AGTTTGATCA GGTGACAGTG TTCTTACACT TCCTGTGGGC AGGACCACTG 660
 CAGGCGATCG CAGTGACTGC CCTACTCTGG ATGAGAGTAG GAATATCGTG CCTTGTCTGG 720
 ATGGCAGTTC TAATCAITCT CCTGCCCTTG CAAAGCTGTT TTGGGAAGTT GTTCTCATCA 780
 25 CTGAGGAGTA AACTGCAAC TTTCACGGAT GCCAGGATCA GGACCATGAA TGAAGTTTAA 840
 ACTGTATAAA GGATAATAAA AATGTACGCC TGGGAAAAGT CATTTTCAAA TCTTATTACC 900
 AATTTGAGAA AGAAGGAGAT TTCCAAGATT CTGAGAAGTT CCTGCCCTAG GGGGATGAAT 960
 TTGGCTTCGT TTTTCAGTGC AAGCAAAATC ATCGTGTATT TGACCTTCAC CACTTACGTG 1020
 CTCCTCGGCA GTGTGATCAG AGCCAGCCGC GTGTTCTGGG CAGTGACGCT GTATGGGGCT 1080
 GTGCGGCTGA CGGTACCTCT CTCTTCCCTC TCAGCCATG AGAGGGGTGC AGAGGCAATC 1140
 30 GTCAGCATCC GAAGAAATCA GACCTTTTGG CTACTGTATG AGATATCACA GCGCAACCGT 1200
 CAGCTGCCGT CAGATGGTAA AAAGATGGTG CATGTGCAGG ATTTTACTGC TTTTGGGAT 1260
 AAGGCATCAG AGACCCCAAC TCTACAAGGC CTTCCTTTTA CTGTGAGACC TGGCGAATTG 1320
 TTAGCTGTGG TTGGCCCGCT GGGAGCAGGG AAGTCATCAC TGTTAAGTGC COTGCTCGGG 1380
 35 GAATTTGGCC CAGTACAGGG GCTGGTCAGC GTGCATGAA GAATTCCTTA TGTGTCTCAG 1440
 CAGCCCTGGG TGTCTCGGG AACTCTGAGG AGTAATATT TATTTTGGGA GAAATACGAA 1500
 AAGGAACGAT ATGAAAAGT CATAAAGGCT TGTCTCTGA AAAAGGATTT ACAGCTGTTG 1560
 GAGGATGGTG ATCTGACTGT GATAGAGAGT CGGGGAACCA CGCTGAGTGG AGGCAGAGAA 1620
 40 GCAAGGTGAA ACCTTGCAAG AGCAGTGTAT CAAGATGCTG ACATCTATCT CTGGGACGAT 1680
 CTTCTCAGTG CAGTACATGC GGAAGTTAGC AGACACTTGT TCGAAGTGTG TATTGTCTCA 1740
 ATTTTGCATG GAAGAAATCA AATTTTAGTG ACTCATCAGT TGCAGTACCT CAAAGCTGCA 1800
 AGTCAGATTC TGATATTGAA AGATGGTAAA ATGGTGCAGA AGGGGACTTA CACTGAGTTC 1860
 CTAAATCTG GTATAGATTT TGGCTCCCTT TTAAGAAGG ATAATGAGGA AAGTGACAAA 1920
 OCTCCAGTTC TCCTAAGTCC CACACTAAGG AATGTAACCT TCTCAGAGTC TTGGGTTTGG 1980
 45 TCTCAACAAT CTCTTAGACC CTCTTGAAGA GATGGTGCTC TGGAGAGCCA AGATACAGAG 2040
 AATGTGCAAT TTAACATATC AGAGGAGAAC CGTCTGAAG GAAAAGTTGG TTTTCAGGOC 2100
 TATAAGAATT ACTTCAGAGC TGGTGCTCAC TGGATTGTCT TCATTTTCTT TATTCTCTTA 2160
 AACACTGCAG CTCAGGTGTC CTATGTGCTT CAAGATTGGT GGCTTTTCTA CTGGGCAAAC 2220
 AAACAAGTGA TCCATAAGT CACTGTAAAT GGAGGAGGAA ATGTAAACCGA GAAGCTAGAT 2280
 50 CTAACTGGT ACTTAGGAAT TTATTCAGGT TTAAGTGTAG CTACCGTTCT TTTTGGCATA 2340
 GCAAGATCTC TATTGGTATT CTACGTCTT GTTAACTCTT CACAACTTT GCACAAACAA 2400
 ATGTTTGAST CAATTCGAA AGCTCCGGTA TTAATCTTTG ATAGAAATCC AATAGGAAGA 2460
 ATTTTAAATC GTTCTCTCAA AGACATTGGA CACTTGGATG ATTTGCTGCC GCTGACGTTT 2520
 TTAGATTTC TCCAGACATT GCTACAAGTG GTTGGTGTGG TCTCTGTGGC TGTGGCCGTG 2580
 55 ATTCCTTGA TCGCAATACC CTGTGTTCCO CTGTGAATCA TTTTCATTTT TCTTGGCGGA 2640
 TATTTTGTGG AAACGTCAAG AGATGTGAAG CGCTGGAAT CTACAACCTG GAGTCCAGTG 2700
 TTTTCCCACT TGTCTATCTC TCTCCAGGGG CTCTGGACCA TCCGGGCATA CAAAGCAGAA 2760
 GAGAGGTGTC AGGAAGCTGT TGATGCACAC CAGGATTTAC ATTCAGAGGC TTGGTTCTTG 2820
 60 TTTTGTACAA CGTCCCGCTG GTTCGCCGTC CGTCTGGATG CCATCTGTGC CATGTTTCTC 2880
 ATCATCGTTG CCTTTGGGTC CCGTATCTG GCAAAAACCT TGGATGCCGG GCAGGTGGGT 2940
 TTGGCACATG CCTATGCCCT CAGGCTCATG GGGATGTTTC AGTGGTGTGT TCGACAAAGT 3000
 GCTGAAGTTG AGAATATGAT GATCTCAGTA GAAAGGOTCA TTGAATACAC AGACCTTGAA 3060
 AAAGAAGCAC CTGGGAATA TCAGAAACGC CCACCACCAG CCTGGCCCA TGAAGGAGTG 3120
 65 ATAATCTTTG ACAATGTGAA CTTCATGTAC AGTCCAGGTG GGCCTCTGGT ACTGAAGCAT 3180
 CTGACAGCAC TCAATTAATC ACAAGAAAAG GTTGGCATTG TGGGAAGAAC CGGAGCTGGA 3240
 AAAAGTTCCT TCAATCTCAG CCTTTTAGA TTGTCAGAAC CCGAAGGTAA AATTTGGATT 3300
 GATAAGATCT TGACAACTGA AATTGGACTT CACGATTTAA GGAAGAAAAT GTCAATCATA 3360
 CCTCAGGAAC CTGTTTGTGT CACTGGAACA ATGAGGAAAA ACCTGGATCC CTTTAATGAG 3420
 70 CACACGGATG AGGAACCTGT GAATGCCTTA CAAGAGGTAC AACTTAAAGA AACCATTGAA 3480
 GATCTTCTGT GTAAATATGA TACTGAATTA CGAAGATCAG GATCCAAATT TAGTGTGGA 3540
 CAAAGACACAT TGGTGTGCTT TGCCAGGGCA ATTCTCAGGA AAAATCAGAT ATTGATTATT 3600
 GATGAAGCGA CCGCAATGTG GGATCCAAGA ACTGATGAGT TAATACAAAA AAAAATCCGG 3660
 GAGAAATTTG CCCACTGCAC CGTGCTAACC ATTCACACA GATTGAACAC CATTTATGAC 3720
 AGGACAGAGA TAATGGTTTT AGATTACAGGA AGACTGAAAG AATATGATGA GCCGTATGTT 3780
 75 TTGCTGCAAA ATAAAGAGAG CCTATTTTAC AAGATGGTGC AACAACTGGG CAAGGCAGAA 3840
 CGCGCTGCC CCCTGTGACC AGCAAAACAG GTATCTTCA AAAGAATTA TCCACATATT 3900
 GGTCACTAGT ACCCATGGT TACAAACACT TCCAATGGAC AGCCCTCGAC CTAACTATT 3960
 TTCGAGACAG CACTGTA

SEQ ID NO:42 PBH5 PROTEIN SEQUENCE

Protein Accession #: NP_005836

5 1 11 21 31 41 51
MLPVQEVKPL NPLQDANLCS RVFFWMLNPL FKIGHKRRLE EDDHYSVLPE DRSQHLGEEL 60
QGFKDKVLR AENDAQKPSL TRAIKCYWK SYLVLGIPFL IEESAKVIQ IFLGKIIDYP 120
BNYDPMDSVA LNTAYAYATV LTFCTLILAI LHLHYFYHVQ CAGERLRVAM CHMTYRKALR 180
10 LSNMAMGKTY TQQTIVNLLSN DVNKFQDQTV FLHPLWAGPL QAIJAVTALLW MEIGISCLAG 240
MAVLIILLPL QSCFGKLPSS LRSKTATFTD ARIRTMNEVI TGIRITIKYA WEKSFNLTIT 300
NLRKKEISKI LRSCLRGEM LASFFSASKI IVFVTFITYV LLSVITASR VFAVATLYGA 360
VRLVTVLPFP SATERVSEAI VSIRRIQTFL LLDEISQRNR QLPDQKXNV HVQDFTAFWD 420
KASETTPFQG LSPTVPRGEL LAVVGPVAG KSSLSSAVLG ELAPSHGLVS VHGRYAVSQ 480
15 QPMVPSGTLR SNILFGKKYB KERYEKVKA CALKDLQLL EDGDLTVIGD RGTTLGGGK 540
ARVNLARAVY QDADIYLLDD PLSAVDAEVS RHLFELCICQ ILHEKITILV THQLQYLKAA 600
SQILLIKDQK MVQKGYTFEF LKSGIDFGSL LKKNNESEQ PPVQPTFLR NRTFSESSVM 660
SQQSSRPSLK DGALESQDTE NVFVTLSEEN RSEGVKGFQA YKNYFRAGAE WIVFIFLILL 720
NIAAQVAYVL QDWMLSYMAN KQSMANVTN GGGNVTEKLD LNWYLGITYG LTUATVLFGI 780
20 ARSLVFPYLR VNSSQTLHMK MFESILKAPV LFFDRNPGR ILNRPSEKDG HLDLLPLTF 840
LDFIQTLQV VGVVSVAVAV IPWLAIPLVE LGIIFIFLR YFLESSEVVK RLESTTRSPV 900
FSLSSSLQG MTTRAYKAE ERCQELFDB QDLHSEAWPL FLTTRMFAV RLDAICAMFV 960
LIVAFSLIL AKYLDAGQVG LALSVALTLM GMPQWCVRS AEVENMHISV ERVIEYTDLE 1020
KEAPWYQNR PPAWPHBQV IIFDNNVFM SPGGPLVLKH LTALIKSQEK VGVVGRGTAG 1080
25 KSSLISALFR LSEPEKQWV DKILATEIGL HDLRKKMSII PQEPVLPFGT MRKNLDPFNE 1140
HTDEELMNAL QEVQLKETTE DLPGKMDTEL AESGSNFSVG QRQLVCLARA ILRKNQILII 1200
DEATANVDK TDELIQKRIE EKPAHCTVLT IAHRLNTIID SDKIMVLDG RLKEYDEPVS 1260
LLQKESLFP KMVQQLGKAE AALATETAKQ VYFKRNYEHI GHTDMVNTNT SNGQPSTLTI 1320
FETAL

SEQ ID NO:43 PBQ7 DNA SEQUENCE

Nucleic Acid Accession #: NM_021233

Coding sequence: 34-1119 (underlined sequences correspond to start and stop codons)

35 1 11 21 31 41 51
ATGGGGAAG TGCTCTGCTG TGGCATGAAA TAAATGAAAC AGAAAATGAT GGCAAGACTG 60
CTAAGAACAT CCTTTCCTTT GCTCTTCCTT GGCCTCTTTG GGGTCTGGG GGCAGCAACA 120
ATTTCATGCA GAAATGAAGA AGGGAAGCT GTGGACTGGT TTACTTTTAA TAAGTTAACC 180
40 AAAAGACAAA ACAGAGGAAAG TGGAGAGACT GGGTTAGAGT ACCTGTACCT AGACTCTACA 240
ACTAGAGCT GAGGAGAGAG TGAGCAACTA ATGAATGACA CCAAGAGTGT TTTGGGAAGG 300
ACATTACAAC AGCTATATGA AGCATATGCC TCTAAGAGTA ACAACACAGC CTATCTAATA 360
TACAAATGAT GAGTCCCTAA ACCTGTGAAT TACAGTAGAA AGTATGGACA CACCAAGGT 420
TTACTGCTGT GGAACAGAGT TCAAGGGTTC TGGCTGATTC ATTCCATGCC TCAGTTTCCT 480
45 CCAATTCCGG AAGAAGGCTA TGATTATCCA CCCACAGGGA GACGAAATGG ACAAGGTGGC 540
ATCTGCATAA CTTTCAAGTA CAACCACTAT GAGGCAATAG ATCTCAGCT CTGTGCTGTC 600
AACCOCACG TCTATAGCTG CTCCATCCCA GCCACCTTTC ACCAGAGCT CATTCACATG 660
CCCCAGCTGT GCACACAGGC CAGCTCATCA GAGATTCCTG GCAGGCTCCT CACCACACTT 720
CAGTCGGCCC AGGGACAAA ATTCTCCAT TTTGCAAGT CGGATTCCTT TCTTGACGAC 780
50 ATCTTTCAG CTTGATGTC TCAACGGCTG AAGACACACT TGTTAACAGA AACCTGGCAG 840
GCAAAAGAAC AAGAGCTTCC TTCAAACTGC TCCCTTCCTT ACCATGTCTA CAATATAAAA 900
GCAATTAAT TATCAGACA CTCTTATTTC AGTCTTATC AAGATCACGC CAAGTGGTGT 960
ATTTCCCAA AGGGCACCAA AAATCGCTGG ACATGTATTG GAGACCTAAA TCGGAGTCCA 1020
CACCAGCCT TCAGAGTGG AGGATTCATT TGTACCAGA ATTGGCAAT TTACCAAGCA 1080
55 TTCAAGGAT TAGTATTATA CTATGAAAGC TGTAAAGTAA CTGTGTGAAA GGACACAGGT

SEQ ID NO:44 PBQ7 Protein sequence

Protein Accession #: NP_067058

60 1 11 21 31 41 51
MYARLLRTSF ALLFLGLPGV LGAATISCRN EEGKAVDWPT FYKLPRQKQK ESGETGLEVL 60
YLDSTTRSWR KSEQLMNDYK SVLGRTLQQL YEAYASKSN TAYLYNDGV PKPVNYSRKY 120
GHTKGLLWN RVQGFWLHS IPQFPPIPEB GYDYPPTGR NGQSGICITF KYNQYBAIDS 180
65 QLLVCNPNVY SCSIPATFHQ ELIHPQLCT RASSSEIPGR LLTTLQSAQG QKPLHFAKSD 240
SFLDDIFAAW MAQRKTHLL TETWQRQRE LPSNCSLPYH VYNIAIKLS RSHYFSSYQD 300
HAKWCESQK TKNRWTCIGD LNRSPHQAQR SGGFICTQNW QIYQARQLV LYYESCK

SEQ ID NO:45 PC08 DNA SEQUENCE

Nucleic Acid Accession #: XM_030453

Coding sequence: 89-1273 (underlined sequences correspond to start and stop codons)

75 1 11 21 31 41 51
CGGTGCCCTG GGGTGGGAATA TCCCTACGA ATTTAAACCA GCGGACTTTA ATGCCACTGT 60
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SEQ ID NO:46 PQ08 Protein sequence
 Protein Accession #: BAB15343

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SEQ ID NO:47 PDG5 DNA SEQUENCE

Nucleic Acid Accession #: AB033036
 Coding sequence: 68-3349 (underlined sequences correspond to start and stop codons)

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	GCAACCTGCT	TGCAGAGCCC	CAGGAAAGCC	TGCTGGTCAA	CAGTCAGATT	ATGCTGTCTC	2940
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55	TAGAGGACCA	CACCTCAAAA	GTTACTAGGC	TGGAGAGACC	CTACCTTCCA	GTGACCCACT	4920
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60	GAGATGCAGA	CCACCTTAGA	ATCTCATCTA	GCTTCACTAG	AAGTTAGTTA	AATCTTCTCT	5220
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SEQ ID NO:48 PDG5 Protein sequence
 Protein Accession #: BAA86524

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5
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15
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SEQ ID NO:49 PAB7 DNA SEQUENCE

Nucleic Acid Accession #: D87742

Coding sequence: 208-3582 (underlined sequences correspond to start and stop codons)

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80

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	TTTCATTGAA AGAAAGTGTA CTGTGCATTA TCCATTACAG TAAAGGATTT CATTTGGCTTC 3660
	AAAAATCCAA AGTTTATTTT AAAAGGTTTG TTGTTAGAAC TAAGCTGCCT TGGCAGTGTG 3720
	CATTTTGTAG CCAAAACAATT CAAAAATGTC ATTTCTTCCC TAAATAAAAA TCACCTTTTA 3780
10	AGCTAGAGCG TCCTTACAAC TTGAAATGT GCAATAAAGA ATACCTGTGT TTTAGCTAAT 3840
	GTAGCATATG TAATTGCCAA ATGATTTAGA ATGTCATGAA AAATATGAAC ATTTCTGTG 3900
	GAAATGCTTT AAGAACAATG ATTTCCATTA TCCTATTTT AGTGACACC AGCTGAATAC 3960
	GGAGCAATGG TGTTTATTAAG CGTTTCTTTA AACTATCTGG TCACAAAGAC TGTACGCTA 4020
	AAAAATGTTA CTAAAAGATC ACTAAACTAT CTCCCTCTT GCTGAAGTTC TTTGTAGTAA 4080
	TAGCTCAATA AAATTTGTTT ATTAATATT CCCAAGTGTG TGTGACTCA TTGGACTGTT 4140
15	ATGAGGCTTG TGCCATTTCG GGAACATGTA AACTCAGGCT CCCAGAACTG AAGATGGTGG 4200
	CTGGTGGCAC ACTTCCGGCT GCTCTCCGT CACCTGTGAA CTCTACAAGT GATGCTCTTT 4260
	TATTTCAAGG AAGTTTATTT CCCACTTGTA TAGCAATCAC ATGCTTCTCT TACGATCTCT 4320
	ATTGCTATT TTCTTGAGAG TTCTTGAGAG TGAGTTTACA TTAGTAGCAA GAGTTGTTTG 4380
	ACCTGATGTT CCATTGTTTT TACCATTCTT GTAGAAAAG GGTGCACAAC AGAAAAATGA 4440
20	AAATGATGTG TCATGGCCAT AAAAGTATAG AAATCTTTAA AAATTTTAAA ATGTACAGTC 4500
	CCTTATCTAT CTTTCCCAT CTCTGCCACT GATTTTGTAG GAATATAATA AAAAGATTGG 4560
	AAGAGTATAA TGCCATGAGA AAGAATGATT TAGGACTGTG AGGGTTATAA CATGCCCTAG 4620
	GTACGCAACC AGAGGTGAA ATCAGTCTCG TTTTAGGGGG AAATGGGGGG GCGACAGAT 4680
	ATTATTCCAA AATTAATATT AATTAATATT TAAACGTGG TGTTTTATT TAAAAATCAG 4740
25	TAACATAACA TCTGGAATTG CACCATACTT AAAGTCTTAT CCATTACTAC ACTGCTCTTA 4800
	AAACAATGTT TCTTTAATA CTCTACAACG TTCTTAAGAA CGAACTTCAG ACATTTTAAAT 4860
	TACAGTATAA ATAGCACTCC TTTTAAGGAG TTTCAGATCC AACTAAAC TAAATCATATA 4920
	AAAGGCTGAT ACTTTTGTTT GCTGCTAGGC TATATTCTTC CATTTCTTGA AGTCCATAGA 4980
	TGTAATATTT TGAACAACCTA GTGTATGCT TGCTACTGTT GTGATATTTA ATCGATTAG 5040
30	AATACCTTGT AAAAAGGAGC AAAAGCTTCA ATGTGAACA ATTTTCTCTC TTTATATAA 5100
	ACAACGTAG ATAGATAGTT TAGAAGATA AGGACCTTTG AAGAAGACA ACTCTGTCAA 5160
	AGTTCATAG GAATATAAAA ATCTCTCAGG AAAAGAGAA TCAATCTATA TGCTCTCCCG 5220
	TTTAATATCA AGAATAGAAG AAATTAAGAG GAAAACCTCA CAGAAGACA TAGGCCACTT 5280
	TTAGCCATGT AAAAATAGA TTAAGTCACA AATACAACCT TTGAATTAC CTGCAATAT 5340
35	CTCTTTAGGA CACAAAACAA TGCTGAAGTT AATATAATTT CTAATTTTAA ATGTCAATTA 5400
	AGTGTAGATT ATGCCATCTA GGAAGGTAAG TAGGAAAGGT AAATTAATC TATTTTAAA 5460
	ATTCAAAATA TTAGAGTATT TTTCCCTCTT AAAGCCTTTT TTGGTGATTA TTCTGTATCT 5520
	GACATAATG AGAAACTAGT AAGCTGTAAA GATTCCAGTG TAGCTTCTCT GAGAAGTTGT 5580
40	GAGCCAGTCC ATAACTGCTT CCTCACATCC ATCTGATGCG ACCATTCTCT CAGCAAAACC 5640
	CAAAAGCAGG TGCCAAATAG CAGATGGCAT AGGAGATATC ATCCCTCAGC CAAATCACTT 5700
	TTCCATCTCT AAAGTTTCAT CTATTTTGA AGTCATCTCC AACTAATGT GTCTGGATT 5760
	AGTTGTCTAA ATTTCTTAT TTATTATGA AGCAGCAATA TTCAGCCTGA AAGCATTTCT 5820
	GCCATAGTGT TTGATCTTAT ATCGCCAATG GCTGATTTT TTCAATGGAA AGTAAATTA 5880
45	AGTAATTCGT GGGATGTTGT ATATTCTGTG TCAACTTCAA GATAATCACT CATTTTCTCG 5940
	TTATATTCAG GTCTGAATTA AAGTTAAGTT AATCAC

SEQ ID NO:50 PAB7 Protein sequence

Protein Accession #: BAA13448

50	1 11 21 31 41 51
	AFLSKVEED YPSEELLEDE NAINAKRSKE KNPGNQGRQF DVNLQVPDRA VLGTIHPDPE 60
	IRESKQETSM ILDEKSTSET AAKGVMTGGR EPNTMVEKER PLADKKQRP FERSDFSDSI 120
55	KIQTPELGEV FQNKDSOYLK NDNPEELKT SGLAGEPEGE LSKEDHGNT E KYMGTESQGS 180
	AAAEFEDDSF HWTPTSVPEP GHSDEKREDLL IISFFKEQQ SLQRFQKYPN VHELEALLQE 240
	MSSKLKSAQ ESFLPNMEKV LDKVFRASES QILSTAEKML DTRVAENRDL GMNENNIPEE 300
	AAVLDDIQL IYFVRYKHS AEETATLVMA PPLEBGLGGA MEEMQPLHED NPSREKTAEL 360
60	NVQVPEEPH LDQVRIGDTH ASEVSQKENT EKDLDFGPVT TETDPMDAID ANKPETAEE 420
	EPASVTPLEN ALLLIYSFMP YLTKSLVATL PDDVQPGPDF YGLFMKFPVI TAPLGIASFA 480
	IFLWRTLVV KDRVYQVTEQ QISEKLRTIM KENTBLVQKL SNEYQKIKES KKHVQETRRQ 540
	NMILSDEAIK YDKIKITL E KQEIILDDTAK NLRVMESEER EQNVKNQDLI SENKKSIEKL 600
	KDVISMNASE FSEVQIALNE AKLSEKVK S ECHRVQEN A RLKKKKEQLQ QEI EDWSKLH 660
65	AELSEQLKSF EKSQKDL E VA LTHKDNINA LINCITQLNL LECESESEGO NRGNDSDHL 720
	ANGEVGGDRN ERKMNQIKQM HDVSRQTAT SVVEEDLKL QLKLRSVST KCNLEDQVK 780
	LEDDRNLSQA AKAGLEDECK TLRQKVEILN ELYQKEMAL QKKLSQEYE QRERERLSA 840
	ADEKAVSAAE EVKTYKRIIE EMEDELQKTE RSFNQIATH EKKAHENWLK ARAAERAE 900
	EKREANLRIH KLLLETQKMA MLQEEFVIVK PMPGKPTQNP PPRRGPPLSQN GSPGSPFVSG 960
70	GECSFPITVE PFVRLSATL NRRDMRSEF GSVDGFLPHP RMSAEASGKP SPSPGSGFTA 1020
	TMNNSSRGS SPTRVLDEBK VNMAKGPFP FPGVPLMSTP MGGFVFPPIR YGFPPLQCGP 1080
	FGFRLPFPF GFGMRPLGL REFAPGVPPG RRDLPFLFRG FLPGHAFPR LGLSGPREYF 1140
	IPGTRLPPT HGPQEPFPF AVRDLLPSGS RDEPPASQS TSQDCSQALK QSP

SEQ ID NO:51 PAB9 DNA SEQUENCE

Nucleic Acid Accession #: NM_006457

Coding sequence: 84-1874 (underlined sequences correspond to start and stop codons)

80	1 11 21 31 41 51
	AGACTGAGGC GGAGGCAGCC CCGCGCCGCG CCGGACCCGA GCATATTTC A TTTCTGTCA 60

5 TTGGACTTTG AGCCATTAGA ACCATGAGCA ACTACAGTGT GTCAGTGGTT GGGCCAGCTC 120
 CTTGGGGTTT CCGGCTGCAG GSCGTAAGG ATTCAACAT GCCTCTGACA ATCTCTAGTC 180
 TAAAAGATGG CGGCAAGGCA GOCAGGCAA ATGTAAGAAT AGGCGATGTG GTTCTCAGCA 240
 TTGATGGAAT AAATGCACAA GGAATGACTC ATCTTGAAGC CCAGAATAAG ATTAAGGGTT 300
 GTACAGGCTC TTTGAATATG ACTCTGCAAA GAGCATCTGC TGCACCCAAG CCTGAGCCGG 360
 TTCTGTGTCA AAAGGGAGAA CCTAAAGAAG TAGTTAAACC TGTGCCCAAT ACATCTCCTG 420
 CTGTGTCCAA AGTCACTTCC ACAAACACAA TGGCCTACAA TAAGGCACCA CGGCTTTTGG 480
 GTTCTGTGTC TTCACCAAAA GTACATCCCA TCCATCACC ATCTGTCTGC TTCACCCAG 540
 10 CCGATGCGAC CACCTCATCA CATGCTTCCC CTTCACCCGT GGCTGCCGTG ACTCCTCCCC 600
 TGTTCGCTGC ATCTGGAAGC CATGCTTAATG CCAATCTTAG TGCTGACCAAG TCTCCATCTG 660
 CACTGAGCGC TGGTAAAACT GCAGTTAATG TCCCACGGCA GCCCACAGTC ACCAGCGTGT 720
 GTTCCGAGAC TTCTCAGGAG CTAGCAGAGG GACAGAGAAG AGGATCCAG GGTGACAGTA 780
 AACAGCAAAA TGGCCACCA AGAAAACACA TTGTGGAGCG CTATACAGAG TTTTATCATG 840
 15 TACCACCTCA CAGTGTATGC AGCAAGAAGA GACTGATTGA GGATACTGAA GACTGGCGTC 900
 CAAGAAGTGG ACAAACCTAG TCTCGCTCTT TCCGAATCCT TCCCCAGATC ACTGGGACTG 960
 AACATTTGAA AGAATCTGAA GCGGATAATA CAAAGAAGGC AAATAACTCT CAGGAGCCTT 1020
 CTCCGCAATT GGCTTCTCTG GTAGCTTCCA CACGGAGCAT GCGGAGAGC CTGACAGGCC 1080
 CAACCTCTGG CAGACCAAGG GTTACCAAGC TCACAACCTG AGCTGCCCTC AAGCCTGTAG 1140
 20 GATCCACTGG CGTCATCAAG TCACCAAGCT GGCACCGGCC AAACCAAGGA GTACCTTCCA 1200
 TCGGAAGTAT CTCAAAACAG GCTACTTACT CAGGATCACT GGCACCAAGC AACTCAGCTT 1260
 TGGGACAAAC CCAGCCAAAGT GACCAGGACA CTTTAGTGCA AAGAGCTGAG CACATCCAG 1320
 CAGGGAAGCG AACTCCGAGT TGCGCCAATT GTAACCAAGT CATCAGAGGA CCATTCTTAG 1380
 TGGCACTGGG GAATCTTGG CACCCAGAA GAAATCAACTG CACTCACTGC AAAAATACAA 1440
 25 TGGCCTACAT TGGATTTGTA GAGGAGAAAG GAGCCCTGTA TTGTGAGCTG TGCTATGAGA 1500
 AATCTTTTGC CCCTGAATGT GGTGATGCC AAAGGAAGAT CCTTGGAGAA GTCATCAATG 1560
 CGTTGAACCA AACTTGGCAT GTTCTCTGTT TTGTGTGTGT AGCCTGTGGA AAGCCATTC 1620
 GGAACAATGT TTTTCACTGT GAGGATGGTG AACCTACTG TGAGACTGAT TATTATGCC 1680
 TCTTTGGTAC TATATGCCAT GGATGTGAAT TTCCCATAGA AGCTGGTGAC ATGTTCTCTG 1740
 30 AAGCTCTGGG CTACACCTGG CATGACACTT GCTTTGTATG CTCAGTGTGT TGTGAAAGTT 1800
 TGGAGAGTCA GACCTTTTTC TCCAAGAAGG ACAAGCCCTT GTGTAAGAAA CATGCTCATT 1860
 CTGTGAATTT TTGAAAGTCA ACAGTTCAGG AGAAGAGAAG GAATTTGAAG AGAAAAAGGA 1920
 AAATTAATAA TACTAATTAA TTTTATGATT CAATATTAT ATGGAGTTT GAAAAATAA 1980
 AGTGGCCCTG AAGGAATAAA TTCCAGCTTT AAAAACCAAG TCTGAGGAAA TATTGTGCTT 2040
 35 CATAAAGTAA AGAGACGGTT TGGCATTAT TATTACTTTT TCCTGTATT TATGCCATA 2100
 AAATAAGCTT TATAAAACCC AATTCTCTGA TGGACTATTA AATTCACTTT AGAATAAAT 2160
 AGTGAAGAT TTATTTTAG AATAAATAAT CCAATCTGAA ATAATTATAC CTCTCTTCT 2220
 TGTTAGTAGT TTATGAGTAA ATCTGCAAAA GGCATGAAA ATGCCCTAAA TTTTATCAAT 2280
 AACAGAAATTA TTGTATTAA AAAAAACTA ATACTTATCT TTAATAAGT AAATAGGATT 2340
 40 TTAACAGAG AATTTTATCA GTAATAGGTG TCAGTTTTTA AAAAATGTCT TGTAGGCTGA 2400
 GCGCGGTGCG TCACGCTGT AATCCAGCA CTTTGGGAGG CCAAGGTGGG TGGACCACT 2460
 GAGGTACAGG GTTTGAGATG AGCCTGGCCA ACATGGTGAA ACCCCATCTC TACTAAAAAT 2520
 ACAGAAATTA GCGGAGCACT GTGGCACGCG CCTGTAATCC CAGCTACTCA AGAGGCTGAG 2580
 GCACGAGAA CACTTGAACC CCGGAGGAG AGGTTCAGT GAGCCAAGAT CGTACCACTG 2640
 45 CACTCCAGCC TGGGTGACAG AGTGAGACTC CGTCTCCAAA AAAAATCTT GCTTGTATAT 2700
 TATTTTTGGC TTACAGTGGG TCATTCTAGT AGGAAAGGAC AATAAGATT TTTATCAAAA 2760
 TGTGTATGCG CAGTAAGAGA TGTATATATC TTTTCTTATT TCTTCCAC CCAAAAATAA 2820
 GCTACCATAT AGCTTATAAG TCTCAAATTT TTGCTTTTA CTAAAATGAG ATTGTTCG 2880
 TFCATTGTGT ATGCTTCATC ACCTATATTA GGCAAATTC ATTTTTCCT TTGCGCTAAG 2940
 50 GTAAAGATTT AATTAAATAA TTTTGGCCTC TCATAGTTTT CTCTCTCTT AAAGAGAATA 3000
 AATAGAGGCG CAGTGTGGT GCGTGACGCC TGTGATCCCA GCCTTTTGGG AGGCCAAGAC 3060
 GGGCGGATCA TGAGGTCAAG AGATCAAGAT CATCTGGGCC AACATGTGTA AACCTGTCT 3120
 CTACTAAAAA TACAAAAAGT AGCTGGGCAT GGTGGGGCGT GCTGTAGTC CCATGTACTT 3180
 55 GGGAGGCTGA GGCAGGAAA TTCTTGAACC CAGGAGACGG AAGTTGCACT GAGCTGAGAT 3240
 CACACCCTG CACTCCAGCC TGGTGACAGA GCAAGACTCC GGCTCTT

SEQ ID NO:52 PAB9 Protein sequence
 Protein Accession #: NP_006448

60 1 MSNYSVSLVG PAPWGFRLQG GKDFNMPLTI SSLKDGKAA QANVRIGDVV LSIDGINAQQ 60
 61 MTHLEAONKI KGCTGSLNMT LQRASAAKPK EPVPVQKSEP KEVVKVPVIT SPAVSKVTST 120
 121 NNMAYNKAPR PFGSVSPFKV TSIPSPSSAF TPAHATSSSH ASPSPVAAVT PFLFAASGLH 180
 181 ANANLSADQS PSALSAGRTA VNVFRQPTVT SVCSETSQEL ABQQRSGSQ DSKQNGPFR 240
 241 KHVIRYTFEP YHVPHSDAS KRRLIEDTED WRPRGTGTS RSFRILAQIT GTEHLKSEA 300
 301 DNTKKANNSQ EPSQLASLV ASTREMPESL DSPTSGRPGV TSLTAAAFK PVGSGTVKS 360
 361 PSWRPFNGOV PSTGRISNSA TYSGSVAPAN SALGQTQPSD QDTLVORAEH IPAGKRTPMC 420
 421 AHCNQVTRGP FLVALGKSWH PEEFNCAECK NIMAYIGPVE ERGALYCELC YEKFPAPBCG 480
 481 RCQRILGEV INALGQTWVH SCFVCVACGK PIRNNVPHLE DGEPYCBTDY YALPGTICGH 540
 541 CEFFIEAGDM FLEALGYTHV DTCFVCSVCC ESLEGQTFPS KKDKFLCKRH AHSVNP

SEQ ID NO:53 PBH7 DNA SEQUENCE

Nucleic Acid Accession #: AA431407

Coding sequence: 1-584 (underlined sequences correspond to start and stop codons)

75 1 ATGGCCAACT GTAAAATGAC CAAAAGCATC AGGTTCCCTG CCCTGGAGCA CTGCTATACT 60
 GCGGGGAGG TCGTGTGGC CAAGATCAG GAGGAGTGA AAAGACGGAC GGGCCTTCTG 120
 80 CTCACAGAGA ACTATGGGCA GTCGGAACG GGACTAATTT GTGCCACCTA CTGGGGAATG 180

5 AAGATCAAGC CGGGTTTCAT GGGGAAGGCC ACTCCACCCT ATGACGTCCA GTTTCATATG 240
 GAGGCGCTCAG TTGAAAACCTG CATTATTGTG AGCATGAACA CCGCTGACCC TGGCAGCCAG 300
 GGCATCACAC ACAGCCTCTTT GCTACAGGTC ATTGATGACA AGGGCAGCAT CCTGCCACCT 360
 AACACAGAAG GAAACATTGG CATCAGAATC AAACCTGTCA GGCGTGTGAG CCTCTTCATG 420
 TGCTATGAGG GTGACCCAGA GAAGACAGCT AAAGTGGAAAT GTGGGGGACTT CTACACACT 480
 GGGGACAGAG GAAAGATGCA TGAAGAGGCC TACATTGTGT TCCTGGGGAG GAGTGTATGAC 540
 ATCATTAAAT CCTCTGGGTA TCGCATCGGG CCTGCAGAGG TTGAAAGCCG TTTGGTGGAG 600
 CACCCAGCGG TGGCGGAGTC AGCCGTGGTG GGCAGGCCAG ACCCGATTGG AGGGGAGGTG 660
 10 GTGAAGGCGT TTATTGTCTT GACCCACAG TTCTGTCTCC ATGACAAGGA TCAGCTGACC 720
 AAGGAAGTGC AGCAGCATGT CAAGTCAGTG ACAGCCCAT ACAAGTACCC AAGGAAGGTG 780
 GAGTTTGTCT CAGAGCTGCC AAAAACCATC ACTGGCAAGA TTGAACGGAA GGAACCTGG 840
 AAAAAGGAGA CTGGTCAGAT GTAAATCGCA GTGAAGTCAG AACGCACTGC ACACCTGAGG 900
 CAAATCCCTG GCCACTTTAG TCTCCCACT ATGGTGAGGA CGAGGGTGGG GCATTGAGAG 960
 15 TGTTGATTGG GGAAGATATC AGGAGTGCCA TGATTCCAAT GTTTTCCTTC TTTTAAATTA 1020
 AATTCAAGTTG TCTCTCTTCC TCCAAGTCTC CTGTATCTTT AGAATTTCOC AGGTGAGCAC 1080
 TCATAACGCA AGTAATAAAA TACTGATATC AACA

SEQ ID NO:54 PBH7 Protein sequence

Protein Accession #: FGENESH predicted

20 1 11 21 31 41 51
 MANCKMTKSI RPPALEHCYT GGEVVLFDQ EEMKRRTGLL LYENYQSET GLICATYWM 60
 25 KIKPFGFMKA TTPYDVQFIM EASVENCIIV SMNTADPGSQ GITHSLLLQV IDDKGSILFP 120
 NTEGNIGIRI KFPVPVSLFM CYEGDPEKTA KVECGDFYNT GDRKMDERB YICFLGRSD 180
 IINASGYRIG PAEVESALVE HPAVAESAVV GSPDPIRGEV VKAFIVLTPO FLSDKDKQLT 240
 KELQGVKSV TAPYKYPRKV EFVSELPKTI TGKIERKELR KKBTGQM

SEQ ID NO:55 PBJ5 DNA SEQUENCE

Nucleic Acid Accession #: AF388200

Coding sequence: 33-137 (underlined sequences correspond to start and stop codons)

35 1 11 21 31 41 51
 GAGAGAGGGA GGCAGAAAGG GAAGTCAGAG CGATGTGCTG TGAAATCTAC TACCGTTTGC 60
 TGTTTGTGAA AATGGAGAAA AAGAGTGAGG AACTGAGAAA CATGGATGCG CTGCGGAACG 120
 TGGAAAGGG TCACTGAAAT GGCACGACAT GAACCTAAGG AGGCTATTTA TGACCATGTC 180
 ATTTGCAACA TGAAGAAAGC TTATCTGGAG TGAAAGTAAA TGAGACCAAC AGAGATAAGA 240
 40 GACCCGGAGA AATCCTGGTT ACACCTGCTG AATCCTGTCA GTCTATATCT GGAGTCTCTG 300
 TAATACAAA TAATAGTAAT AATCCCTCTG TTTCTTATGT TTATGCCAAC TTCAACAAAA 360
 AGAACTTGA CTAAAGACA ATATAAGAAC TTAATGTGTA ATTAAGAAAG AACTCTCCAC 420
 CACGGGGAAAT GTGAAAGGTA TATGAGTCCG TTTTCACGAT GCGATGTCAAT GTCTTTTAAA 480
 TAAGCCATAC TTATATTTCA ATAAAAAGAG AATAAGCAGG A

SEQ ID NO:56 PBJ5 Protein sequence

Protein Accession #: AAK83352

50 1 11 21 31 41 51
 MCCEIYRL VLMKKSE LRNDGLGNV EKGH

SEQ ID NO:57 PBJ7 DNA SEQUENCE

Nucleic Acid Accession #: AA876910

Coding sequence: 1-2064 (underlined sequences correspond to start and stop codons)

55 1 11 21 31 41 51
 ATGGACAGTT GCCTGCAACA TATGAGAGAC CTACTTTACC TCCTTCAGGA GCTCAGGTGT 60
 60 TTAATCCAG CTACACTACT CCCTGATCCA GACTCCACTA CTCTGTTC TAAGTGTTCAG 120
 GATCTGTGG AACTACCAA AACTGGCCAA CCTGATCTTC AAGATGTGCC CTTAGAAAAG 180
 GCAGATGCCA CTGTGTTTAC AGATGGTAGC AGCTTCCTCG AGCAGGGAGA ACGAAAAGCT 240
 GTTCTTTTC CACAGCCAGA TCTGCTGAC AATCCACAT ACTCAACAGA AGAAGAAAAA 300
 CTGGCTTCAG ATCTGGAGC AATAAAAAAT CAGGAAGGAC GTGTATTCGC AAACACTACT 360
 65 TGGAGGGCG GTACCTCCAA GGAAGTCTCC TTTGCAGTTG ATTTATGTGT ACTGTTCCCA 420
 GAGCCAGCTC GTACCCATGA AGAGCAACAT AATTGCGCG TCATAGGAGC AGGAAGTGTG 480
 GACCTTCAG CAGGATTTGG ACACCTCTGG AGCCAAACTG GATGTGGAAG CTCCAAAGGT 540
 CAGAAAAAG GGCCTCAAAA TGTGTACTTT TACCTCTGTC CTGGAATACA CCCTGACGCT 600
 AGCTGTAGAG ATACTTACCA GTTTTCTGCT CCTGATTGGA CATGTGTAAC TTTAGCCACC 660
 70 TACTCTGGGG GATCAACTAG ATCTTCAACT CTCTCCATAA GTGCTGTTC TCATCTCAA 720
 TTATGTACTA GAAAAATGT TAATCTCTT ACTATAACTG TCCATGAACC TAATGCAGCT 780
 CAATGCTATT ATGGCATGTC ATGGGGATTA AGACTTTATA TCCAGGATT TGATGTTGGG 840
 ACTATGTTCA CCATCCAAA GAAATCTTG GTCTCATGGA GCTCCCCCAA GCCAATCGGG 900
 CCTTTAAGTG ATACTAGTGA CCTATATTG CAGAAACACC CTGACAAAGT TGATTTAACT 960
 75 GTTCTCTGCT CATCTCTAGT TCCTAGACCC CAGCTACAAC AACACATCT TCAACCCAGC 1020
 CTAATGCTTA TACTAGGTGG AGTACCCAT CTCTTAACC TCACCCAGCC TAACTAGCC 1080
 CAAGATTGTT GGCTATGTT AAAAGCAAAA CCCCCTTATT ATGTAGGATT AGGAGTAGAA 1140
 GCCACACTTA AACGTGGCCC TCTATCTGT CATACAGGAC CCGTGCTCT CCAATAGGA 1200
 GATGTGTCTG GAAATGCTG CTGTCTGATT AGTACGGGT ATAACCTATC TACTCTCTCT 1260
 80 TTTAGGCTTA CTGTGTAATCA GTCCCTGCTT ACTTCCATAA GCACCTCAGT CTCTTACCAA 1320
 GCACCCACA ATACCTGTTT GGCTGCACC TCAGGTCTCA CTGCTGCAT TAATGGAAT 1380

	GAACACGGAC	CTCTCCTGTG	CGTGTAGTT	CATGTACTTC	CCCAGGTATA	TGTGTACAGT	1440
	GGACACGAAG	GACGACAACT	CATCGCTCCC	CCTGAGTTAC	ATCCACAGTT	GCACCAAGCT	1500
	GTCCACACTC	TGGTTCOOCF	ATTGGCTGGT	CTTAGCATAG	CTGGATCAGC	AGCCATTGGT	1560
5	ACGGCTGCC	TGGTTCACGG	AGAAACTGGA	CTAATATCCC	TGTCTCAACA	GOTGGATGCT	1620
	GATTTTAGTA	ACCTCCAGTC	TGCCATAGAT	ATACTACATT	CCCAGGTAGA	GTCTCTGGCT	1680
	GAACTAGTTC	TTCAAAACTG	CCGATGCTTA	GATCTGCTAT	TCCTCTCTCA	AGGAGGTTTA	1740
	TGTGACGCTC	TAGGAGAAAG	TTGTTGCTTC	TATGCCAATC	AATCTGGAGT	CATAAAAGGT	1800
	ACAATAAAAA	AAGTTCGAGA	AAATCTAGAT	AGGCACCAAC	AAGAACGAGA	AAATAACATC	1860
10	CCCTGGTATC	AAAGCATGTT	TAATCGGAAC	CCATGGCTAA	CTACTTTAAT	CACCTGGGTTA	1920
	GCTGGACCTC	TCCTCATCTC	ACTATTAAAT	TTAATTTTTC	GGCCTTGAT	ATTAAATTCG	1980
	TTTCTTAATT	TTATAAAACA	ACGCATAGCT	TCTGTCAAA	TTACGTATCT	TAAAGCTCAA	2040
	TATGACACCC	TTGTTAATAA	CTGA				

15 SEQ ID NO:58 PB17 Protein sequence
Protein Accession #: FGENSEH predicted

	1	11	21	31	41	51	
20	MDSCLOHMRD	LLYLLQELRC	LNPATLLPDP	DSTTFVHDQ	DLLETKTKGQ	PDLQDVPLEK	60
	ADATVTFDGS	SFLBQGERKA	VSPFPQDLPD	NPTYSTEREK	LASDVGANKN	QEGRVFANTT	120
	WRAGTSKEVS	FAVDLCVLPF	EPARTHEEQH	NLPVIGAGSV	DLAAGPGRSG	SQTGCGSSKG	180
	AEKGLQNVDF	YLCFQNHEDA	SCRDTYQFFC	FDWTCVFLAT	YSGGSTRSST	LSLSRVPHFK	240
	LCTRKNCNPL	TIIVHDFNAA	QWYVGMWSGL	RLYIPGFDVG	TMPTIQKKIL	VSWSSEPKPIG	300
25	FLTDLGDPPI	QKHPDQVLDL	VPLPFLVPRP	QLQQHQLQPS	LSILGGVHE	LLNLTPKPLA	360
	QDCMLCLKAK	PYYVGLGVE	ATLKRGLPSC	HTFRALITIG	DVSGNASCLI	STGYNLSASP	420
	FQATCQNSLL	TSISTSVSYQ	APNNITWLACT	SGLTRCINGT	EPGFLLCVLV	HVLFPQVIVYS	480
	GPBGRQLIAP	PELEPRLHQA	VPLLVPLLAG	LSIAGSAAIG	TAALVQGETG	LISLSQCVDA	540
	DFSNLQSAID	ILHSQVESLA	BVVLQNCRLC	DLLEPLSQGGL	CAALGESCCF	YANQSGVIRG	600
30	TVKVERENLD	RHQQRERNMI	PWYQSMFNWN	PWLFTLITGL	AGPLLLILLS	LIFGPCILNS	660
	FLNFIKORIA	SVKLTYLKTQ	YDTLVNN				

SEQ ID NO:59 PCQ1 DNA SEQUENCE

35 Nucleic Acid Accession #: NM_019005
Coding sequence: 182-1885 (underlined sequences correspond to start and stop codons)

	1	11	21	31	41	51	
40	TGATGGTGGG	AAATTCCTGA	AACCGCTCTC	GTAATTGGCC	ACGTGCTGTT	GCAAAATATTC	60
	TGGTGAATGA	ACACAGAATC	AGCATGGCTT	TCCTTTGCTG	AGAAATCACT	GATGGGAAGT	120
	GAGACTTGT	AAACTTGA	GTGAATGGAC	CTGAGTGGAC	CCTTTGATCA	CATCAGTAAA	180
	CATGAGCGGT	ACCAAACTCG	ATATTTTATG	GGCACCACAC	CATGTTGATA	GATTGTGTGT	240
	GTGTACTCA	GAATCAAGTC	TTTATCATGT	GGAACTCACT	GTGAATTCAG	AACTCAAAGC	300
	TGGATCTTTA	CGTTTATCTG	AAAGACTCTGC	AGCTACATTA	CTGTCAATAA	ATTTCAGATAC	360
45	ACCTATATG	AAATGTGTTG	CCTGGTATCT	TAATATATGAT	CCTGAATGTC	TGCTGGCAGT	420
	TGGACAGACA	AATGGTCCAG	TTGTACTTAC	AAGCCTTGCT	CAAGATCATA	ACTCAAAGTT	480
	CAAGATTTG	ATAGGAAAAG	AGTTTGTTC	AAAACATGCA	CGCAATGTGA	ATACCCCTGC	540
	CTGGAATCA	CTGGAATGTA	ACTGGCTAGC	TGCTGGTTTA	GATAAGCACA	GAGCTGACTT	600
	TTCACTGCTA	ATATGGGATA	TCTGCAGCAA	ATATACTCCT	GATATAGTTC	CCATGGAAAA	660
50	AGTGAAACTT	TCAGCAGGTG	AAACTGAAAC	AACATTATTA	GTAAACAAAC	CACCTTTATGA	720
	GTTAGAGCTG	TAGGATGCTT	GTCTGTCTCT	TTGTTGGCTT	CCACGAGACC	AGAAACTTCT	780
	CCTTGTCTGT	ATGCATGCTA	ACCTAGCTAT	ATTGTATCTT	CGGAATACAA	GCCAAAGGAT	840
	GTTCGTAAAT	ACAAAAGCTG	TTCAAGGTGT	GACGGTAGAC	CCATATTTC	ACGATCGTGT	900
	TGCTTCTTTC	TATGAAGGTC	AGGTTGCAAT	ATGGGATCTT	AGAAAATTTC	AGAAAGCCAGT	960
55	TTTGACATTC	ACTGAGCAAC	CAAAACCCCT	AACAAAAGTA	GCATGGTGTG	CCACTAGGAC	1020
	TGGTCTACTT	GCCACTTTAA	CAAGGGATAG	TAATATTATT	AGATTGTATG	ATATGCAGCA	1080
	TACACCCACT	CCCATTTGGG	ATGAAACTGA	ACCCACAATA	ATTGAAAGAA	GTGTGCAACC	1140
	TTGTGACAA	TACATTGCTT	CCTTTGCGTG	GCATCCAACA	AGTCAAAATC	GAATGATAGT	1200
	TGTAACTCCC	AACCGAACAA	TGTCAAGACT	CACGTGTTTT	GAAAGGATAT	CTCTTGCTCTG	1260
60	GAGCCCAATT	ACATCTTTAA	TGTGGGCTTG	TGGTCGTAT	TTATATGANT	GTACGGGAAG	1320
	AGAAAATGAT	AATTCTTTAG	AAAAAGATAT	AGCAACGAAG	ATGCGTCTTC	GGGCTTTATC	1380
	AAGGTATGGA	CTTGATACAG	AGCAGGTGTG	GAGGAACCA	ATTTTAGCTG	GAAATGAAGA	1440
	TCCACAGCTC	AAGTCACTCT	GGTATACTCT	GCACCTTTATG	AAGCAATACA	CAGAAGATAT	1500
	GGATCAGAAA	TCTCCAGGCA	ACAAAGGATC	ATTGTTTAT	CGAGGAATTA	AATCAATTGT	1560
65	AAAGTCATCG	TTGGGAATGG	TGGAAAGCAG	CAGACATAAT	TGGAGTGGGT	TGGATAAGCA	1620
	AAGTGATATT	CAAAACTTAA	ATGAAGAGAG	AATCTTAGCT	TTACAGCTTT	GTGGGTGGAT	1680
	AAAGAAAGCA	ACGGATGTAG	ACGTGGGGCC	ATTTTGAAC	TCCTTTGTAC	AAGAAGGGGA	1740
	ATGGGAAGCA	GCTGCTGCTG	TGGCATTTGT	CAACTTGGAT	ATTCGCCGAG	CAATCCAAAT	1800
	CCTGAATGAA	GGGCACTCTT	CTGAAAAAGG	CAGGAGATCT	GAATCTCAAT	GTGGTAGCAA	1860
70	TGGCTTTATC	GGGTTATACG	GATGAGAGA	ACTCCCTTTG	GAGAGAAATG	TGTAGCACAC	1920
	TGGATATACA	GCTAAATAAC	CCGTATTTGT	GTGTCAATGT	TGCATTCTG	ACAAGTGAAA	1980
	CAGGATCTTA	CGATGGAGTT	TTGTATGAAA	ACAAAGTTGC	AGTACGTGAC	AGAGTGGCAT	2040
	TTGCTTGTA	ATTCTCTTAGT	GATACTCAGA	TACATCGAAA	AGTTGACCAA	TGAAATGAAA	2100
	GAGGCTGGAA	ATTTGGAGGG	AAATTTGCTT	ACAGGCCTTA	CTAAAGATGG	AGTGGACTTA	2160
	ATGGAGAGTT	ATGTTGATAG	AACCTGGAGAT	GTTCAAACAG	CAAGTTACTG	TATGTTACAG	2220
75	GGTTCACCTT	TAGATGTTCT	TAAAGATGAA	AGGGTTCACT	ACTGGATTGA	GAATATATAGA	2280
	AAATTTATAG	ATGCTCGGAG	GTTTTGGCAT	AAACGAGCTG	AAATTTGATAT	TCACAGGAGT	2340
	AAGTTGGATC	CCAGTTCCAA	GCCTTTAGCA	CAAGTTTTTG	TGAGTTGCAA	TTTCTGTGGC	2400
	AAGTCAATCT	CCTACAGCTG	TTCAAGCTGT	CCTCATCAGG	CGACAGGTTT	TAGTCAGTAT	2460
80	GGTGTGAGTG	GCTCAACCA	GAATCTTAA	GTCAAAAGTT	GTCTGGCTG	TGCAAAACCA	2520
	CTTCTCGAT	GTGGCGTTTG	TCTCATTAAT	ATGGGAACAC	CAGTTTCTAG	CTGTCTGGA	2580

5 GGAACCAAT CAGATGAAA AGTGGACTTG AGCAAGGACA AAAAATTAGC CCAATTTAAC 2640
 AACTGGTTTA CATGGTGTCA TAATTCGAGG CACGGTGGAC ATGCTGGACA TATGCTTAGT 2700
 TGGTTCAGGG ACCATGCAGA GTGCCCTGTG TCTGCATGCA CGTGTAATG TATGCAGTTG 2760
 GATACAACGG GGAATCTGGT ACCTGCAGAG ACTGTCCAGC CATAAAATGT TACCACCTTA 2820
 AGAGAACCT TCAAGTGTGG AGCTTTCTAG TAGGTGTCTT TCATAGCTCA GAAACATACC 2880
 TCAGAACAG CCAATTCATGA CTTACCTGTA ATGGGAAAT AAATCATTTCT ATCAGAAAAA 2940
 AAAAAAAAAA AAAAAAAAAA

10 SEQ ID NO:60 PCQ1 Protein sequence
 Protein Accession #: NP_061878

15 1 11 21 31 41 51
 MSQTKFDILW APHHVDRFV CSELSLYHV ESTVNSELKA GSLRLSEDSA ATLLSINSDT 60
 PYMKCVAWYL NYDFECLLAV QANGRVVLT SLGQDHSKF KDLIGKEFVP KHARQCNTLA 120
 WNPLDSNWLA AGLDKHRADF SVLIWDICSK YTPDIVPMEX VKLSAGETET TLLVTKPLYE 180
 LGQNDACLSL CMLPRDQKLL LAGMHRNLAI FDLRNTSQKM PVNTKAVQGV TVDPYPHDRV 240
 ASFYEGQVAI WDLRKFKEFV LTLTEQPKPL TKVACPTPT LLLATLRDS NIIRLYDMQH 300
 TPTPIGDETE PTLIERSVQP CDNYIASPAW HPTSONRMTV VTPNRTMSDF TVFERISLAW 360
 SPITSLMWAC GRILYECTEE ENDSLEKDI ATKMLRLALS RYGLDTEQW RHILAGNED 420
 PQLKSLWYTL HPMKQYTEDM DQKSPGNKGS LVIYAGIKSIV KSSLQMVES RHNSGLDKQ 480
 SDIQNLNER ILALQLCGWI KKGTDVDVGP FLNSLVQEGE WERAAVALF NLDIRRAIQI 540
 LNEGASSEKG RRSESCQGSN GFILGYG

SEQ ID NO:61 PDG3 DNA SEQUENCE

25 Nucleic Acid Accession #: U42359
 Coding sequence: 563-775 (underlined sequences correspond to start and stop codons)

30 1 11 21 31 41 51
 TTGTACATCT TAACAACCTT AAGCTGTACA AATAGANCAA TAATATCTAA ATGGTGTGAT 60
 GATCAGCCCA CAGTACACAT CATTGATGAG AATTTCACTG GTCTCAACCT TTCTCATGCT 120
 GAGTCTTGGC TTGTGTAAT GACTTATAAA GGTCCAAGGA TTAGAGATG ATTAAGAGAT 180
 AAGCTGGCAT TCTGTAAAG CACCATCGTC TATCCCTGT CTTATCTAGA TAAAGAATGT 240
 AGTGCTAAAT CTGTGTAATA TATTGTACAA ATGGAATTC AATCTTAAGG ATTATTTTTT 300
 CCATATTGTT GTATTTCATT GTGGTGTATT GGAAAGTGAT CTGGACTTTG AGTGAGAAGA 360
 TGTGATTGG ACCATGGCAC TTAATAAATC TATAACCTCA GGCAAGTCTT TTAATCTTCT 420
 CTGAGCTCA GTTTTCTCTCA TTTTTCAAAT ATAGAGAGTA TAACATTTAT CTCATAAGAC 480
 AAGTGTAGT AAATTACTGT TTTACAAATG TAAGATAACT TTTAACTGTG AGATTCCATA 540
 TTCCAGCTTT ACATTATTAT GTTTATCTGC CACAGGGAGA AGTCCCTCAGA TAAAAATGTC 600
 TACCAAAAGC CTGACAGGTG GAGTTAATCA TTTGACAGAT GCAAAATGCTT CCACCCCAAA 660
 CAAATATACT TTCTTTAATC TCTGTGTGGG TATCACTTAG GGAAAAAAG GCAGGCAACA 720
 AAATATTTT TAATTCTATC TTAGGAAAAA TTGTAGNCAA ATCTTTTINT CCCATTAAAC 780
 AATAATGTAA GCCTTAATAT TCAAGGGGTA ATAAAAATAC AAGTCTTCC AACACGGTAA 840
 CTACTCTGAA AACTTT

50 SEQ ID NO:62 PDG3 Protein sequence
 Protein Accession #: AAB18375

55 1 11 21 31 41 51
 MGARGAPSRH RQAGRRRLRYL PTGSFFFLLL LLLLCIQLGG GQKKKENLLA EKVEQLMEWS 60
 SRSIFRMRG DKRFKFIKAP FRNYSIVMF TALQPORQCS VCRQANEYQ ILANSWRYSS 120
 APCNKLFSM VDVDEGTDVF QQLMNSAET FXHXPXKGRF KRADTFDLQR IGFAAQBLAK 180
 WIADRTDVI RVPFPNYSG TIALALLVSL VGGLLYXRN NLEPTYNKQ WAMVSLCIVP 240
 AMTSGGMNH IRGPPYAHN PHNGQVSYIH GSSQAQFVAE SHILLVNAI ITMGVLLNE 300
 AATSKGDVKG RRIICLVGLG LVVFFPSPLL SIFRSKYEGY FYSDLDFE

SEQ ID NO:63 PDG3 DNA SEQUENCE

60 Nucleic Acid Accession #: AL080235
 Coding sequence: 245-453 (underlined sequences correspond to start and stop codons)

65 1 11 21 31 41 51
 GGTCGCCCA CCGGCGGCTT CCGGCGGCCC GCGGCGGCCA GCGGCGGCGC CGCCACCGCC 60
 GGGGCGGCCA CCGGCGGCTT AGCCTACCCC GCGGCGGAGC CGCCCGGCCC GCTGTGGCTG 120
 CAGGGCGGAG CGCTGCATTT CTGCTGCCCTA GACTTCAGCC TGGAGGAGCT GCAGGCGGAG 180
 CCGGCGTGGC GGCTGAACCG TAAGCCCAT T GAGTCCACGC TGGTGGCGTG CTTCATGACC 240
 CTGCTCATCG TGGTGTGGAG CGTGGCGGCC CTCATCTGCC CGGTGCCCAT CATGCGCGGC 300
 TTCTGTCGCA ACGGCATGGA ACAGGCGCGG ACCACCGCCA GCACCAACGC AGCCACCCGC 360
 GCGCGAGTGC CCGCAGGAGC CACCGCAGCC GCGGCGGCGC CGCCCGCTGC CGCCCGCGCC 420
 GCGGCGGCTA CTTCGGGGGT GCGGACCAAG TGACCGGCTC CGCTCCTCCC TGTGTCCGTC 480
 CTGTGTCCG GCGGCGGCGT GCCTTTCCCG CCGGCGGACTC GCGCGGTGTG CTTCGTGCTG 540
 TAGTTATCGT TAGTTCTCTT TCCCGAGATG GGGCGGCGCA GAGACCCAG CGCCTTTGAA 600
 AAGCAAGGTT TGTGCTGGC TTCCAGTTCC GAAAAGCAGA TGTTTAAGCC CTTGACTTGA 660
 GGGTGGGATC GCAGCTCCGA AGACGGAGAG GAGGGAAATG GGGCCCTTTC CCTCTATTG 720
 CATCCGCCCTG CCGGACTCCT TCCCGCACCC CACGTGCCCT AGATTATCG CAGAAAAATGA 780
 CCAAATCTGT TGTATTGTT TTATATATTT AATAACTGTT TTAATGAAA GTTTTAGTAA 840
 AAAAAATACA AAACAAAAG ATTAAATGCT TATTGCTGTA GTAAGAGAG CTCTTTGTAT 900
 CTGAACATAG TTGATTTTGA AATTTGTGGT TTTTAAATTT ATTTAAATTT GGGGGGAGGG 960

CATGGGAAGG ATTTAACCAC GATATATTGT TACCGCTGAA AATGAACCTT ATGAACCTTT 1020
TCCAAGTTGA TCTATCCAGT GACGTGGCCT GGTGGCGGTT TCTTCTGTGA CTTATGTGGT 1080
TTTTTGGCTT TTAATACAGA CATTTCCTCT CAAAAAAGG

5 SEQ ID NO:64 PDQ8 Protein sequence
Protein Accession #: CAB45781

1 11 21 31 41 51
10 GRRTGRLRPA AAPSAATAA GAPALPAYP AAEPFGLWL QGEPLHPCCL DFSLEELQGE 60
FGWRLARKEI ESTLVACFET LVIVVWSVAA LIWVPIIAG FLNGMEQRR TFASTTAATP 120
AAVPAAGTTAA AAAAAAAAAA AAVTSGVATK

15 Nucleic Acid Accession #: NM_006765
Coding sequence: 149-1195 (underlined sequences correspond to start and stop codons)

20 1 11 21 31 41 51
CGGCGCGGCG CGGGTCCCT CGCAAGCCG CTGCCATCCC GGAGGSCCA GCCAGCGGCG 60
TCCCGGAGGC TGGCCGGGCA GCGGTGGTGC GCGGTAGGAG CTGGGCGGCG ACCTGACCG 120
CGCGTGGAGG AGACACTGCC CTGCCGCGAT GGGGGCGCGG GCGCTCCTT CACGCGTAG 180
GCAAGCGGGG CGCGCGTGC GTTACCTGCC CACCGGGAGC TTTCCTCTCC TTCTCTGCT 240
25 GCTGCTGCTC TGCATCCAGC TCGGGGAGG ACAGAAGAAA AAGGAGAATC TTTTAGCTGA 300
AAAAGTAGAG CAGCTGATGG AATGAGATTC CAGACGCTCA ATCTCCGAA TGAATGGTGA 360
TAAATCCGA AATTTATAA AGGCACCACC TCGAACTAT TCCATGATG TTATGTTTAC 420
TGTCTTCAG CACTAGCGGC AGTGTTCGT GTGAGGCAA GCTAATGAAG AATATCAAT 480
ACTGGCGAAC TCTTGGCGCT ATTCACTGCC TTTTGTAAAC AAGCTCTCT TCACTATGGT 540
30 GGAATATGAT GAGGGGACAG ACGTTTTTCA GCAGCTCAAC ATGAATCTCT CTCCTACATT 600
CATGATTTW CCTCAAAAG GCAGACCTAA GAGAGCTGAT ACTTTGACC TCCAAAGAAT 660
TGGATTTGCA GCTGAGCAAC TAGCAAGTG GATTGCTGAC AGAACGGATG TTCATATTCG 720
GTTTTTCAGA CCACCAACT ACTCTGTTAC CATTGCTTTG GCGCTGTAG TGTGCTTGT 780
TGGAGTTTG CTTTATGTA GAAGGAACAA CTTGAGATTC ATCTATAACA AGACTGGTGT 840
35 GGCCATGGTG TCTCTGTGA TAGTCTTTC TATGACTTCT GGCCAGATGT GGAACCATAT 900
CGGTGGACCT CCATATGCTC ATAAGAACC ACACATGGA CAGTGAGCT ACATTCATGG 960
GAGCAGCCAG GCTCAGTTTG TGCCAGAATC ACACATTAIT CTGCTACTGA ATGCGCTAT 1020
ACCATGGGG ATGGTCTTC TAAATGAAG AGCAACTTCG AAGGCGATG TTGGAAGAG 1080
ACGATTAAT TGCTAGTGG GATTGGGCTT GGTGGCTTC TTCTTCAGTT TTCTACTTTC 1140
40 AATATTTCTG TCCAGTACC ACGGCTATCC TTATAGTGAT CTGCACTTTG AGTGAGAAGA 1200
TGTGATTTGG ACCATGGAC TTAAGAACTC TATAACCTCA GCTTTTAAAT TAAATGAAGC 1260
CAAGTGGGAT TTGCATAAG TGAATGTTA CCATGAAGAT AAAGTGTTC TGACTTATA 1320
CTATTTGAA TCACTCAT TCAATGATG CAGCTAGCTT ATTCTGTGT ACTTTTTTAA 1380
45 AACTGTGGGT TTCTAGTA AATTTAATT ACAGAAATCA ATGATAGCAT TTAGTAATCT 1440
ACAAAGGAAA TATCAAGTG TTTTCAAGC CTGTTATATY CAGTGTGTC CACAGGATG 1500
CAATAAAGA CAATGAAT A

50 SEQ ID NO:66 PDM1 Protein sequence
Protein Accession #: NP_006756

1 11 21 31 41 51
55 MGARGAPSR RQAGRLRYL PTGSPFFLL LLLLCIQLG GQKKENLLA EKVEQLMEWS 60
SRSLFRMG DKRFKIKAP FRNYSIMVF TALQPORQS VCRQANEYQ ILANSWRYSS 120
APCNLFPSM VDYDEGTVF QQLAMNSAPT FXHPPKGRP KRADTFDLQ IGFAADQLAK 180
WIADRTDVI RVRFPNYSG TIALALLVSL VGLLYXRRN NLEFIYNKG NAMVSLCIVF 240
AMTSGQWNNH IRGPPYAHKN FHNGQVSYLH GSSQAQFVAE SHILVINA A ITMGMVLLNE 300
60 AATSKGDVVK RRLICLVGLG LVVFFSFLL SIPRSYEGY PYSDLDFE

65 Nucleic Acid Accession #: NM_000947
Coding sequence: 88-1617 (underlined sequences correspond to start and stop codons)

70 1 11 21 31 41 51
GGTTTCATAT GAACCTCTCC GCCACCCGGG AACAGCTGGC TGCCACCGTT TGTGTTTCC 60
GAGTTGTAT TCTTGAGGT GACCAAGATG GAGTTTCTG GAAGAAAGCG GAGGAAGCTG 120
AGGTGGCAG GTGACCAGAG GAATGCTTCC TACCTCAT TCCCTCAGTT TACTTGCAG 180
CCACCTCTG AATACATATC TTTAACAGAA TTTGAAACT TGGCTATTGA TAGAGTTAA 240
75 TTGTTAAAT CAGTTGAAA TCTTGAGTG AGCTATGTA AAGGAAGTGA ACAATACCAG 300
AGTAAGTGG AGAGTGAGCT TCGGAAGCTC AAGTTTCTC ACAGAGAGAA GCTAGAAGAT 360
GATATGAAC CACGAAGAG AGATCATATT TCTCATTTA TTTTGGGCT TGTATTATG 420
CAGTCTGAAG AACTTAGAG CTGGTTCATT CAACAAGAAA TGGATCTCT TCGATTAGA 480
TTTAGTATT TAGCCAAGGA TAAATTCAG GATTTCCTAA AGGATAGCCA ATTGAGTTT 540
GAGGCTATAA GTGATGAAGA GAAGACTCTT CGAGAACAGG AGATTGTGTC CTCATCACC 600
80 AGTTAAGTG GACTTAAGTT GGGGTCGAG TCCATTATA AGATCCCTTT TGTGATGCT 660
CTGGATTCT TCGAGGAAG GAAAGTCTAT TTGGAAGATG GCTTTGCTTA CGTACCATT 720

5 AAGGACATTG TGGCAATCAT CCTGAATGAA TTTAGAGCCA AACTGTCCAA GGCTTTGGCA 780
 TTAACAGCCA GGTCTTGGCC TGCTGTGCAG TCTGATGAAA GACTTCAGCC TCTGCTCAAT 840
 CACCTCAGTC ATTCTACAC TGGCCCAAGAT TACAGTACCC AGGGAAATGT TGGGAAGATT 900
 TCTTTAGATC AGATTGATTT GCTTCTTACC AAATCCTTCC CACCTTGCAT GCGTCAGTTA 960
 CATAAAGCCT TGGCGGAAAA TCACCATCTT CGTCATGGAG GCCGAATGCA GTATGGCCTA 1020
 TTCTCGAAGG GCATTGGTTT AACTTTGGAA CAGGCATTGC AGTTCTGGAA GCAAGAATTT 1080
 ATCAAAAGAA AGATGGATCC AGACAGTTT GATAAAGTTT ACTCTTACAA CATCCGTCAC 1140
 AGCTTTGGAA AGGAAGGCCA GAGGACAGAC TATACACCTT TCAGTTGCCT GAAGATTATT 1200
 CTGTCCAATC CACCAAGCCA AGGGGATTAT CATGGGTGCC CATTCGGTCA CAGTGATCCA 1260
 GAGCTGCTGA AGCAAAAGTT GCAGTCATAC AAGATCTCTC CTGGAGGGAT AAGCCAGATT 1320
 TTGGATTAGT TAAAGGGGAC ACATTACCAG GTAGCCTGTC AAAAATACTT TGAGATGATA 1380
 CACAATGTGG ATGATTGTGG CTTTCTTTTG AATCATCCCTA ATCAGTTCTT TGTGAGAGC 1440
 CAACGTATTG TAAATGGTGG TAAAGACATA AAGAAGGAAC CTATCCAACC AGAAACTCCT 1500
 CAAGCCAAAC CAAGTGTCCA GAAAACCAAG GATGCATCAT CTGCTCTGGC CTCCTTAAAT 1560
 TCCTCTCTGG AAATGGATAT GGAAGGACTA GAAGATTACT TTAGTGAAGA TTCCTAGGCA 1620
 GTTTTATAAC CCTTTTTCCT CAATAGCCTG TTTCTGTGTT TTAAGATTTT GCCTTTGTTG 1680
 TTGAAAAGAG GTTTCACCTG CACCAAGGCT TAGTGCAGTG ACACAATTAC AGCTGATTGC 1740
 AGCCTTGAGC TTCCAGCTC AAGTGTCTCT OCTACCTCAG CCTCCAAGT AGTTAGGACA 1800
 CACAGTGTGG CACCTCATAT CCAGATAATT TTTTCAATT TTTTGTGTA GAGGTGGGGG 1860
 GTCTCCCTAT GTTGCCGAGG CAGATCTCAG ACTCCTGGGC TCAAGCGATC CTCACACCTC 1920
 AGCCTCCAG AGTCTGCGGA TTACAGTTGT GAGCCACTGT GCCTGGCCTT TTTTTTTTTT 1980
 TAACCTTTTC GTTFAACTTC TCTCTTCACT GCATCCCAAT CCATCTACAG GCATGCACAC 2040
 TTATTAGGAA AGGAGGTTTG AGGTAACAAC AGAGACTTTC ACTATATTTT GCTTTGACAG 2100
 AAGGAAGAG GAGGAGTTTC TATTAATAAT TGTCACTTGA GTGATGTCTT TTAAGTCCCA 2160
 TTTTAGGAGA TAAAAACACC TTTGGGCACT GGTAAAGTC CCCAGAAAC TACAATAAAG 2220
 AACAACTTTT GTTTTAACTC TTAATCACTT TGTAAATTTG ACTCAATCCT TTTCTGGACC 2280
 ATTTTGTGTA ATAAATATCA AAGTGT

30 SEQ ID NO:68 PDM2 Protein sequence
 Protein Accession #: NP_000938

1 11 21 31 41 51
 35 MEFSGRKRRK LRLAGDQRNA SYPHCLQFYL QPPSENISLT EFENLAIDRV KLESVENLG 60
 VSYVKGTBEQY QSKLESELK LKPSYREKLE DEYEPRRRDH ISHFILRLAY CQSEELRRWF 120
 IQQMDLLRF RFSILPKDKI QDPLKDSQLQ FEASIDEERT LREQEIVASS PSLSGKLKGF 180
 ESITKIFPFD ALDLFRGRKV YLEDGFAYVP LEDIVAILIN EPRKLSKAL ALTARSLPAV 240
 QSDERLQPLL NHELSHSYTG DYSTQGNVGR ISLDQIDLLS TKSFPPCMRQ LKALRENEH 300
 40 LRHGGRMQYQ LPLKIGLGLL DQALQFWKQR FIKGKMDPKR FDKGYSYNIR HSPKBEGRKT 360
 DYTTPFSLCKI ILSNPPSQGD YHGCPFRHSD PELLKQKLQS YKISPGGISQ ILDLVKGTHY 420
 QVACQKYFEM LHNVDGCFPS LNHFNQPFCE SQRILNGGKD IKKEPIQPET PQPKPSVQRT 480
 KDASSALASL NSSLEHMEG LEDYFSEDS

45 SEQ ID NO:69 PDM3 DNA SEQUENCE
 Nucleic Acid Accession #: NM_024840
 Coding sequence: 108-491 (underlined sequences correspond to start and stop codons)

50 1 11 21 31 41 51
 AATTCAATCA GGAGAGAGT CATATATATG CAGTGATTGT GGAAAAGGCT TCATCAAGAA 60
 GTCTCGGCTC ATTAAATCAT AGAGAGTTCA TACAGGAGAG AAACCACATG GATGCAAGCT 120
 GTGTGGGAAG GCCTCTCCCA AAAGGTCCAG GCTCACTGAA CACCAGAGAA CTCATACAGG 180
 AGAGAAGCCC TATGAATGCA CTGAATGTGA CAAAGCAATC CGCTGGAAAT CACAGCTCAA 240
 55 TGCACATCAG AAAGCTCACA CAGGAGAGAA GTCATATATA TGCCGTGATT GTGGAAGAG 300
 CTTTCATCAG AAGGAAATC TCATTGTACA TCAGOGAATT CACTCTGGAG AAAAACCCCTA 360
 TATATGCAAT GAATGTGGAA AAGGCTTCAT CCAAAAGGCG AACCTCCTTA TTCATCGAG 420
 TACTCACTCT GGAGAGAAAC CCTATGAATG CAATGATATG GGGAAAGGCT TCAGCCAGAA 480
 60 GACATGTTTA ATATCCATC AGAGATTTC CACAGGAAAG ACACCCCTTG TATGTACTGA 540
 GTGTGGAAAA TCCTGCTCAC ACAAGTCAGG TCTCATTAAC CACCAGAGAA TTACACACAG 600
 AGAGAAACCC TATACATGCA GTGACTGTGG GAAAGCTTTC AGAGATAAAT CATGCTCTAA 660
 CAGACATCGG AGAATCATATA CAGGGGAGAG ACCGTATGGA TCCTCTGATT GTGGGAAAGC 720
 TTTCTCCAC TTGTCTATGC TTGTTTATCA TAAGGGGAATG CTGCATGCAA GAGAGAAATG 780
 TGTAGGTTCA GTCAAAATGG AAAATCCTTG CTCAGAGAGT CATAGCTTAT CACATACAG 840
 65 TGATCTCATA CAGGATAAAG ACTCTGTTAA CATGGTGACT CTGCAGATGC CTCTCTGTGC 900
 AGCTCAGACC TCATTAACTA ACAGTGGCTT CCAAGCAGAG AGCAAGTAG CCATTGTGAG 960
 CCAGCTGTTT GCCAGAAAGT CAGTCTCAGC AGATAGTAGA ATTTGCACAG AATAAAACCC 1020
 ATATGAATGC AGTGAATGTG GTAGTGCTTT CAGTGATCAA TTACATCATA TGTCACAAAA 1080
 AACACAGAGG AACAACTGCA TATATTCAAG GTGGAAAGCC CTTGAATAAA ACCTTATGGC 1140
 70 TAATAAGACT ATACTCAGAG AAAAATAGTA TGAAGTGGAG ACTGGGAAAT TCTTTTATGG 1200
 GAAGATAGAT CTCTCATCA CTGACCATAG ATCACAATCT CAGTGAGCTT ATAGTTGGTA 1260
 GAAATATAAT GATCATGGAA AAGTCTTGTG TCAGAAACAG TACGCCAGTA GGTATCAGGG 1320
 GGTTTACACA GGAGAGAAAC TTTTGAAGA CCTTTGAAGG CTATGAATGT GGCAGGGTTG 1380
 CTAGTGGTAC ATCTCGCTTT ATCCTCAGAG GGAATCATAT AGAAATATAA CTATGAAAT 1440
 75 GTAATAGAAA CATCTCATC AAAATATGAA AGAACACAGG AAGCAATATA GCCCTGTGAA 1500
 AAGGAGTATT TATGAGATT CGATCAGAAA TCTAACATCA TTATATGGCA GATAATATA 1560
 AGGATGTGTA TTTTAGGACA ATATACCTTG AATCACTAGT TGATATGTC AATGACTAAT 1620
 AAAAGGGGTT GTCAAGTTTA CACATCATTT GTTAAATTTA TAGCACATG TACCTCTTCC 1680
 CCTTTTGTG ATAGAGATCT TCTATTCCCA ACCAAGATCA TTATATGATT AGCTCTTGTG 1740
 80 TTTCTTTGAT TCCAAATTTT TTTACTTGTG ATTTTCAGACT ACTGAAGCTC TTCAAAAGGA 1800

AAAATGTAAT TAATTTAATA ATGTAACACA ACAAGTTTGG ATGTGTTTAA CTTTATAAAT 1860
AATCACCCCA GAGGAATGAA GTTCAAAAC TGTGAATAAC C

5 **SEQ ID NO:70 PDM3 Protein sequence:**
Protein Accession #: NP_079116

1 11 21 31 41 51
10 MDAACVGRPS PKGPGSLNTR ELIQERSPMN ALAVTKHSAG NHSSMHIRKL TQERSHIYAV 60
IVERKASFRRE ISLYISEFIL EKNPIYAMNV ERASSKRAT S LPIDVLTLEK NPMNAMNVGK 120
ASARRHV

15 **SEQ ID NO:71 PDM3 DNA SEQUENCE**
Nucleic Acid Accession #: NM_018455
Coding sequence: 341-855 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
20 AATTTCGGCA CGGGGGGGGAG GCACAGTGTAG TCCACTGGGG CACGGCAGCG TCTAAGCCAC 60
AAGCCGACTG ACATAAGCCA GGTCCCTAACG GAGCCTATGT GTAACTCCAC TACTGGTGCA 120
AGGTTCACCA CTCTTAAGAA GAGCGGCGTG GGGGGCTGGG CGACCTTCGC TTCAGTCGCT 180
CCCCCGTGCA GTCCCTCTGTG CCCAAGACAC AGCCTGATGC TTGTGCTCCG GTGGGCGGAC 240
TTGGAGGCGG CGGGAAGTGC AATTGGTGGC TTTGAAGGGC GCGGAGCGGG AACAGCTCTT 300
25 GAGGAGTGAG ACTGCAGGAG ATGTGGGCGG TGCCAAAGAG ATGGATGAGA CTGTTGCTGA 360
GTTTCATCAAG AGGACCATCT TGAAAAATCC CATGAATGAA CTCGACACAA TCCTGAAGGC 420
CTGGGATTTT TTGTCTGAAA ATCAACTGCA GACTGTAAAT TTCCGACAGA GAAAGGAATC 480
TGTAGTTTCAG CACTTGATCC ATCTGTGTGA GGAAAAGCGT GCAAGTATCA GTGATGCTGC 540
30 CCTGTAGAC ATCATTATA TGCAATTICA TCAGCACCAG AAAGTTTGGG ATGTTTTC 600
GATGAGTAAA GGACAGGTG AAGATGTTGA CCTTTTGTAT ATGAACAAT TTAATAATTC 660
GTTCAAGAAA ATTCTTCAGA GAGCATTAAG AAATGTGACA GTGAGCTTCA GAGAAACTGA 720
GGAGAATGCA GTCTGGATTG GAATTGCTTG GGGAAACACG TACACAAAGC CAAACCACTA 780
CAAACTTACC TAGCTGGTGT ACTACTCCCA GACTCCGTAC GCCTTCACGT CCTCCTCCAT 840
35 CCTGAGGCGC AATACACCGC TTCTGGGTCA GGAATTAGAA GCTACTGGGA AAATCTACCT 900
CCGACAAGAG GAGATCATTT TAGATATTAC CGAAATGAAG AAGCTGTGCA ATTAGTGAAC 960
ATGAAGGAA AATAAAATTT CCTCACAGTC AAAAAAAAAA AAAAA

40 **SEQ ID NO:72 PDM8 Protein sequence:**
Protein Accession #: NP_060925

1 11 21 31 41 51
40 MDETVAEFIK RTILKIFMNE LTTILKAWDF LSENQLQTVN FRQKESVVQ HLHLCEEKR 60
ASISDAALLD ILYMQFHQHQ KVWDVFMQSK GPGEVDVDFD MKQFKNSFKK ILQRLKNVT 120
45 VSPRETEBNA WIRLIANGTQ YTKFNQYKPT YVVYYSQTFY APTSSSLMR NTPLLGQELE 180
ATGKIYLRQE EILLDITENK KACN

50 **SEQ ID NO:73 PDM9 DNA SEQUENCE**
Nucleic Acid Accession #: NM_016192
Coding sequence: 1-1125 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
55 ATGCTGCTGT GGGAGTCCCC GCGGCAGTGC AGCAGCTGGA CACTTTGCCA GGGCTTTTGC 60
TGGCTGCTGC TGCTGCCCCG CATGCTACTC ATCGTAGCCC GCGCGGTGAA GCTCGCTGCT 120
TTCCTACCTT CCTTAAGTGA CTGCCAAACG CCCACGGCTT GGAATTCGTC TGGTTATGAT 180
GACAGAGAAA ATGATCTCTT CCTCTGTGAC ACCAACACCT GTAAATTGTA TGGGGAATGT 240
TTAAGAATFG GAGACACTGT GACTTGCGTC TGTCAATTCA AGTCAACAA TGAATATGTG 300
60 CCTGTGTGTG GCTCCAATGG GGAGAGCTAC CAGAATGAGT GTTACCTGGG ACAGGCTGCA 360
TGCAAAACAG AGAGTGAGAT ACTTGTGGTG TCAGAAGGAT CATGTGCCAC AGATGCAGGA 420
TCAGGATCTG GAGATGGAGT CCATGAAGGC TCTGGAGAAA CTAGTCAAAA GGAGACATCC 480
ACCTGTGATA TTTGCCAGTT TGTGTCAGAA TGTGACGAAG ATGCCGAGGA TGTCTGGTGT 540
GTGTGTATAA TTGACTGTTT TCAAAACCAAC TTCATCCCC TCTGCGCTTC TGATGGGAAA 600
TCTTATGATA ATGCATGCCA AATCAAAGAA GCATCGTGTG AGAAACAGGA GAAATTTGAA 660
65 GTCATGTCTT TGGGTGATG TCAGATAAC ACAACTACAA CTACTAAGTC TGAAGATGGG 720
CATATGCAA GAACAGATTA TGCAGAGAA GCTAACAAAT TAGAAGAAAG TGCCAGAGAA 780
CACCACATAC CTGTTCGGGA ACATTACAAT GGCTTCTGCA TGCAATGGGA GTGTGAGCAT 840
TCTATCAATA TGCAGGAGCC ATCTTGCCAG TGTGATGCTG GTTATAGTGG ACAACACTGT 900
70 GAAAAAAGG ACTACAGTGT TCTATACGTT GTTCCCGGTC CTGTACGATT TCAGTATGTC 960
TTAATGCGAG CTGTGATTGG AACAAATCAG ATTGCTGTCA TCTGTGTGGT GGTCTCTGTC 1020
ATCACAGGA AATGCCCCAG AAGCAACAGA ATTCACAGAC AGAAGCAAAA TACAGGCGAC 1080
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SEQ ID NO:74 PDM9 Protein sequence:
Protein Accession #: NP_057276

5 1 11 21 31 41 51
1 MVLWESPRQC SSWTLCEGFC WLLLLFVMLL IVARFVKLAA FPTSLSDCQT PTGWNCSGYD 60
61 DRENDFLCD TWTKCFDGEK LRIGDTVTCV CQFKCNNDYV FVCGSNESY QNECYLRQAA 120
121 CKQSQEILVV SEGSCATDAG SGSODGVHEG SGETSQKETS TCDICQFGAE CDEDAEDVWC 180
181 VCNIDCSQYN FNFICASDGK SYDNACQIKE ASCQKQEKIE VMSLGRQDIN TTTTTSKSDG 240
241 HYARTDYAEN ANKLEESARE HHIPCFEYHN GPCMHGKCEH SINMQEPCSR CDAGYTGQHC 300
301 EKKDYSVLVY VPGFVRPQYV LIAAVIGTIQ LAVICVVVLC ITRKCFRNR IHRQKQNTGH 360
361 YSSDNTTRAS TRLI

SEQ ID NO:75 PDI1 DNA SEQUENCE

15 Nucleic Acid Accession #: NM_014324
Coding sequence: 89-1237 (underlined sequences correspond to start and stop codons)

20 1 11 21 31 41 51
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CTCGTAGTGT CTGGAACCTGA AGCAGCGCGG GAGCGCGCGT GCTGCGGCGT CTGTGCAAGC 300
GGTGGGATGT GCTGCTGGAG CCTTCCGCC GCGGTGTCAT GGAGAAACTC CAGCTGGGCC 360
25 CAGAGATCTT GCAGCGGGAA AATCCAAGGC TTATTTATGC CAGGCTGAGT GGATTTGGCC 420
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30 CACACGCACT GACAAGGGTC AGGTCAATGA TGCAAAATAT GTGGAAGGAA CAGCATATTT 660
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CATGTTGGAT GGTGGAGCAC CTTTCTATAC GACTTACAGG ACAGCAGATG GGGAAATTCAT 780
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GTCTGATGAA CTTCGCCAATC AGATGAGCAC GGATGATTGG CCAGAAATGA AGAAGAAAGTT 900
35 TGCAGATGTA TTTGCAAGA AGACGAAGGC AGAGTGGTGT CAAATCTTTG ACGGCACAGA 960
TGCTGTGTGT ACTCCGGTTC TGACTTTTGA GGAGGTTGTT CATCATGATC ACAACAAGGA 1020
ACGGGGCTCG TTTATCACCA GTGAGGAGCA GGACGTGAGC CCGCGCCTTG CACCTCTGCT 1080
GTTAAACACC CCAGCCATCC CTTCTTCCAA AGGGGATCCT TTCATAGGAG AACACACTGA 1140
GGAGATACCT GAAGAATTGG GATTCAAGCG AGAAGAGATT TATCAGCTTA ACTCAGATAA 1200
40 AATCATTAAG AGTAATAAGG TAAAAGCTAG TCTCTAAGT CCAGGCCAC GGCTCAAGTG 1260
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45 TGATATTAG ATTCTTTGAT TATATTTTGA ATGGGTTCTA GTGAAAAAGG AATGATATAT 1560
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50 CTGAAAAAAG CATATCCAAA ATAATGAGGA AATGTTTGG CTCACTACGT AGAGTCCAGA 1860
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55 AAAAAAAAAA AAAAAAAAAA AAAAAAAAA

SEQ ID NO:76 PDI1 Protein sequence:
Protein Accession #: NP_055139

60 1 11 21 31 41 51
1 MALQGISVVE LSLGAPGRXC AMVLADFGAR VVRVDRPGSR YDVSRLGRGK RSLVLDLKQP 60
61 REPRAAASVQ AVGCAAGALP FRCHGETPAG PRDAAAGKSK AYLCQAEWIV FVQESFCRLA 120
121 GHDINYLALS GVLSKIGRSG ENFYAPLNLV ADFAGGGLMC ALGIIMALFD RTRTDKQVI 180
181 DANMVEGTAY LSSPLWKTQK SSLWEAPRGQ NMLDGGAPPY TTYRTADGEF HAVGAIEPQF 240
241 YELLIKLGLL KSELEFNQMS TDDWPEMKKK FADVPAKRTK AEWCIQFDGT DACVTFVLTF 300
301 EEVVKHDKNK ERGSPITSEE QDVSPRLAPL LLNTPAIPSS KGDPFIGEET EBILEEPGFS 360
361 REEYQLNSD KIIESNKKVA SL

SEQ ID NO:77 PDOS DNA SEQUENCE

70 Nucleic Acid Accession #: AB028951
Coding sequence: 97-1128 (underlined sequences correspond to start and stop codons)

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GTTAAATCCT TACTTTACCA GATTCTTGAT GGTATCCATT ACCTCCATGC AAATGGGTG 60
CTTCACAGAG ACTTGAATCC AGCAAAATATC CTAGTAATGG GAGAAGGTCC TGAGAGGGG 120
AGAGTCAAAA TAGCTGACAT GGGTTTGGCC AGATTATTCA ATTCTCCTCT AAGGCCACTA 180
GCAGATTTGG ATCCAGTAGT TGTGACATTT TGGTATCGGG CTCACAGACT TTTGCTTGGT 240
80 GCAAGGCATT ATACAAAGGC CATTGATATA TGGGCAATAG GTTGATATTT TGCTGAATTG 300
TTGACTTGGG AACCTATTTT TCACTGTGCT CAGGAAGATA TAAAAACAG CAATCCCTTT 360

	CATCATGATC	AACCTGGATCG	GATATTTAGT	GTCATGGGGT	TTCTGTCAGA	TAAAGACTGG	420
	GAAGATATTA	GAAAGATGCC	AGAATATCCC	ACACTTCAAA	AAGACTTTAG	AAGAACAACG	480
	TATGCCAACCA	GTAGCCTCAT	AAAGTACATG	GAGAAACACA	AGGTCAAGCC	TGACAGCAAA	540
5	GTGTTCTCT	TGCTTCAGAA	ACTCCTGACC	ATGGATCCAA	CCAAGAGAAT	TACCTCGGAG	600
	CAAGCTCTCG	AGGATCCCTA	TTTTCAGGAG	GACCCCTTGC	CAACATTAGA	TGTATTTGCC	660
	GGCTGCCAGA	TTCCATACCC	CAAAACGAGAA	TTCCCTTAATG	AAGATGATCC	TGAAGAAAAA	720
	GGTGACAAGA	ATCAGCAACA	GCAGCAGAAC	CAGCATCAGC	AGCCACAGC	CCCTCCACAG	780
	CAGCAGCAG	CCCTCCACCA	GGCGCCCCA	CCACAGCAGA	ACAGCACCCA	GACCAACGGG	840
10	ACCGCAGGTG	GGGCTGGGGC	CGGGGTGGGG	GGCACCGGAG	CAGGCTTGCA	GCACAGCCAG	900
	GACTCCAGCC	TGAACCAAGT	GCCTCCAAC	AAGAAGCCAC	GGCTAGGGCC	TTCAGGCGCA	960
	AACTCAGGTG	GACCTGTGAT	GCCTCGGAT	TATCAGCACT	CCAGTTCTCG	CCTGAATTAC	1020
	CAAGCAGCG	TTCAGGGATC	CTCTCAGTCC	CAGAGCACAC	TTGGCTACTC	TTCTCTGCTC	1080
	CAGCAGAGCT	CAGCATACCA	CCCATCTCAC	CAGGCCACCC	GGTACTGACC	AGCTCCCGTT	1140
15	GGGCCAGGCC	AGCCACGCC	AGAGCAGCAG	CTCCAGCAAT	ATGCTGTCAT	TGAAAAGAAC	1200
	CAAAAATATG	CAAACTAGTA	TGCCATTAA	AACCTATACA	CAATGGAGGA	AAACCTTATA	1260
	TACTGAGCAT	TGTGACGAGC	TGATAGCTCT	TCTTTATTGA	CTTAAAGAG	ATTCTTGTGA	1320
	AGTTTCCCA	GCACCCCTTC	CCTGCATGTG	TTCCATTGTG	ACTTCTCTGA	TAAAGCGTCT	1380
	GATCTAATCC	CAGCATCTCC	GTAACCTTCA	GCATTTCCTT	GAAGGATTTC	CTGGTGCACC	1440
20	TTTCTCATGC	TGTAGCAATC	ACTATGGTTT	ATCTTTTCAA	AGCTCTTTTA	ATAGGATTTT	1500
	AATGTTTTAG	AAACAGGATT	CCAGTGGTGT	ATAGTTTTAT	ACTTCATGAA	CTGATTAGC	1560
	AACACAGGTA	AAATGCACC	TTTAAAGCA	CTACGTTTTC	ACAGACAATA	ACTGTCTCTC	1620
	TCATGGAAGT	CTTAAACAGA	AACTGTTACT	GTCCCAAAGT	ACTTTACTAT	TAGGTTCTGA	1680
	TTTATCTAGT	TTCAGGGAGG	GTCTAATAAA	AAGACAAGCG	GTGGGACAGA	GGGAACCTAC	1740
25	AAOCAAATAC	TGCCATGATC	TTTGCAGTTA	TGTGCTTTAT	GGCAGGAGAA	ACTGAAGTAT	1800
	TTGGTAAATT	TTATAGATTC	ATTCAATATG	AACTGAGTTC	CCAGCATCAT	CTTATTCTGA	1860
	ATAGCATTCA	GTAATTAAGA	ATTACAATTT	TAACCTTTCAT	GTAGCTAAGT	CTACCTTAAA	1920
	AAGGGTTTCA	AGAGCTTTGT	ACAGTCTCGA	TGGCCACAC	CAAAACGCTG	AAGAGAGTAA	1980
	CAACTGCATC	AGGATTTCTG	TAAGGAGTAA	TTTTGATCAA	AAGACGTGTT	ACTTCCCTTT	2040
30	GAAGGAAAG	TTTTTAGTGT	GTATTGTACA	TAAAGTCGGC	TTCTCTAAAG	AAOCCATGGT	2100
	TTCTTCACAT	CTGGGTCTGC	GTGAGTAACT	TTCTTGACATA	ATCAAGGTTA	CTCAAGTAGA	2160
	AGCCTGAAA	TTAATCTGCT	TTTAAATATA	AGAGCAGTGT	TCTCCATTCT	TATTTGTATT	2220
	AGATATAGAG	TGACTATTTT	TAAAGCATGT	TAAAAATTTA	GGTTTTATTCT	ATGTTTAAAG	2280
	TATGTATTAT	GTATGCATAA	TTTTGCTGTT	GTACTGAAA	CTTAATTCTA	TCAAGAATCT	2340
35	TTTTCAATGC	ACTGAATGAT	TTCTTTTGCC	CCTAGGAGAA	AACTTAATAA	TTGTGCTTAA	2400
	AAACTATGGG	CGGATAGTAT	AAGACTATAC	TAGACAAAGT	GAATATTGCA	ATTTCATTAA	2460
	TCTATGAATT	AGTGGCTGAG	TTCTTTCTTA	GCTGCTTTAA	GGAGCCCTTC	ACTCCCCAGA	2520
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40	GTCTCTCTGA	ATGCTTACTAG	CAGCAACCAG	CTTGTTTTAA	ATGTTTTCTT	GAGCTAGAGG	2640
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	TTATCTACAT	CTGGTGTGTA	CTGTGGGTCC	ATACACAAGT	AAATAAGAT	TAGACAGAGG	2760
	CCAGTATACA	TTTTGCACATA	TTGATGTGAT	ACTGTAGCCA	GGCAGGACCT	TACTGATCTC	2820
	AGCATATATA	TGCTCACTAA	TAATGAAGTC	TGCTATAGTA	CACCTATCAA	GACTGAAGAT	2880
	GAGCAGGTT	AGCTGCTCCA	TTGGAAGGAG	TTTCTGATAG	TCTCTGCTG	TTTTACCCCT	2940
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	TTTATCCCTG	GGCTTAAAGC	CTCACTGTCC	AGAGCTGTGT	GTCACTAGAT	GCTTATTGCA	3060
	CCCTCACCAT	GTGCTGTGTG	CCCTGCTGGG	TAGAGAACAC	AGAGGACAGG	GCATCTTCT	3120
	TGTCTTTAAG	GAGCTTGCTA	TCTGTGACAG	TAGCCCTCC	TGGGATGCT	GTGCCATGTG	3180
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50	ACTTGGGTAG	TTACTATCCC	CAAACTGTTT	CTGTAAATAA	TATTATGGAA	GGGTTTCTAT	3300
	GTCACTTACT	GGTATAGAAA	GCCAGTGATT	CAATATCACA	AAAGGCAITG	ACGTATCTTT	3360
	GAAATGTICA	CAGCAGCCTT	TTAAACAACA	CTGGGTGGTC	CTGTAGGCA	GAACATATCT	3420
	TCTTAAGTGG	TTGTAGGAAA	TTGCAAGGAA	ATAGAAGGT	CTGTCTTGC	TCTCAAGGAG	3480
	GTACCTCTGA	ATAAAGAGAG	ACAAACCCAG	ATAGATATGT	AAACCAAAAT	ACTATGCCCC	3540
55	TTAATACTTT	ATAAGCAGCA	TGTGTAATA	GTCTTACGC	TTATACATTC	ACAGAACTAC	3600
	CCTGTTTTCC	TTGTATATAA	TGACTTTTGC	TGGCAGAACT	GAATATATA	CTGTAGGGG	3660
	ATTGCTGAG	TTGCTCCAG	TATACAATAT	CCTCCAGGAC	ATAGCCAGAA	ATCTCCATTC	3720
	CACACATGAC	TGAGTTCTTA	TCCCTGCACT	GGTACTGGCT	CTTTCTCCT	CTTTCTTGC	3780
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	GTGATCTCC	TGCTCAGCC	TCCCGAGTAG	CTGGGACTAC	GGGCAGCCAC	CACCACGCT	4020
	GGCTAATTTT	TGTTATTTTA	GTAGAGATGG	GGTTTCACCC	TATTTGTCAG	GCTGGTCTTG	4080
	AATTOCTCAC	CTCAGGTCAT	CGCCTGTCT	CGCCTCCCG	AAGTGTGGG	ATTATAGGTG	4140
65	TGAGCCACCG	CACCCAGTTG	GGAACAAAGC	CTTTTAAACA	CACGTAAGGG	CCCTCAAACC	4200
	GTGGGACCTC	TAAGGAGACC	TTTGAAGCTT	TTTGAAGGCA	AACCTTACCT	TTTGGTCC	4260
	CAAAATGATG	CATTCTCTT	TGAAATTTAT	TAGATACTGT	TATGTCCCC	AAGGGTACAG	4320
	GAGGGGCATC	CCTCAGCTA	TGGGAACACC	CAAACTAGGA	GGGTTTATG	ACAGGAAGGA	4380
	ATGAATCCAA	TGAAGGCTT	TCTGCTCTTC	GTGTTACAAA	CCAGTTTCAG	AGTTAGCTTT	4440
70	CTGGGGAGGT	GTGTTTGTG	GAAAGGAAT	CAAGTGTG	AGGACAGAT	AGCTCAAGGT	4500
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	GATCATGAG	TGACATACAA	AGACCAAGGA	TTATGTATAT	TTTTATATCT	CTGTGGTTTT	4620
	GAACTTTTAT	TACTTAGAAT	TTTGCCCTTC	TGCACTACTC	TTTTGCTCTT	ACGAACATA	4680
	TGGACTCTTA	AGAAATGGAA	GGGATGACAT	TTACCTATGT	GTGCTGCCCT	ATTCCTGGTG	4740
75	ANGCAACTGC	TACTTGTCTT	CTATGCCTCT	AAAATGATGC	TGTTTTCTCT	GCTAAAGGTA	4800
	AAAGAAAGGA	AAAAAATAGT	TGGAATAATA	GACATGCAAC	TTGATGTGCT	TTTGAGTAAA	4860
	TTTATGCAAG	AGAACTATA	CAATGAAGGA	AGAATCTTAT	GGAAATTACA	AATCCAAAC	4920
	TCTATGATGA	TGCTTCTCTA	GGGAGTAGAG	AAAGGCAGTG	AAATGCCAGT	TAGACCAACA	4980
	GAGGCTTGAA	GAATTCAGT	ACAAGTATA	TTTTGTATAA	AACATAGCAG	TTTAGGTCCT	5040
80	CATATCTCT	AAAAATAGTC	ACAAATATAA	CAAGTTCAT	TGTTTTAGGG	TTTTTAAAAA	5100
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10
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ACCTGTCTCT GTCCTCTTTT TCAGTCATT TCTGCACGCA TCCCCCTTTA TATGGTTATA 5460
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AGCGAGGCTT GCTCCATGGA GTGCAGGAGC AGCTACTGCT TTTGAGCGAG GGTTCCTGTC 5580
TTTGTAGTTG ACCTGACTTC CTCTCTGAAA TGACTGTAA AACTAAAATA AATTACATTG 5640
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SEQ ID NO:78 PD03 Protein sequence
Protein Accession #: BAA82980

15
20
1
11 21 31 41 51
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HHDQLRLIFS VMGFPADKIM EDIRKMEYFP TLOKDFRRT YANSSLIKYM EKHKVKPDSK 180
VFLLQLKLLT MDPTKRITSE QALQDPYFQE DPLPTLDVFA GCQIPYFKRE FLNEDDFEEK 240
GDKXQQQQQN QHQQTAPPQ QAAAPPAFP PQQNSTQTHG TAGGAGAGVG GTGAGLQHSQ 300
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QQSSQYHPSH QAHRY

SEQ ID NO:79 PD05 DNA SEQUENCE

25
Nucleic Acid Accession #: XM_002922
Coding sequence: 1-2190 (underlined sequences correspond to start and stop codons)

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65
1
11 21 31 41 51
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AACTATCCAC TGAGCAITGC CTTCATTGTG GTGAATGAAT TCTGCGAGCG CTTTTCCTAT 180
TATGGAATGA AAGCTGTGCT GATCCTGTAT TTCTGTATT TCTGCACTG GAATGAAGAT 240
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TATCTGTTTG TTATTACTAA TAACACCAAT CAGGGTCTTC AGGCCTGGAA GATTGAAGAC 1800
ATTCCAGCCA ACAAAATGTC CATTGCGTGG CAGCTACCAC AATATGCCCT GGTACAGCT 1860
GGGAGAGTCA TGTCTCTGT CACAGGTCTT GAGTTTCTT ATTCTCAGGC TCCCTCTAGC 1920
ATGAAATCTG TGCTCCAGGC AGCTTGGCTA TTGACAATTG CAGTTGGGAA TATCATCTGT 1980
CTGTGTGTGG CACAGTTCAG TGGCTGTGTA CAGTGGGCCG AATTCATTT GTTTTCTGTC 2040
CTCTGCTGG TGATCTGCTT GATCTCTCC ATCATGGGCT ACTACTATGT TCTGTAAAAG 2100
ACAGAGGATA TCGGGGTCC AGCAGATAAG CACATCTCTC ACATCCAGGG GAACATGATC 2160
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SEQ ID NO:80 PD05 Protein sequence
Protein Accession #: XP_002922

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75
80
1
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YVLGEVKSLL QALPLGGQV VHTVLSLIGL SLIALGTGGI KPCVAAPGD QFEKHAEER 180
TRYFSVFYLS INAGSLISTF ITFHLRQDVQ CPGEDCYALA FGVPGLLHVI ALVVFAAGSK 240
IYNKPPPEGN IVAQVFECIN FAISNRFKNR SGDIKPRQHW LDWAERKYPK QLIEDVKALT 300
RVLFYLYPLP MFWALLDQQG SRWTLQAIM NRNLGFFVLQ FDMQVLANPF LVLIPIPLFD 360
FVIYRLVSKC GINPSSLRKM AVGHILACLA PAVAAVAEIK INEMAPAQSG PQEVPLQVLN 420
LADDEVKTVV VGNENSLILI ESIRSFQTFP HYSKLHLKTK SQDFPHILKY HNLSTYTES 480

5 VQEKWYSLV IREDGNSISS MMVKDTESKT TNGMTTVRFV NTLKEDVNIS LSTDTSLAVG 540
EDYGVSAVYT VQRGEYPAYH CRTEDKNFSL NLGLLDFGAA YLFVITNMTN QGLQAMKIED 600
IPANKMSLAW QLPQYALVTA GEVMFSVTGL EFSYSQAPSS MKSVLQAMML LTIAGVNIIV 660
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SEQ ID NO:81 PD08 DNA SEQUENCE

Nucleic Acid Accession #: NM_020448

Coding sequence: 1-1221 (underlined sequences correspond to start and stop codons)

10 1 11 21 31 41 51
ATGGAAGGAT CCCACAGCGC AGCCCTGAAG CTGCAGCAGC TGCCCTCCAC AAGTAGCTCC 60
AGGCGCGTAA GCGAGGCTTC CTCTCTCTAC AAGGAAAACC TGATTGGGCG CCTCTTGGCG 120
15 ATCTTGGGCG ACCTCGTGGT CAGCATTGCA CTTAACCTCC AGAAGTACTG CCACATCCGC 180
CTGCAGGCT CCAAGGATCC CCGGGGCTAT TTCAAGACCA AGACATGGTG GCTGGGCGTG 240
TTCTGATGC TTCTGGGCGA GCTGGGTGTG TTGCGCTCCT ACGCTTTCGC GCGCTGTGCA 300
CTCATCGTGC CCTCAGCGC AGTTTCTGTG ATAGCTAGTG CCATCATAGG AATCATATTC 360
20 ATCAAGGAAA AGTGAAGACC GAAAGACTTT CTGAGGCGCT ACGTCTGTGC CTPTGTGGGC 420
TGCGGTTTGG CTGTCTGTGG TACCTACCTG CTGGTGACAT TCGCACCCAA CAGTCACGAG 480
AAGATGACAG GCGAGAATGT CACCAGGCAC CTCGTGAGCT GGCTTTCTCT TTGTACATG 540
CTGGTGGAGA TCATTCTGTT CTGCTTGCTG CTCCTACTTC AAGAGGAGAA GAACGCCAAC 600
AACAATGTGC TGATTCTTCT CTTGGTGGCG TTAATGGGCT CCATGACAGT GGTGACAGTC 660
25 AAGGCGGTGG CTGGGATGCT TGCTCTGTCC ATTCAAGGGA ACCTGCAGCT TGACTACCCC 720
ATCTTCTACG TGATGTTCTG GTGCATGGTG GCAACCGCCG TCTATCAGGC TGGGTTTGTG 780
AGTCAAGCCT FRKTIWMLGL FLMLLGLGV PASYAFAPLS LIVPLSAVSV IASAIIGIIF 840
ACAAACATG CTATCACAGC AGGTGCAATA TTTTACCTGG ACTTCATCGG GGAGGACGTC 900
CTGCACATCT GCATGTTTGC ACTGGGGTGC CTCATTGCAT TCTTGGGGGT CTTCTTAATC 960
30 ACGGTATACA GGAAGAAGCC CATTCCTATT GAGCCCTATA TTTCATGGA TGCCATGCCA 1020
GGTATGCAGA ACATGCACGA TAAAGGGATG ACTGTCCAGC CTGAACCTAA AGCTTCTTTT 1080
TCTATGGGG CTCTGGAATA CAATGACAA ATTCTGAGA TCTACGCTCC TGCCACCCGT 1140
CCAGTATGC AGAAGAGCA CGGCTCCAGA AGTGCCTCTG GGTGCCCTCA COGAGTCCCTA 1200
GAGCACACCA AGAAGGAATG A

SEQ ID NO:82 PD08 Protein sequence

Protein Accession #: NP_065181

40 1 11 21 31 41 51
MDGSHSAALK LQQLPPTSSS SAVSEASFSY KENLIGALLA IFGHLVVSIA LNLQRYCHIR 60
LAGSKDPFRAY FRKTIWMLGL FLMLLGLGV PASYAFAPLS LIVPLSAVSV IASAIIGIIF 120
IKEKWKPKDF LRRYVLSFVG CGLAVVGTYL LVTFAPNSHE KMTGENVTRH LVSWPFLLYM 180
LVEILLFCLL LVFYKERIAN NIVVILLVA LLGSMIVTVV KAVAGMLVLS IQGNLQLDYP 240
45 IFYVHFVCMV ATAVVQAAPL SQASQMYDSS LIASVGYILS TTIATAGAI FYLDPIGEDV 300
LHICMFALGC LIAFVGFLVI TRNRKPIPF EPIYSEDAMP GNONHDKGM TVQPELKASF 360
SYGALENNND ISEIYAPATL PVMQEERGSR SASGVPRYVL ERTKKE

SEQ ID NO:83 PD08 DNA SEQUENCE

Nucleic Acid Accession #: NM_032712

Coding sequence: 555-908 (underlined sequences correspond to start and stop codons)

50 1 11 21 31 41 51
CACTCATTA A GAACAGAGGA GGCTGCCTGT TACTCTGGT GTTGCAATCC TCCAGACACT 60
55 CTGCTGTTC CTGCTAGGC GTGGCTGCAG CCATGGCTAG GAAAGCGCTG CCACCCACCC 120
ACCTGGGCCA GAGCTGGTTC TGCTCTGCT GCAGGGACAC TGAGCTGGCT ATCTCGGCGC 180
TTGGGGCAG AACTGCAACA GGCTCTCTG GGTCTCTGAG GTGTACAGCC GGGCCCTGTC 240
CTGTGCTCT AGCTCTCGAG AGCTGCTGCT GCGGGGTGAC CTGATCCAAC CTGATAAGGT 300
60 GCCATCTTCA GCTACCACTG CAAGGCCCTG AGGGCAACAG CAGCACGGCA CTGCCACCCC 360
GGCTGCTGAT GGCTGGTGC CAGCTGGGAG TCCTCCCGGC ACTTCGAGGC CACTGAGCCA 420
CCCTTCCAGC CCCAGCCAC CATGGACAGG GGTATCCAGC TTCTCTCTCA ACCTGCTCCT 480
CTGCCCTGA GCCAGTGACG CCCAAGGACA TGCTCTTAC CCAGGTCTCT TACCAGCACT 540
AGCTGGTCAA GGCCATGACA GTGCTGGAGG CCGTCTTGGA GATCCAGGCC ATCACTGGCA 600
65 GCAGGCTGCT CTCTATGGTG CCAGGGCCCG CCAGGCCACC AGGCTCATGC TGGGACCCAA 660
CCCAGTGAC AAGGACTTGG CTGCTGAGCC ACACACCCAG GAGAAGGTGG ATAAGTGGGC 720
TACCAAGGCC TTCTGCAAG CTAGGGGAGG AGCCACCCCG GCTTCCCTAT TGTGACAGG 780
CCTATGGGGA GGAGCTGTCC ATACGCCACC GTGAGACCTG GGCTGGCTC TCAAGGACAG 840
70 ACACGCGCTG GCTGTGCTCT CCAGGGGTGA AGCAGGCCAG AATCTTGGGG GAGCTGTCTC 900
TGGTTTGAAG TGCAATTCAGG AAGTGCAGGA CATGGTAGGG GAGGCCAAAA GCCTTGGGCA 960
CTACCTCTCC TGTGGAGCTG TTCGGTGTCC GTGAGCTAG CCACACCCCT ACACCATGTT 1020
CAAGGTTACC GGAAGAGAGG GGTGTCTGCC CCAACCTCC CTTGTGGGTG TCACTGGCCA 1080
GATGTATAGA GGAAGACAGG CCTGTGAGT GGACACTGAC CATGAGTCCC TGGGGGGAGT 1140
GATCCCCAG GCATGCTGTG CCATGTGCA CTCTGCCCA GGCAGCAGGG TGGGTGGGTA 1200
75 CCATGGGTGC CCACCCCTCC ACCACATGGG CCCCCAAAGC ACTGCAGGCC AAGCAGGGCA 1260
ACCCACACC CTTGACATAA AAGCATCTTG AAGCTTTTAA AAAAAA AAAAAA

SEQ ID NO:84 PD08 Protein sequence

Protein Accession #: NP_116101

80 1 11 21 31 41 51

MTVLEAVLEI QAITGSRLLS MVFGPARPPG SCWDPTQCTR TWLLSHTPRR RMISGLPRAS 60
CRLGEEPPFL PYCDQAYGEE LSIRERETWA WLSRTDTAWP GAGPVQARI LGELLLV

5

SEQ ID NO:85 PDT1 DNA SEQUENCE

Nucleic Acid Accession #: NM_000693

Coding sequence: 53-1591 (underlined sequences correspond to start and stop codons)

10 1 11 21 31 41 51
AGCCGCTGCG CGGCAGACTA GGGCGCCTCG GGCCAGGGAG CGCGGAGGAG CCATGGCCAC 60
CGCTAACGGG GCGCTGGAAA ACGGGCGAGCC GGACGGGAAG CCGCCGGCCC TGCCGCGCCC 120
CATCCGCAAC CTGGAGGTCA AGTTCACCAA GATATTTATC AACAAATGAAT GGCACGAATC 180
CAAGAGTGGG AAAAAGTTTG CTACATGTAA CCCTTCAACT CGGGAGCAAA TATGTGAAGT 240
15 GGAAGAAGGA GATAAGCCCG ACGTGGACAA GCGTGTGGAG GCTGCACAGG TTGCCTTCCA 300
GAGGGGCTCG CCATGGCGCC GGCTGGATGC CCTGAGTCGT GGGCGGCTCG TGCACCAAGT 360
GGCTGACCTT GTGGAGAGGG ACCGGGCCAC CTGTGGCCGC CTGGAGACGA TGGATACAGG 420
GAAGCCATT CTTCATGCTT TTTTCATCGA CCTGGAGGGC TGTATTAGAA CCCTCAGATA 480
CTTTGCAGGG TGGGACAGCA AAATCCAGGG CAAGACCATT CCCACAGATG ACAACGTCTG 540
20 ATGCTTCACC AGGCATGAGC CCATTTGTTG CTGTGGGGCC ATCACTCCAT GGAACCTTCC 600
CCTGCTGATG CTGCTGTGGA AGCTGGCACC CGCCCTCTGC TGTGGGAACA CCATGGTCTT 660
GAAGCCTCGG GAGCAGACAC CTCTCACC GCCTTCTCTG TCAAGTAGGC 720
CGGTTCCCT CCGAGGTGG TGAACATTGT GCCAGGATTC GGGCCACAG TGGGAGCAGC 780
AAATTTCTCT CACCTCAGA TCAACAGAT CGCCTTCACC GGCTCCACAG AGGTTGGAAA 840
25 ACTGGTTAAA GAGCTGCGT CCGGAGCAA TCTGAAGCG GTGACGCTGG AGCTGGGGGG 900
GAAGAACCCC TGCATGTTGT GTGCGGACGC TGACTTGGAC TTGGCAGTGG AGTGTGCCA 960
TCAGGAGTGT TTCTTCAACC AAGGCCAGTG TTGCACGGCA GCCTCCAGGG TGTTCGTGGA 1020
GGAGCAGGTG TACTCTGAT TTGTCAAGCG GAGCGTGGAG TATGCCAAGA AACGGCCCGT 1080
GGGAGACCCC TTGATGTACA AAACAGAAAC GGGGCTCAG ATTGATCAA AGCAGTTCGA 1140
30 CAAAATCTTA GAGCTGATCG AGAGTGGGAA GAAGGAAGGG GCCAAGCTGG AATCGGGGG 1200
CTCAGCCATG GAAGACAAGG GGCTCTTCAT CAACCCCAT GTCTTCTCAG AAGTCACAGA 1260
CAACATGGCG ATTGCCAAG AGGAGATTTT CGGGCCAGTG CAACCAATAC TGAAGTTCAA 1320
AAGTATCGAA GAGTGTATAA AAGAGCGGAA TAGCACCGAC TATGGACTCA CAGCAGCCGT 1380
GTTCACAAA AAATCTGACA AAGCCCTGAA GTTGGCTTCT GCCTTAGAGT CTGGAAGCGT 1440
35 CTGGATCAAC TGCATCAACG CCCTCTATGC ACAGGCTCCA TTTGGTGGCT TAAAAATGTC 1500
AGGAATGGC AGAGAAGTAG GTGAATACGC TTTGGCCGAA TACACAGAAG TGAAGTCTGT 1560
CACCATCAAA CTGGGCGACA AGAAGCCCTG AAGGAAAGGC GGGGCTCCTT CCTCAACAT 1620
CGGACCGGCG AATGTGGGAG ATGAAATGTG CTGGAGGAAA AAAATGACAT TTCTGAGCTT 1680
40 CCGGAGACAC ATTCTTCTGG AGGCTTTACA TCTACTGGAG TTGAATGAT CTGTGTTTCC 1740
TCTCACTCTA CTGTCTTATC ACCAGACTGG GGTGCTCTAT AGGTTGTCTG TGAATTCGCA 1800
GTCTGCTGCG GGGAGGGAGC TGTGCGCAT TTCTGTGTTT CCTTTAAAC CAGATCCTGG 1860
AGACAGTAGG ATACTCAGGG CGTTGTTAAC AGGGAGTGGT ATTTGAAGTG TCCAGCAGTT 1920
CGTTGAAATG CTTTGCCGAA TCTGACTCCA GTAAGAATGT GGGAAAACCC CCTGTGTGTT 1980
45 CTGCAAGCAG GGCCTCTTGA CCAGCGGTCT CCTCAGGGTG GACCTGCTTA CAGAGCAAGC 2040
CAGCGCTCTT TCCGAGGTGA AGGTGGGACC ATTCTTTGGG AAAGGATTCA CAGTAAGGTT 2100
TTTTGCTTTT TGTTTTTTGT TTTCTTGT TTAAAAAAG GATTTACAG TGAGAAAGTT 2160
TTGGTTAGTG CATACCGTGG AAGGGGCCCA GGGTCTTTGT GGATTTGATG TTGACATTGA 2220
CCGTGAGATT CGGCTTCAAA CCAATCTGCT CTTTGGAATA TGACAGAATC AATAGCCGAG 2280
50 AGAGCTTAGT CAAGAGCAT ATCAAGGTCT ACCTTAACCA AGGCACCTTC TTAAGCAGAA 2340
AATATTGCTG AAGTTACTTT TGCTGCTAAA GATCCAACTC TCTAACGCCA CAACAGCATA 2400
GCAAACTCTA GGATAATTCA CCTCCTCAIT TGACAAATCA GAGCTGTAT TCACTTTAAC 2460
AAATTAGCCA TTCTATACCA GTTCACTAAC AGCTTATGAT AAGTCTGTGT AGTCTTCTT 2520
TTCTCCAGTT CTGTACACCA ATTTAGATTA GTAAAGOGTA CACAACTGGA AAGACTGCTG 2580
55 TAATAACACA GCCTTGTAT TTTTAAGTCC TATTTTGATA TTAATTTCTG ATTAGTTAGT 2640
AAATAACACC TGGATTCTAT GGAGGACCTC GGTCTTCAT CAAGTGGGCT GAGTATTTC 2700
CTGGCAGGTT GTGAATTTT CTTTTCTCTT TTGGGAATCC AAATGATGAT GTGCAATTT 2760
ATGTTTAAAC TTGGGAAACT GAAAGTGTTC CCATATAGCT TCAAAACAA AAACAATGT 2820
60 GTTATCCGAC GGATACTTTT ATGTTACTA ACTAGTACT TCCTAATTGG GAAAGTAGTG 2880
CTTAAGTTTG CAATTAAGT TGGGGAGGGC AATAATAAAA TGAGGGCCCC TAACAGAAC 2940
AGTGTGTGTA TAACGAAAAC CATGTATAA ATGGGCTAT CACCTTGTG AGAGATATA 3000
ATTACCACAT TTGGCTTCCC TTCAATCAGT AACACTTATC ACTTACTATA CCAATAACT 3060
GTTAAATCAG GATTGTGCTT CATACACTGA ATTTTCAGTA TTTTATCTCA AGTAGATATA 3120
GACACTAACC TTGATAGTGA TACGTTAGAG GGTTCCTATT CTTCATTTGT ACGATAATGT 3180
65 CTTTAATATG AAATGTCTA TTAATTTATA TTGTTAGAGT TATTTGATCT TTTTATAGTT 3240
GTAAGTACAC AGAGGTGGTA TATTTAACT TCTGTATAT ACTGTATTTA GAAATGGAAA 3300
TATATATAGT GTTAGGTTTC ACTTCTTTTA AGGTTTACCC CTGTGGTGTG GTTTAAAAAT 3360
CTATAGGCTT GGAATTCGG ATCTAGCTG CAGATCGCAT CCCACATGC GAGAAATGATA 3420
AATAAATTT GGTATTTTGA GA

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SEQ ID NO:86 PDT1 PROTEIN SEQUENCE

Protein Accession #: NP_000684

75

1 11 21 31 41 51
MATANGAVEN GQPDGKFPAL FPIRNLEVK FTKIFINNEW HESKSGKKFA TCNPFSTREQI 60
CEVEEGDKPD VDKAVEAQQ AFQPGSPMRR LDALSRGRLL HQLADLVERD RATLAALESTM 120
DTGKFFLEAF FIDLEGGCIRT LRYFAGWADK IQGKTIPTDD NVVCPTRHEP IGVCGAITPW 180
NPFLLHLVWK LAPALCCGNT NVLKFABQTP LTALYLSLI KBAGPFFGVV NIVPGFGPTV 240
GAAI6SHPIQ NKLAFTGSTB VGKLVKEAAS RSNLKRVTLE LGGRNFCIVC ADADLDLAVE 300

CAHQGVFFNQ GQCCTAASRV FVEEQVYSEF VRRSVEYARK RPYGDPFDPVK TEQGPQIDQK 360
 OFDKLELIE SGRKKGAKLE CGGSAMEDKG LPIKPTVPSE VTDNMRIAKE EITGFPVQPI 420
 KFKSLIEVLIK RANSTDYGLT AAVPTKNLKD ALKLASALEK GTVWVINCYNLYAQAFFGGP 480
 KMSGNGRELQ EYALAEYTEV KTVTKLGDGK NP

5

SEQ ID NO:87 PDV3 DNA SEQUENCE

Nucleic Acid Accession #: NM_032642

Coding sequence: 184-1263 (underlined sequences correspond to start and stop codons)

10 1 11 21 31 41 51
 GACCATTAGC AGGCACCCAG GCCTGTCTTT GGCTCGGAAA CGGTGGCCCC CAATGTAGCC 60
 TAGTTTGAAC CTAGGAACCTG CAGGACCAGA GAGATTCCAC TGGAGCCTGA TGGACGGGTG 120
 ACAGAGGGAA CCCTACTCTG GAAACTGTCA GTCCACGGGC ACTGGGGAGG GCTGAGGCCG 180
 ACCATGCCCA GCTGTCTGCT GCTGTTCACG GCTGCTCTGC TGTCCAGCTG GGCTCAGCTT 240
 CTGACAGACG CCAACTCTCT GTGGTTCATTA GCTTTGAACC CGGTGCAGAG ACCCGAGATG 300
 TTATCATCCG GTGCCACGCG CGTGTCCAGT CAGCTTCCCG GGCTCTCCCG TGGCCAGAGG 360
 AAGCTGTGCC AATTGTACCA GGAGCACATG GCCTACATAG GGGAGGGAGC CAAGACTGGC 420
 ATCAAGGAAT GCCAGACCA GTTCCGGCAG CGCGGTGGA ATTGCAGCAC AGCGGACAAC 480
 GCATCTGTCT TTGGGAGAGT CATGCAGATA GGCACCGGAG AGACCGCCTT CACCCACGCG 540
 GTGACGCGCG CGGGCGTGGT CAACGCCATC AGCGGCGCTT GCCCGGAGG CGAGCTCTCC 600
 ACCTGCGGCT GCAGCCGGAC GCGCGCGGCC AAGGAOCTGC CCCGGACTG GCTGTGGGGC 660
 GGCTGTGGGG ACAAGCTGGA GTACGGCTAC CGCTTCGCCA AGGAGTTTGT GGATGCCCGG 720
 GAGCGAGAGA AGAAGCTTGC CAAAGGATCA GAGGAGCAGG GCCGGTGCT CATGAACCTG 780
 CAAAACACG AGCGCGGTGC CAGGGCTGTG TATAAGATGG CAGACGTAGC CTGCAAAATG 840
 CACGCGCTCT CGGGTCTCTG CAGCCTCAAG ACCTGCTGGC TGCAGCTGGC CGAGTTCCGC 900
 AAGGTCCGGG ACCGCTGAA GGAGAACTAC GACAGCGCG CGCCATGCG COTCAACCGC 960
 AAGGCGCGG TGGAGCTGGT CAACAGCGCG TTCAOCCAGC CCACCCCGGA GGACTCTGGT 1020
 TATGTGGACC CCAGCCCGCA CTACTGCTG CGCAACGAGA GCACGGGCTC CCTGGGCAAG 1080
 CAGGCGCGCC TCTGCAACAA GACCTCGGAG GGCACTGATG GCTGTGAGCT CATGTGCTGC 1140
 GGGCGTGGCT ACAACAGATT CAAGAGCGTG CAGGTGGAGC GCTGCCACTG CAAGTTCCAC 1200
 TGGTCTGCTG TCGTCAGTG TAAGAACTGC ACGAGATCG TGGACCACTA CATCTGTAAA 1260
 TAGCCCGGAG GCGCTGCTCC CGGCCCGCCC TGCACTCTGC CTCACAAAGG TCTATATTAT 1320
 ATAAATCTAT ATAAATCTAT TTTATATTG TATAAGTAAA TGGGTGGGTG CTATACAATG 1380
 GAAAGATGAA AATGGAAGG AAGAGCTTAT TTAAGAGAGC CTGAGATCT CTGAGGAGTG 1440
 GACTTGTCTG GTTCTCTCTT CTGTGTGGGT GGGAGACAGG GCTTTTCTC TCCTCTGGC 1500
 GAGGACTCTC AGGATGTAG GACTTGGAAA TATTTACTGT CTGTCCACCA CGGCCTGGAG 1560
 GAGGGAGGTT GTGGTGTGAT GGAGGAGATG ATCTTGTCTG GAAGTCTAGA GTCTTTGTG 1620
 GTTAGAGGAC TGCTGTGTAT CTTGCCACT AGGCCAAGAG GCCCTATGAA GGTGGCGGGA 1680
 AACTAGCTC AACTCTGAT TCTTCAGGT CTGTCCAGA ATGTAGATGG GTTCCGTAAG 1740
 AGGCTGTGTG CTCTCTACT CTTTCATCCA CGTGCACTG TCGGCGATCT CGAGTTTACA 1800
 GGAACGGCTC CTTCCCTAAA ATGAGAACTC CAAGGTCTAT TCTGGCCAG TGACCACAGA 1860
 GAGATCTGCA CTTCCCGGAC TTCAGGCTG CCTTTCCAGC GAGAATCTT CATCTCCAC 1920
 GGTTCACCTG CTCTCTACT AAGAGGAAAG GGGGCCATT GACCTGACAT GTCAAGAAAG 1980
 CCTTAACTC AATGTTTGG CCTGGGCTGC AGAAGCCAGG GTGCATGACC AGGCTGCGTG 2040
 GAGTTTATAC TGTCTTCCC CACCCCGGG GAGGGGAAGC TTGAGCTGCT GCTGTCACTC 2100
 CTCCACCGAG GGAGGCTCA CAAACACAG GACGCTGCAA CGGCTCAGG TGGCGGGCCC 2160
 GGCCTGTCTA TCATCTCTGC CCCAGGTGTA CGGTTTCTCT CTGACATTAA ATGCCCTTCA 2220
 TGGAAAAAAA AAAAAGAAAA AAAAAAAAAA AA

50

SEQ ID NO:88 PDV3 Protein sequence

Protein Accession #: NP_116031

55 1 11 21 31 41 51
 MFSLLLLFTA ALLSSWAQLL TDANSWWSLA LNFVQRPMP IIGAFVCSQ LPGLSPGQRK 60
 LCQLYQEHMA YIGEGAKTGI KECQHQFRQR RWCNSTADNA SVFGRVMQIG SRETAPTHAV 120
 SAAGVVAIS RACREGELST CGCSRTARPK DLPRDWMGG CGDNVEYGYR FAKEFVDARE 180
 REKNFARGSE EQGRVLMNLQ NNEAGRRVAV KMDVACKCH GVSGSCSLKT CWLQAEFRK 240
 VGDRLEKEYD SAAAMRVTRK GRLELVNSRF TQPTPEDLVY VDPSPDYCLR NESTGSLGTQ 300
 GRLCNKTSSE MDGCELMCCG RGYNQFKSVQ VERCHCKPFW CCFVRCKKCT EIVDQYICK-

65

SEQ ID NO:89 PDT9 DNA SEQUENCE

Nucleic Acid Accession #: NM_033280

Coding sequence: 58-636 (underlined sequences correspond to start and stop codons)

70 1 11 21 31 41 51
 GGCAGCCGTC TGTGCCACCC AGAGCCGGCG GGCGGCTAGG TCCCGGAGGA CCTGTCTATG 60
 GTGCGTGGCG GCGCGTGGGG GGCTCATCTC CCGCGGTCCG GCTTGGATAT CTTCGGGGAC 120
 CTGAAGAAGA TGAACAACCG CCAGCTCTAT TACCAGGTTT TAACTTCGC CATGATCGTG 180
 TCTTCTGCAC TCATGATATG GAAAGGCTTG ATCGTGCTCA CAGGCAGTGA GAGCCCATC 240
 GTGGTGTGTC TGAGTGGCAG TATGGAGCCG GCCTTTCACA GAGGAGACCT CCTGTCTCTC 300
 ACAAAATTCC GGGAGAGACC AATCAGAGCT GGTGAAATAG TTGTTTTTAA AGTTGAAGGA 360
 CGAGACATTC CAATAGTTCA CAGAGTAATC AAGTTTCATG AAAAGATAA TGGAGACATC 420
 AATTTCTTGA CTAAAGGAGA TAATAATGAA GTTGATGATA GAGGCTTGTA CAAAGAAGGC 480
 CAGAACTGCC TGGAAAAGAA GGACGTGGTG GGAAGAGCAA GAGGGTTTTT ACCATATGTT 540
 GGTATGCTCA CCATAATAAT GAATGACTAT CCAAAATCA AGTATGCTCT TTTGGCTGTA 600
 ATGGGTGCAT ATGTGTTACT AAAACGTGAA TCCTAAAATG AGAAGCAGTT CCTGGGACCA 660
 GATTGAAATG AATCTCTGTTG AAAAAAGAAA AACTTAATAT ATTTGAGATG TTCCATTTC 720

80

TGTATAAAG GGAACAGTGT GGAGATGTTT TTGTCTTGTC CAAATAAAG ATTCAACAGT 780
 AAAAAAAAAA AAAA

SEQ ID NO:90 PDV9 Protein sequence

Protein Accession #: NP_150596

5

1 11 21 31 41 51
 10 MVRAGAVGAH LPASGLDIFG DLKQMKRQL YYQVLNFAMI VSSALMIWKG LIVLTGSESP 60
 IVVVLSGSME PAFHRGDLIF LTNFRDPIR AGEIVVFKVE GRDIPIVHRV IKVHEKINGD 120
 IKPLTRGDNN EVDDRGLYKE QQNWLEKRDV VGRARGFLPY VGMVTIIMND YPKFKYALLA 180
 VMGAYVLLER ES

SEQ ID NO:91 PDV5 DNA SEQUENCE

Nucleic Acid Accession #: NM_016590

Coding sequence: 691-975 (underlined sequences correspond to start and stop codons)

15

1 11 21 31 41 51
 20 GATTACTCAC ACAGTCTTGA AGATGCAATG TCAGCTATTT AGGACAGAAA CATCCAAGGC 60
 CGGTCTCAGAA CTCGAATACG ACTACATATG CATTAAGGCA GGAAGTGGCA GGCCTCAGGG 120
 TAGGCCAATC ATAGGACTCG TGCTTCTCGT ACGCTGGGCT ATAATCTATG AAAGTGAAGT 180
 CCAGAGCCAG CCAATCACTT AGCTCCTCAT AACCAAGTCTA ACTGGCTCTG GAAAGCTGAA 240
 AGGGCTGCAC TGGACAACAA CAGATGAGAT ATTCTACACA TTAATCTACT TATCTGGAAT 300
 25 CACTTTGGCT CTAAGGGCCA GAGAAAAATC ACAGCTTCCT TGTCGGAGGG GAAAAGGACA 360
 GGTGATCTGG GGAAGACGCA GCTACACCTG GAGCAAGGTC TCTTCCCGGC TTGGCAATCT 420
 CAGCTGTGCG GCGCTACGG GACCCGAGCC GTCCAGAAA CCAAGGGCCA GGCACGGCAG 480
 CAACGCGCTG AGTGTCTGCTG CCTTCGGTGA CTATATGAGA ATGGAACACT CTAAAGGAAGC 540
 CAGGTGTGTA GAATGTGTAC CCCCTTTACT CAGAGATAAC ATAGATTATC CAGGCTGAGA 600
 30 TGGAAAAACA GCCCTTTAAT GAATTTTCAA CACAGACTCC CTGCTTCTCA TCTCCTTAAT 660
 AAAATTTTCA TAAATCCCC TTGAATCCCT ATGTTCAAAT CTCCATTGTG TGACAGACAA 720
 AGCCAACAAT ACTCTAAACT GAGGCTGCA AGTCAATTTCA TTTGTATTTT TGTCAGAAA 780
 TTTCCCATAG GAAGACTTCA CCTCCTACAA CTCGGAAGAA AACCTTACTG GTCCAAGACC 840
 GTCAACGACA ACCATCCGCA GTCAATCAAG TGGAAAGCTT CACAGCTTTT GTACATTCTC 900
 35 TGTGTCAATG TACAAGTGGG TTACAGACTG TCCCCTGGCT CCCTGACCCCT TACAACACT 960
 AAAGTGTGTT TTTGACTCAA CTCAAGCTG CTCATCTGTT AGTAAGTATG GTTCACTCCA 1020
 GAACACATTC ATGATGAGAA CTCTCTAATA GACCAGCACT GCTCTTCCCT TCCTATAATC 1080
 ATAATAATCA TGATAACCTG AAACATGTTA CTGGGACTCG ACATTTTCTC GGGGATTGAA 1140
 ATCTTTAGTC TTTGGAGCTG TCACATAGCA GGGGCAACCT CACACTGAAA CAAAGGAAGT 1200
 40 GATGTCCCAT TATTATCCAC CCTGAGCCAC CATAAATATG TGTATACATT TATTTCTCTC 1260
 AGCTGTGACA AAACAAAGCA ATGGAAGAGG AAATAAATA ATATACATAC TAGTACCAAT 1320
 ATCTCTTTT GCTTAAATTT ACTAATGCAC CAGCTCAGTC TGCTTCTCTC AGGCATCAAT 1380
 CTCATTTCTT CAGGACTTGT ATTAGCAGGT TCTGGCTAGA GAGACTATCT CCTGTATCAT 1440
 CGATCAATTA ATGTTTCTG GTGATCACAT CAGGCCATAT CTAAGAAGCT CATGGTATAC 1500
 45 AAGGGTCAAC CAAATAGCTG AGTGCAGTCC TTGCTCATAT TTCTTCTATC TTAACCCCGC 1560
 AAACAAGAAAT TAAGATGATC CCAATAAAG AAATAATGCT CAGGAAGACT AACCTTTTTC 1620
 TGAACCAAGC ACTGTGAGCA AATCTCAGGT ATTAGAGCAA CTATGTTTGA TTGAAGAGT 1680
 TCTCAAAATC TGGGCCAAGA ATGATGCTA GGTCCATAAG CTAATTTGTC TGGCCTTGCC 1740
 ATTTACGTAA GCCAAGAAA GTCACTCATG AGTAACATAT AGAAAACGTT CAGACCCATC 1800
 50 CTGTTAGTAT GTCAAAATCAA CTAAGACTGG CAGGGTATTA ACTCATTCCT AGGTGACATG 1860
 GATAAAGAGC CCCATTAATT TCACAGTGCC AGCCTCTACC TAAGGAAGCC CTAGAACTTG 1920
 GAACCAAGTT CCTGTGAGGG AACTGCTGAC AGTTTCAATG CTGACAGTGT GAGCCAATGC 1980
 CTCATAGTGT AAAGTGAAG AAAAATAGTT GCTTTTAAAA ATGTGAGCAA GAAGGCTGCT 2040
 55 CTCATCTTAA CAAAGCAAAA AAAAATGCTT TAATTCAAT TAATAATCAT GATACTAAAA 2100
 AAAAAAAA

SEQ ID NO:92 PDV5 Protein sequence

Protein Accession #: NP_057674

60

1 11 21 31 41 51
 MQCQLFRIT SKAVSELNYD YICIKAGTGR PQGTPTIGLV LLVRWAIYB TELQSQPII

SEQ ID NO:93 PEE6 DNA SEQUENCE

Nucleic Acid Accession #: NM_002606

Coding sequence: 61-1842 (underlined sequences correspond to start and stop codons)

65

1 11 21 31 41 51
 70 CGCGGCGGCT GCGCTCGGGA AAGTACAGTA AAAAGTCCGA GTGCAGCCGC CGGGCGCAGG 60
 ATGGGATCCG GCTCTCCAG CTACCGGCC AAGGCCATCT ACCTGGACAT CGATGGACGC 120
 ATTCAAGAG TAATCTTCAG CAAGTACTGC AACTCCAGCG ACATCATGGA CCTGTCTGTC 180
 ATCGCCACCG GCTGCTCGG GAACACGACC ATCTCCCTGC TGACACCGA CGAGCCCATG 240
 75 GTCTCCATCG ACCCCACCAT CCGCGCGAAT TCAGAAAGCA CTCGTACAA AGTGAGACCT 300
 GTGGCCATCA AGCAACTCTC CGCTGGTGTG GAGGACAAGA GAACCAAGC CCGTGGCCAG 360
 TCTGCTGAGA GACCACTGAG GGACAGACGG GTTGTGGGCC TGGAGCAGCC CCGGAGGGAA 420
 GGAGCATTTG AAAGTGGACA GGTAGAGCCC AGGCCACAGG AGGCCACAGG CTGCTACCA 480
 GAAGGACGCG GCATCCCTCC AGAGAGAGAA GAATTAATCC AGAGCGTGCT GGCAGCGGTT 540
 GCAGAGCATG TCTCAAGAGC ATTCAAAATC AATGAAGTGA AAGCTGAAGT TGCAATCAC 600
 80 TTGGCTGTCC TAGAGAAAG CGTGGAAATG GAAGGACTAA AAGTGTTGGA GATTGAGAAA 660

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TGCAAGAGTG ACATTAAGAA GATGAGGGAG GAGCTGGCGG CCAGAAGCAG CAGGACCAAC 720
TGCCCTCTGA AGTACAGTTT TTTGGATAC CACAAGAAGT TGACTCCTCG ACCCGATGTT 780
CCCACTTACC CCAAGTAOCT GCTCTCTCCA GAGACCATCG AGGCCCTGCG GAAGCCGACC 840
TTTGAGCTCT GGCTTTGGGA GCCAATGAG ATGCTGAGCT GCCTGGAGCA CATGTACCAC 900
GACCTCGGGC TGGTCAGGGA CTTCAGCATC AACCTGTCA CCTCAGGAG GTGGCTGTTC 960
TGTGTCCAGG ACAACTACAG AAACAACCCG TTCCACACT TCCGGCACTG CTTCTGCCGTG 1020
GCCAGATGA TGTACAGCAT GGTCTGGCTC TGCACTCTCC AGGAGAAGTT CTCACAAACG 1080
GATATCCTGA TCCTAATGAC AGCGGCCATC TGCCACGATC TGGACCATCC CGGCTACAAAC 1140
AACACGTACC AGATCAATGC CCGCACAGAG CTGGCGGTCC GCTACAATGA CATCTCACCG 1200
CTGGAGAACC ACCACTGCGC CGTGGCCCTC CAGATCCTCG CCGAGCCTGA GTGCAACATC 1260
TTCTCCAAAC TCCACCTGGA TGGGTTCAAG CAGATCCGAC AGGGAATGAT CACATTAATC 1320
TTGGCCACTG ACATGGCAAG ACATGCAGAA ATATTGGATT CTTTCAAAGA GAAATGGAG 1380
AATTTTGA CTACGCAACGA GGAGCACATG ACCCTGCTGA AGATGATTTT GATAAAATGC 1440
TGTGATATCT CTAACGAGGT CCGTCCAATG GAAGTCGCAG AGCCTTGGGT GGACTGTMTA 1500
TTAGAGGAAT ATTTTATGCA GAGCGACCGT GAGAAGTCAG AAGGCCCTTC TGTGGCACCG 1560
TTCATGGACC GAGACAAAGT GACCAAGGCC ACAGCCAGA TTGGGTTTCA CAGTTTGTG 1620
CTGATCCCAA TGTTTGAAAC AGTGACCAAG CTCTTCCCA TGGTTGAGGA GATCATGCTG 1680
CAGCCACTTT GCGAATCCCG AGATCGCTAC GAGGAGCTGA AGCGGATAGA TGACGCCATG 1740
AAGAGTTTAC AGAAGAAGAC TGACAGCTTG ACGTCTGGGG CCAACGAGAA GTCCAGAGAG 1800
AGAAGCAGAG ATGTGAAAAA CAGTGAAGGA GACTGTGCTT GAGGAAAGCG GGGGCCCTGG 1860
CTGCACTTCT GGACGGGCTG GCGGAGCTGC CCGGATCCT TGTGCAGGGA AGAGCTGCC 1920
TGGGCACTG GCACCAACAG ACCATGTTTT CTAAGAACCA TTTTGTTCAC TGATACAAA 1980
AAAAAAAAA A

SEQ ID NO:94 PEE6 Protein sequence
Protein Accession #: NP_002597

1 11 21 31 41 51
1
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HGSGSSSYRP KATYLDIDGR IQKVIKSKYC NSSDIDMLFC IATGLPRNTT ISLLTTDDAM 60
VSIDTFMFPAN SERTPYKVRP VALKQLSAGV EDKRTTTRGQ SAERPLRDRR VVGLEQPRRE 120
GAFESGQVEP RREPQGCYQ EGQRIPPERE ELIQSVLAQV ABQPSRAFKI NELKAEVANH 180
LAVLEKRVEL EQLKVVELEK CKSDIKKMR ELLAARSSRTN CPCKYSFLDN HKKLTPRRDV 240
PTYPKYLSP ETIEALRKPT FDVWLWEPNE MSLCLEBMYH DLGLVRDFSI NPVTLRRLWP 300
CVHDYRNNP FHNFRHPCPV AQMYSMVWL CSLQEKPSQT DILILMTAAI CHDLDPGYN 360
NTYQINARTE LAVRYNDISP LENHCAVAF QILAEPCNI FSNIPDFGPK QIRQGMITLI 420
LATMARRAE IDMSFKERME NFDYSNEEHM TLLKMLIKC CDISNEVRPM EVAEPWVDCL 480
LEEYFMQSDR EXSEGLPVAP FMDRDKVTKA TAQIGFIKPV LIPMFETVK LPMFVEEIML 540
QPLWESDRY EBLKRIIDAM KELQKTDLS TSGATEKRE RSRDVKNSEG DCA

SEQ ID NO:95 PEG4 DNA SEQUENCE

Nucleic Acid Accession #: none
Coding sequence: 41-559 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
1
45
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CAGTCACAGG CGAGAGCCYT GGGATGCACC GGCCAGAGGC ATGCTGCTGC TGCTCACGCT 60
TGCCCTCCTG GGGGGCCCCA CCTGGGCAGG GAAGATGTAT GGCCCTGGAG GAGGCAAGTA 120
TTTCAGCACC ACTGAAGACT ACGACCATGA AATCACAGGG CTGGCGGTGT CTGTAGGTCT 180
TCTCTGGTGG AAAAGTGTCC AGGTGAACT TGGAGACTCC TGGGACGTGA AACTGGGAGC 240
CTTAGGTGGG AATACCCAGG AAGTCACCTT CGAGCCAGGC GAATACATCA CAAAAGTCTT 300
TGTGCCCTTC CAAGCTTTCC TCCGGGGTAT GGTATGTATC ACCAGCAAGG ACCGCTATTT 360
CTAATTTGGG AAGCTTGATG GCCAGATCTC CTCTGCCCTAC CCCAGCCAAG AGGGGCGAGT 420
GCTGTGGGGC ATCTATGGCC AGTATCAACT CCTTGGCATC AAGAGCATTG GCTTTGAATG 480
GAATATCCCA CTAGAGGAGC CGACCACTGA GCCACCACTT AATCTCACAT ACTCAGCAAA 540
CTCACCCGTG GGTCTGCTAGG GTGGGGTATG GGGCCATCCG AGCTGAGGCC ATCTGTGTGG 600
TGGTGGCTGA TGTACTTGA GTAACTGAGT CCGGACGCTG AATCTGAATC CACCAATAAA 660
TAAAGCTTCT GCAGAAATCAG TGAATAAAAAA A

SEQ ID NO:96 PEG4 Protein sequence
Protein Accession #: FGENSEH predicted

1 11 21 31 41 51
1
65
70
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MLLLLTALL GGPTWAGKMY GPGGGKYFST TEDYDHEITG LRVSVGLLLV KSVQVKLGDS 60
WDVKLGALGG NTQEVTLQPG EYITKVPVAF QAFLRGVMYH TSKDRYFYFG KLDGQISSAY 120
PSQEQVILVG IYQYQLLGI KSIGFEMNYP LEEPTTEPPV NLTYANSFV GR

SEQ ID NO:97 PEL9 DNA SEQUENCE

Nucleic Acid Accession #: NM_006953
Coding sequence: 33-898 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
1
75
80

CCGTTCCCGG CTCTGGCGGC TCCTCCCGGG CGATGCTTCC GCTCTGGGCC CTGCTGGCCC 60
TGGGCTGCTT GGGGTTGGGC TCGGCTGTGA ACGTCAGCC CCACTGGGCC AGTGTGACTT 120
TGCCACACAA CAACCCACCA CTTACCACTG TGGCCTTGGG AAGGCTCTC TGCAATGTTG 180
ACAGCAAAAG GGCCTCACT GGCACCCAGG AGGTCTACT GTATGTCTG GTGCACTCAG 240
CCATTTCCAG GAATGCCTCA GTGCAAGACA GCACCAACAC CCACTGGGC TCAACGTTCC 300

TACAAACAGA GGGTGGGAGG ACAGGTCCCT ACAAAGCTGT GGCCTTGTAC CTGATCCCTT 360
 GCAGTGACCT GCCAGGCTG GATGCCATG GGGATGTGTC CAAGGCTCA CAGATCCTGA 420
 ATGCTTACTT GGTGAGGGTG GGTGCCAAGC GGACCTGCCT GTGGGATCCC AACTTCCAGG 480
 GCCTCTGTAA CGCACCCTG TCGGCAGCCA CGGAGTACAG GTTCAAGTAT GTCTTGGTCA 540
 ATATGTCCAC GGGCTGTGTA GAGGACCAGA CCTGTGGTTC GGACCCATC CGCACCAACC 600
 AGTCAACCCC ATACTCGACC ATCGACACGT GGCACGGCCG CGCGAGCGGA GGCATGATCG 660
 TCATCACTTC CATCTGAGG TCCCTGCGCT TCTTCTACT TGTGGGTTT GCTGGCGCCA 720
 TTGCTCTGAG CCTCTGTGAC ATGGGGAATT CTGATGGGGA AACGACTCAC GACTCCCAA 780
 TCACTCAGGA GCTCTGTCC AGTGTGCTGG GGGCTCCGGA GTCTTCTAC ACCTCCGTA 840
 ACCGGGGGCC GCCACTGGAC AGGGCTGAGG TGTATTCCAG CAAGCTCCAA GACTGAGCCC 900
 AGCACCAACC CTGGGCAGCA GCATCTCTCT CTCTGGCTTT GCCCAGGCC CTGCAGGGT 960
 GGTGTGTACA CCTGACTTC AGGGAAGGTG AAACAGGCTT TGTCCTCCA ACTGCAGGAA 1020
 AACCTTAAT AAAATCTTCT GATGAGTTCT AAAAAAAAA

SEQ ID NO:98 PEL9 Protein sequence
 Protein Accession #: NP_008884

1 11 21 31 41 51
 MPPLMALLAL GCLRFGSAVN LQPLASVTF ATNNPTLITV ALEKPLCMFD SKEALTGTHER 60
 VLYLVLDISA IERNASVQDS TNYPLGSTFL QTEGGRTGPF KAVAFDLIPC SDLPFLDAIG 120
 DVSKASQLLN AYLVRVGANG TGLWDPNFG LCNAPLSAAT EYRFKYVLVN MSTGLVEDQT 180
 LMSDFIRNQ LTFYSTIDTW PGRRSGGHIV ITSILGSLEF FLVVGFGAI ALSLVDMGSS 240
 DGETHDSQI TQEAVPKSLG ASESSTSVN RGPPLDRAEV YSKLQD

SEQ ID NO:99 PEN1 DNA SEQUENCE

Nucleic Acid Accession #: NM_012391

Coding sequence: 416-1423 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 GTCTGACTTC CTCCAGCAC ATTCCTGCAC TCTGCCGTGT CCACACTGCC CCACAGACCC 60
 AGTCTCTCAA GCTCTGCTGC AGCTCCCTGC AAGCCCTCA GGTGGGCTT TGCCACGGTG 120
 CCAGCAGGCA GCCCTGGGCT GGGGGTAGGG GACTCCCTAC AGGCACGCAG CCTGAGACC 180
 TCAGAGGGCC ACCCTTTGAG GGTGGCCAGG CCCCAGTGG CCAACTGAG TGCTGCCCTT 240
 GCCACACGCC CTGCTGGGCG CTGGTTCCGC TGGCCCCCA GATGCTTGGC TGAGACAGC 300
 CAGTGGCTTC AGCTGCCAC ACCTCTTCCC GGCCTCGAA GTTGGCACTG CAGCAGACAG 360
 CTCCCTGGGC ACCAGGCGAG TAACAGACAC AGCCGCGAGC CCAACAGCA GCGGCATGG 420
 CAGCGCCAGC CCGGCTCTGA GCAGCGTATC CCCCAGCCAC CTCTGCTGTC CCCCCGACAC 480
 GGTGTCCGGG ACAGGCTTGG AGAAGGCGGC AGCGGGGCA GTGGGTCTCG AGAGACGGGA 540
 CTGGAGTCCC AGTCCACCCG CCACGCCCGA GCAGGCGCTG TCGCTTCTT ACCTCTCTTA 600
 CTTTGACATG CTGTACCTTG AGGACAGCAG CTGGGCGACC AAGGCCCTG GGGCCAGCAG 660
 TCGGAGGAGG CACCTGAGG AGCCTGAGCA GTGCCCGTTC ATTGACAGCC AAGCCCGAGC 720
 GGGCAGCCTG GACTTGTGTC CCGGCGGGCT GACCTTGGAG GAGCACTGCC TGGAGCAGGT 780
 GCAGTCCATG GTGGTGGGCG AAGTCTCTCA GGACATCGAG ACGGCTTCA AGCTGCTCAA 840
 CATCACCGCA GATCCCATGG ACTGGAGCCC CAGCAATGTG CAGAAGTGGC TCTGTGGAC 900
 AGAGACCAA TACCGGCTGC CCCCAGTGG CAGGCGCTTC CAGGAGCTGG CCGGCAAGGA 960
 GCTGTGGGCC AAGTGGGAGG AGCAGTCCG CCAGCGCTCG CCGCTGGGTG GGGATGTGCT 1020
 GCACGCCAC CTGGACATCT GGAAGTCAGC GGCCTGGATG AAAGAGCGGA CTTCACCTGG 1080
 GGCGATTCT TACTGTGCTT CGACCACTGA GGAGAGCTGG ACCGACAGCG AGGTGGACTC 1140
 ATCATGCTCC GGGCAGCCCA TCCACTGTG GCAGTTCTTC AAGGAGTTGC TACTCAAGCC 1200
 CCACAGCTAT GGGCCCTTCA TTAGGTGGCT CAACAAGGAG AAGGGCATCT TCAAAATTGA 1260
 GGACTCAGCG CAGGTGGGCC GGCCTGTGGG CATCCGCAAG AACCTGCCG CCATGAACCTA 1320
 CGACAAGCTG AGCCCTCCA TCGCCAGTA TTACAAGAG GGCATCATCC GGAAGCCAGA 1380
 CATCTCCAG CGCTCTGCTT ACCAGTCTGT GCACCCATC TGAATGCCCT GCCCAGGGCC 1440
 TGAAACCCG CCTCAGGGGC CTCTCTCTG CTTGCCCTGC CTCAGCCAGG CCTGAGATG 1500
 GGGGAAACG GGCAGTCTGC TCTGCTGCTC TGACCTTCCA GAGCCCAAGG TCAGGGAGGG 1560
 GCAACCAACT GCGCCAGGGG GATATGGGTC CTCTGGGGCC TTGGGACCA TGGGGCAGGG 1620
 GTGCTTCTC CTCAGGCCCA GCTGCTCCCT TGGAGGACAG AGGGAGACAG GGTGCTCCC 1680
 AACACCTGCT CTCTGACCCC AGCATTTCCA GAGCAGAGCC TACAGAAGGG CAGTGACTCG 1740
 ACAAGGCCA CAGGCAGTCC AGGCTCTCT CTGCTCCATC CCGCTGCCCT CCATTTGCA 1800
 CCACACCTGG CATGCTGAGC GGAGACATCT GCACCCCTGA GTTGGGCAGC CAGGAGTGCC 1860
 CCGGGAATG GATAATAAAG ATACTAGAGA ACTG

SEQ ID NO:100 PEN1 Protein sequence
 Protein Accession #: NP_036523

1 11 21 31 41 51
 HGSASPLGSS VSPSHLLLP DTVSRTGLEK AAAGAVGLER RDWSPSPPAT FEQGLSAPYL 60
 SYFDMLYPED SSWAAKAPGA SSREEPPEEP EQCPVIDSQA PAGSLDLVPG GLTLEHSL 120
 QVQSVVGEV LKDIETACKL LINITADPMW SPENVKWLL WTEHQVRLFP MGKAPQELAG 180
 KELCAMSEBQ FRQRFPLGGD VLHAHLDIWK SAAMKERTS PGAIHYCAST SEBSWTDSEV 240
 DSSCSQPIH LMQFLKELL KPHSYGRPIR WLAKKEGIFK IEDSAQVARL WGRKNRPAM 300
 NYDKLSRSIR QYYKKGIIRK FDISQLVYQ FVHPH

SEQ ID NO:101 PEN3 DNA SEQUENCE

Nucleic Acid Accession #: NM_000742

Coding sequence: 555-2144 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
GAGAGAACAG CGTGAGCCTG TGTGCTTGTG TGTGAGCCCT TCATCCCTTC CTGGGGCCAG 60
GCTTGGGTTT CACCTGCAGA ATCGCTTGTG CTGGGCTGCC TGGGCTGTCC TCAGTGGCAC 120
CTGCATGAAG CCGTCTCTGC TGGCAGAGCT GGACAGCCCC AGGAAAACCC ACCTCTCTGC 180
AGAGCTTGCC CAGCTGTCCC CGGGAAGCCA AATGCTCTCT ATGTAAGTCT TCTGCTCGAC 240
GGGGTGTCTC CTAAACCTTC ACTCTTCAGC CTCTGTTTGA CCATGAAATG AAGTGACTGA 300
GCTCTATTCT GTACCTGCCA CTCTATTCTT GGGGTGACTT TTGTGAGCTG CCGAGAATCT 360
CCAAGCCAGG CTGGTCTCTT GCATCTTTTC AATGACCTGT TTCTCTGTGT AACCAAGGTT 420
TCGGTGGTGA GAGGAAGCCT CGCAGAATCC AGCAGAATCC TCACAGAAATC CAGCAGCAGC 480
TCTGCTGGGG ACATGGTCCA TGGTGCACCC CACAGCAAAAG CCGTGAACCTG ACCTCTCTGAT 540
GCTCAGGAGA AGCCATGGGC CCGTCTCTGT CTGTGTTCCCT GTCCCTCACA AAGCTCAGCC 600
TGTGGTGGCT CTTCTCTGACC CCAGCAGGTG GAGAGGAAGC TAAGCGCCCA CCGTCCAGGG 660
CTCTCGGAGA CCGACTCTCC TCTCCAGCTC CCAGCGGATT GCGCCAGGGA GGCCTGCATA 720
CCGAGACTCT CGAACCGCTC TTCAAACACC TCTTCCGGGG CTACAACCGC TGGGCGCGCC 780
CGGTGCCCAA CACTTCAGAC GTGGTGTATG TGGGCTTTGG ACTGTCCATC GCTCAGCTCA 840
TCGATGTGGA TGAGAAGAAC CAAATGATGA CCACCAAGCT CTGGCTAAAA CAGGAGTGGGA 900
GGGACTACAA ACTTCCGCTGG AACCCGCTG ATTTTGGCAA CATCACATCT CTCAGGTTCC 960
CTTCTGAGAT GATCTGGATC CCGGACATTC TTCTCTACAA CAATGCAGAT GGGGAGTTTG 1020
CAGTGAACCA CAGTGAACCA GCGCACTCTT TCTCCACGGG CACTGTGACAT TGGGTGCCCC 1080
CGGCCATCTA CAAGAGCTCC TGCAGCATCG ACGTCACTTC CTGCCCTTC GACCAGCAGA 1140
ACTGCAAGAT GAGTCTTGGC TCTTGGACTT ATGACAAGGC CAGATCCGAC CTGGAGCAGA 1200
TGGAGCAGAT TGTGAGACTG AAGGACTACT GGGAGAGCGG CGAGTGGGCC ATCGTCAATG 1260
CCAGCGGCAC CTACACAGC AAGAAGTACG ACTGCTGCGC CGAGATCTAC CCGCAGCTCA 1320
CTTACGCTCT CGTCAATCCG CGGCTGCGGC TCTTCTACAC CATCAACCTC ATCATCCCT 1380
GCGTGTCTAT CTCTGCTCTC ACTGTGCTGG TCTTCTACCT GCGCTCCGAC TGCAGCGAGA 1440
AGATCAAGCT GTGCAATTCG GTGCTGCTGT CACTCACCGT CTTCCTGCTG CTCATCACTG 1500
AGATCATCCC GTCCACTCG CTGGTCAATC CGCTCATCGG CGAGTACCTG CTGTTCACCA 1560
TGATCTTGT CACCTCTGCC ATCGTCAATC CCGTCTCTGT GCTCAATGTC CACCAACGCT 1620
CCCGCAGCAC CAGCACAAG CCGCACTGGG TGGGGGGGGC CCTTCTGGGC TGTGTGCCCC 1680
GGTGGCTTCT GATGAACCGG CCGCCACAC CCGTGGAGCT CTGCCACCCC CTACGCTCTA 1740
AGCTCAGCCC CTCTTATCAC TGGCTGGAGA GCAACGTGGA TGGCAGGAG AGGGAGGTGG 1800
TGGTGGAGA TGGGACACGA TGGGCATGTG CAGGTCAATG GCGCCCTCT GTGGGCACCC 1860
TCTGAGGACA CGGCCACCTG CACTCTGGGG CCTCAGGTCC CAAGGCTGAG GCTCTGCTGC 1920
AGGAGGGTGA CTGTCTGCTA TCACCCACA TGCAGAAGGC ACTGGAAGGT GTGCACTACA 1980
TTGCCGACCA CTGCGGTCT GAGGATGCTG ACTCTTCGGT GAAGGAGGAC TGGAAGTATG 2040
TTGCCATGGT CATCGACAGG ATCTTCTCTT GCGTGTATTAT CATCGTCTGC TTCTGCGGGA 2100
CCATCGGCTT CTCTCTGCTT CCGTCTCTAG CTGGAATGAT CTGACTGCAC CTCCCTCGAG 2160
CTGGCTCCCA GGGCAAAAGG GAGGGTCTCT GATGTGTGAA GGGCTTTGAA CAATGTTTAG 2220
ATTTGGAGCT CAGCCCAAG TGGCAGGGAG AACAGCCAGG TGAAGTGGGA GGTGGAGAG 2280
CCAGGTGAGG TCTCTCTAAG TCAGGCTGGG GTTGAAGTTT GAGTCTGTCT CGAGTTTCCA 2340
GGGTGCTGAG TGTATGCTG CAGCAGGGGA GTAAATAGGG CTCTTCCGGA AGGGAGGGA 2400
GCGGAGGACA GCGCTGCACC TGAATGGAG GTACAGGGAG ATCTTCCCTA CCGGGGAGG 2460
ATGGATGTTT GGATACAGGT GCGTGGGCTA TTCCATCCAT CTGGAAGCAC ATTTAGAGCT 2520
CCAGCTTCTT CTTGACGCTT ATTCCTCTCC TTCTTGTCTG CAAATAGGCT GTGACCCAGC 2580
CGGCCCCAG GAGTCTTGGC AGAGCTGAGA GGCATGGCT GCAGGGGCTC CATATGTCCC 2640
TACCGGTGCA CGAGGCAAC AAGA

SEQ ID NO:102 PENS Protein sequence
Protein Accession #: NP_000733

1 11 21 31 41 51
MGFSCFVFLS FTKLSLWMLL LTPAGGEEK RPPFRAPGDP LSSPSPTALP QGGSHTETED 60
RLFKLHFRGY NRKAREVPT SDVIVVRFLG SIAQLIDVDE KNGMTTNVW LKQWSDYKL 120
RWNPADPQNI TSLRVFSEMI WIPDIVLYNN ADGEPAVTHM TKAHLESTGT VHWVPPAIYK 180
SSCSIDVTFP PFDQONCKMK FGSWTYDKAK IDLEQMEQTV DLKDYWESGE WAIVNATQTY 240
NSRKYDCCAE IYEDVTYAPV IRRPLPFTYI NLIIICLLIS CLTVLVFVLP SDCGKITLC 300
ISVLLSLTVF LLLITEIIPS TSLVIPLIGE YLLFTMIFVT LSVITVTVFL NVHRSPTSTH 360
TMFHWVRGAL LGCVRMLLM NRPPFVELC HPLRLKLSFS YEWLESNVDA EREVVVEEE 420
DRWACAGHVA PSVGTLCSHG HLESGASGEK AEALLQEGEL LLSFEMQKAL EGVHYIADHL 480
RSEDADSSVK EDWKYVAMVI DRIFLWLFH VCFLTGTLGF LPFFLAGMI

SEQ ID NO:103 PELU4 DNA SEQUENCE

Nucleic Acid Accession #: NM_018670
Coding sequence: 87-693 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
CACGAGGCTG GAAGGGGCCA CTTACACACT CGGGCTCGGC ATAAAGCGGC GCGCGCGCCG 60
CGGCCCCAG ACGCGCCGCC GCTGCCATGG CCCAGCCCTT GTGCCGCGCC CTCTCCGAGT 120
CCTGGATGCT CTCTGCGGGC TGGGGCCCAA CTGCGCGGCC GCGCGCCCTC GACAGGAGCT 180
GCGCGCGCTC CCTGCTCTCG TCCCCAGACT CATGGGCGAG CACCCAGGCC GACAGCCCGC 240
TGGCGAGCCC GCGCGCGCCA GGCACCTTCC GGGACCCCGG CCGCCCTTCC GTAGGTAGGC 300
GCGCGCGCGC CAGCAGCCGC CTGGGCGAGG GGCAGAGCCA GAGCGCCAGT GAGCGGAGGA 360
AACTGGCAT GCGCACGCTG GCGCGCGGCC TGCAGGAGCT GCGCGCGCTT CTACCGCCGT 420
CCGTGGCGCC CCGCGGCGAG AGCTGAGCCA AGATCGAGAC GCTGCGCGCT GCTATCCGCT 480
ATATCGGACA CTTCTCGGCC GTGCTAGGCC TCAGCGAGGA GAGTCTCCAG CCGCGGTGCC 540
GGCAGCGCGG TGACGCGGGG TCCCTCGGG GCTGCGCGCT GTGCCCGAC GACTGCGCCG 600
GCGAGTGA GACACGGACG CAGGCTGAGG GCGAGGGCCA GGGGCGCGGG CTGGGCGCTG 660

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10
TATCCGCCGT CCGCGCCGGG GCGTCTGGG GATCCCGCC TGCCTGCCCC GGAGCCCGAG 720
CTGCACCCGA GCCCGCCGAC CCGCTCGCG TGTTCGCCGA GCGCGCGTGC CCGGAAGGGC 780
AGGCGATGGA GCCAAGCCCA CCGTCCCGC TCCTTCGGG CGACGTGCTG GCTCTGTGG 840
AGACCTGGAT GCCCTCTCG CCTCTGGAGT GGCTGCCCTGA GGAGCCCAAG TGACAAGGGA 900
CAACTGACGC CGTCTCTGTG AGCACCGAGG CTTTTTGGCC TCAGCACCTT CGAAGTGGTT 960
CCTTGGCAGA CTGCTTTTCC TGAAGAGGG CACGGGCGAT CCCGACGGGG GCATTCTCTC 1020
GGGTGAGAGC CGTCCCGACC GCGCGCGCCC TTCTCAGCCC CTCCCTCCAT GGAGGGAGCC 1080
ATAGGGCTAG ACACCTTTAG GCAAGCAGGA GCGCTCGCCT AATGTGAATT TATTATTATT 1140
TGAATAAACT GTACTGGTGT CAAAAA AAAA A

SEQ ID NO:104 PEU4 Protein sequence
Protein Accession #: NP_061140

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1 11 21 31 41 51
MAQFLCPPLS ESWMLSAAWG PTRRPPPSDK DCGRLSVSP DSWGSTPADS FVASPARPGT 60
LRDPFRAPSVG RRGARSRSLG SGQRQSASER EKLRLMRLAR ALLELRRLFLP PSVAPAGQSL 120
TKIETLRLAI KYIHLASAVL GLSEESLQRR CRQRDAGSP RGCPLCPDDC PAQMOTRTQA 180
EGQGQGLGLG LVSAVRAGAS WGSPPACPGA RAAPEPRDPP ALFAEAACFE GQAMEPSPFS 240
PLLPGDVLAL LETWMLPSPL EWLPEEPK

SEQ ID NO:105 PEU5 DNA SEQUENCE

Nucleic Acid Accession #: NM_017636

Coding sequence: 324-3374 (underlined sequences correspond to start and stop codons)

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1 11 21 31 41 51
CCACGGAGAA GCCCACCGAT GCCTACGGAG AGCTGGACTT CACGGGGGCC GCGCCCAAGC 60
ACAGCAATTT CCGCCGGCTC TCTGACCGAA CGGATCCAGC TGCACTTTAT AGTCTGGTCA 120
CAGCGACATG GGGCTTCOGT GCCCGGAACC TGGTGGTGTG AGTCTGGGGG GGATCGGGGG 180
GCCCGCTGCT CCAGACCTGG CTGCAGGACC TGCTGCGTGG TGGGCTGGTG CCGGCTGCCC 240
AGAGCACAGG AGCCTGGATT GTCACTGGGG GTCTGCACAC GGGCATCGGC CGGCATGTTG 300
GTGTGGCTGT ACGGGACCAT CAGATGGCCA GCACCTGGGG CACCAAGGTG GTGGCCATGG 360
GTGTGGCCCC CTGGGGTGTG GTCCGGAAAT GAGACACCTT CATCAACCCC AAGGGCTGGT 420
TCCCTGCGAG GTACCGGTGG CGCGGTGACC CGAGGAGCGG GGTCCAATTT CCCCTGGACT 480
ACAACCTACT GGCCTTCTTC CTGGTGGAGC ACGGCACACA CGGCTGCGTG GGGGGCGAGA 540
ACCGCTTCGG CTGCGGCTTG GAGTCTTACA TCTCACAGCA GAAGACGGGC GTGGGAGGGA 600
CTGGAATTGA CATCCCTGTC CTGCTCTCTC TGATTGATGG TGATGAGAAG ATGTTGACGC 660
GAATAGAGAA CGCCACCCAG GCTCAGCTCC CATGTCTCCT CGTGGCTGGC TCAGGGGGAG 720
CTGCGGACTG CTGGGGGAG ACCCTGGAAG ACACCTTGGC CCCAGGGAGT GGGGGAGCCA 780
GCCAAGCGGA AGCCCGAGAT CGAATCAGGC GTTCTTTTCC CAAAGGGGAC CTTGAGGTCC 840
TGCAGGCCCA GGTGGAGAGG ATTATGACCC GGAAGGAGCT CCGTACAGTC TATTCTTTCTG 900
AGGATGCTGC TAGGGAATTC GAGACCATAG TTTTGAAGGC CCTTGTGAAG GCCTGTGGGA 960
GCTCGGAGGC CTCAGCTTAC CTGGATGAGC TGCGTTTGGC TGTGGCTTGG AACCGCGTGG 1020
ACATTGCGCA GATGAACTTC TTTGGGGGG ACATCCAAAT GCGGTCTTTC CATCTCGAAG 1080
CTTCCCTCAT GAGCGCCCTG CTGAATGACC GGCCTGAGTT CGTGGCTTGG CTCATTTCCTC 1140
ACGGCTTCAG CCGGGCCAC TTCTTGACCC CGATGCGCCT GCGCCAACTC TACAGCGCGG 1200
CGCCCTCCAA CTGCTTCACT CGCAACCTTT TGGACCAAGC GTCCACAGC GCAGGACCCA 1260
AAGCCCCAGC CTTAAAGGG GAGAGTGGG AGCTCCGGCC CCGTACAGTG GGGCATGTGC 1320
TGAGGATGAG CCGGGGAGG ATGTGCGGCG CGAGGTACCC CTCGGGGGCC GCCTGGGACC 1380
CTCACCCAGG CCAGGGCTTC GGGGAGAGCA TGTATCTGCT CTCGGACAG GCCACCTGCG 1440
CGCTCTGCTG GATGCTGTC CTGCGGCGAG CCCCTGGAG CGACCTGCTT CTTTGGGCAC 1500
TGTGTCTGAA CAGGGCACAG ATGGCCATGT ACTTCTGGGA GATGGGTTC AATGCAATTT 1560
CCTCAGCTCT TGGGGCTGTT TTGCTGCTCC GGGTGTATGG ACGCCCTGAG CCGTACGCTG 1620
AGGAGGCAGC ACGGAGGAAA GACCTGGCGT TCAAGTTTGA GGGGATGGGC GTTGACCTCT 1680
TTGGCGAGTG CTATCGCAGC AGTGAAGTGA GGGCTGCCCC CCGCTCTCTC CGTGGCTGCC 1740
CGCTCTGGGG GATGCCACTT TGCCTCCAGC TGGCCATGCA AGCTGACGCC CGTGGCTTCT 1800
TTGCCCAGGA TGGGTACAG TCTCTGCTGA CACAGAAGTG GTGGGGAGAT ATGGCCAGCA 1860
CTACACCCAT CTGGGCGCTG GTTCTCGCTT TCTTTTGGCC TCACCTCATC TACACCGGCC 1920
TCATCAGCTT CAGGAAATCA GAAGAGGAGC CCACACGGGA GGAGCTAGAG TTTGACATGG 1980
ATAGTGTCTT TAATGGGGAA GGGCCTGTGG GGACGGCGGA CCCAGCCGAG AAGACGCCGC 2040
TGGGGGTCCC GGGCCAGTCG GGGCGTCCGG GTTGTGCGGG GGGCGCTGC GGGGGCGGCC 2100
GGTGCTTACG CCGCTGTGTC CACTTCTGGG GCGCGCCGGT GACCATCTTC ATGGGCAAGC 2160
TGGTCAGCTA CCGTCTGTTT TTGCTGCTTT TCTCGCGGGT GCTGCTCGTG GATTTCACGC 2220
CGGCGCCGCG CCGCTCCCTG GAGCTGCTGC TCTATTCTG GCGTTTCAGC CTGCTGTGGG 2280
AGGAACGTGG CCAGGGCCTG AGCGGAGGCG GGGGCGAGCT CCGCAGCGGG GGGCCCGGCC 2340
CTGGCCATGC CTCAGTGAGC CAGCGCCTGC GCCTCTACCT CCGCGACAGC TGGAAACGAT 2400
GCGACCTAGT GCGCTTCAAC TGCTTCTCTC TGGGCGTGGG CTGCGGCTG ACCCGGGGTT 2460
TGTAACCACT GGGCGGCACT GTCTCTGCA TCGACTTCAT GGTTTTCAAG GTGCGGCTGC 2520
TTCACTCTT CAGGGTCAAC AAACAGCTGG GGGCCAAAGT CGTCACTCGT AGCAAGATGA 2580
TGAAGGAGCT GTTCTTCTTC CTCTTCTTCC TCGGCGTGTG GCTGGTAGCC TATGGCGTGG 2640
CCACGGAGGG GCTCTGAGG CCAAGGGACA GTGACTTCCC AAGTATCTCT GCGCGGCTCT 2700
TCTACCTGTC CTACTGCAAG ATCTTGGGGC AGATTCCCA GAGGACATG GACGTGGGCC 2760
TCATGAGACA CAGCACTCG TCGTGGAGC CCGGCTTCTG GGCACACCTT CCGGGGCCCC 2820
AGCGGGCCAC CTGGCTCTCC CAGTATGCCA ACTGGCTGGT GGTGCTGCTC CTGCTCATCT 2880
TCTGCTGCTG GGCCACATC CTGCTGTGTA ACTTGTCTCAT TGCCATGTTT AGTTACACAT 2940
TCGGCAAGT ACAGGGCAAC AGCGATCTCT ACTGGAAGGC GCAGCGTTAC GCGCTCATCC 3000
GGGAATTTCA CTCTGGGCC GCGCTGGCCC GCGCTTTTAT CGTCACTTCC CACTTGGGCC 3060
TCTGCTCAG GCAATGTGC AGGGAGCCCC GGAGCCCCCA GCGCTCTTCC CCGGCCCTCG 3120
AGCATTTCCG GGTTTACCTT TCTAAGGAAG CCGAGCGGAA GCTGTAAAG TGGGAATCGG 3180

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TGCATAAGGA  GAACTTTCTG  CTGGCACGCG  CTAGGGACAA  GCGGGAGAGC  GACTCCGAGC  3240
GTCTGGAGCG  CACGTCCGAG  AAGGTGGACT  TGGCACTGAA  ACAGCTGGGA  CACATCCGCG  3300
AGTACGAACA  GCGCCTGAAA  GTGCTGGAGC  GGGAGGTCCA  GCAOTGTAGC  CGCGTCTCTG  3360
GGTGGGTGAC  GTAGGCGGTT  AGCAGCTCTG  CCATGTTGCC  CTCAGGTGGG  CCGCCACCCC  3420
TTGACCTGCA  TGGGTCCAAA  GAGTGAGCCA  TGCTGGCGGA  TTTTAAGGAG  AAGCCCCAC  3480
AGGGGATTTT  GCTCTTAGAG  TAAGGCTCAT  GTGGGCTCG  GCGCCCGCAC  CTGGTGGCCT  3540
TGCTCTGAG  GTAGGCGCCA  TGTCATCTG  GGCCACTGTC  AGGACCACT  TTGGGAGTGT  3600
CATCCTTACA  AACCACAGCA  TGCCCGGCTC  CTCACAGAAC  CAGTCCAGC  CTGGGAGGAT  3660
CAAGGCTCG  ATCCCGGGCC  GTTATCCATC  TGGAGGCTGC  AGGGTCTCTG  GGGTAACAGG  3720
GACCACAGAC  CCTCACACC  TCACAGATTC  CTCACACTGG  GGAATAAAG  CCATTTCAGA  3780
GAAAAA      AAAAAA      AAAAAA

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SEQ ID NO:106 PEU5 Protein sequence

Protein Accession #: NP_060106

15
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30
35

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1      11      21      31      41      51
|      |      |      |      |      |
MASTGGTKVV  AMGVAFWGVV  RNRDTLINPK  GSFPARYRWR  GDPEDGVQFF  LDYNYSAFFL  60
VDDGTHCCLG  GENRFLRLLE  SYISQKRTGV  GGTGIDIPVL  LLLIDGDERM  LTRINATQA  120
QLPCLLVAGS  GGAADCLAET  LEDTLAPGSG  GARQGEARDR  IRRFFPKGDL  EVLQAQVERI  180
MTRKELLTVV  SSEGSGEEFE  TIVLKALVKA  CGSSEASAVL  DELRLAVAMN  RVDIAQSELE  240
RGDIQNRSPH  LEASLMDALL  NDRPEFVRLI  ISHGSLGHP  LTFMRLAQLY  SAAPSNSLIR  300
NLLDQASHSA  GTKAPALKGG  AAELRPPDVG  HVLRLMLGKM  CAPRYPSSGA  WDPHPGQGGF  360
ESMYLLSDKA  TSPLSLDAGL  GQAPWSDLL  WALLLNRAQM  AMYFWEMGSN  AVSSALGACL  420
LLRWARLEP  DAEBAARRKD  LAFKFEQMGV  DLPGECYRSS  EVRAARLLLR  RCPLWGDATC  480
LQLAMQADAR  AFFAQDGVQS  LLTQKWMGDM  ASTTPIWALV  LAFFCPPLIY  TRLITFRKSE  540
EPTREZELEF  DMSVINGEG  PVGTADPAEK  TPLGVPRQSG  RPGCCCGRGG  GRCLLRWFH  600
FWGAPVTIFM  GNVVSYLLFL  LLFSRVLLVD  FQPAPPGSL  LLLYFWAFTL  LCEELRQGLS  660
GGGSGLASGG  PGPBASLSQ  RLRLYLADSW  NQCDLVALTC  PLLGVGCRLT  PGLYHLGRTV  720
LCIDFMVFTV  RLLEIFTVNK  QLGFIVIVS  KMKDVFFFL  FFLGVMLVAY  GVATEGLLRP  780
RDSDFPSILR  RVFYRPVLQI  FQGIPOEDMD  VALMEHSNCS  SEGPFWAHP  GAQAGTCVSQ  840
YANWLVLVLL  VIFLLVANIL  LVNLLIAMP  YTPGKVQGSN  DLYWKAQRYR  LIREFHSRPA  900
LAPFFIVISH  LRLLLRQLCR  RPRSPQSSP  ALEHFRVYLS  KEAERKLLTW  ESHVENPLL  960
ARARDKRES  SERLETSQK  VDLALKQLGH  IREYBQRLV  LEREVQCSR  VLGWVT

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SEQ ID NO:107 PEW3 DNA SEQUENCE

Nucleic Acid Accession #: NM_005982

Coding sequence: 276-1130 (underlined sequences correspond to start and stop codons)

40
45
50
55
60
65

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1      11      21      31      41      51
|      |      |      |      |      |
GGTAGCAGCA  TCCACCGGGC  GGGAGGTCCG  AGGCAGCAAG  GCCTTAAAGG  CTACTGAGTG  60
CGCCGGCGGT  TCCGTGTCCA  GAACCTCCCC  TACTCTCTTC  CTTTCTCTTC  CTGGCCGCGC  120
CACGCCAACA  TTCCGACTCC  GGTTTTGCCG  TTGCAAAAGC  CTAAGGAGGA  GGTTAGGAAC  180
AGCCGGCGCC  CCTCTCCCTG  GGCCGCGCGC  CCTGCTCTCT  CGGCTCTGCT  CCTTCCGCGC  240
TGCCCTTGCG  CCGTGCGCC  CGGCAGCGCG  CAGCCATGTC  GATGCTGCGC  TCGTTTGGCT  300
TTACGCAGGA  GCAAGTGGCG  TGCCTGTGCG  AGGTTCGCA  GCAAGGCGGA  AACCTGGAGC  360
GCTTGGCGAG  GTTCTGTGG  TCACTGCGCG  CCTGCGACCA  CCTGCACAAG  AACGAGAGCG  420
TACTCAAGGC  CAAGGCGGTG  GTGCGCTTCC  ACCGCGGCAA  CTTCCGTGAG  CTCTACAAGA  480
TCTCTGAGAG  CCACGAGTTC  TCGCCTCACA  ACCACCCCAA  ACTGCAGCAA  CTGTGGCTGA  540
AGGGGCATTA  CGTGGAGGCC  GAGAAGCTGC  GCGGCCGACC  CCTGGGCGCC  GTGGGCAAT  600
ATCGGGTGGC  CCGAAAATTT  CCACTGCGCG  GCACCATCTG  GGACGGCGAG  GAGACCAGCT  660
ACTGCTTCAA  TGAGAAGTGC  AGGGGTGTCC  TGCGGGAGTG  GTACGGCGAC  AATCCTTACC  720
CATCGCCGCG  TGAGAAGCGG  GAGCTGCGCG  AGGCCACCGG  CCTCACCCAC  ACCCAGGTCA  780
GCAACTGGTT  TAAGAACCGG  AGGCAAGAG  ACCGGGCGCG  GGAGGCCAAG  GAAAGGGAGA  840
ACACCGAAAA  CAATAACTCC  TCCTCCAACA  AGCAGAACCA  ACTCTCTCTC  CTGGAAGGGG  900
GCAAGCCGCT  CATGTCCAG  TCAGAAGAGG  AATTCTCAAC  TCCCAAGAGT  CAGACCCAGA  960
ACTCGGTCTC  TCTGCTGCAG  GGCAATATGG  GCCACGCCAG  GAGCTCAAAC  TATTCTCTCC  1020
CGGGCTTAAC  AGCCTGCGAG  CCCAGTCAAG  GCCTGCAGAC  CCACAGCAT  CAGCTCCAAG  1080
ACTCTCTAGT  CGGCCCTCTC  ACCTCCAGTC  TGGTGGACTT  GGGGTCTTAA  GTGGGGAGGG  1140
ACTGGGCGCT  CGAAGGGATT  CCTGGAGCAG  CAACCACTGC  AGCGACTAGG  GACACTTGTA  1200
AATAGAAATC  AGGAACATTT  TTGCAGCTTG  TTTCTGGAAT  TGTTCGCGCA  TAAAGGAATG  1260
GTGGACTTTC  ACAATATCTC  TTTTAAAAAT  CAAAACCAAC  AGCGATCTCA  AGCTTAATCT  1320
CCTCTCTCT  CCAACTCTTT  CCACTTTTGC  ATTTTCTCTC  CCAATGCAGA  GATCAGGG

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SEQ ID NO:108 PEW3 Protein sequence

Protein Accession #: NP_005973

70
75

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1      11      21      31      41      51
|      |      |      |      |      |
MSMLPSFGPT  QEQVACVCEV  LQQGGNLERL  GRFLWSLPAC  DHLERNESVL  KAKAVVAFHR  60
GNFRELKYL  ESHQPSFPH  FKLQQLMLKA  HYVEAEKLRG  RPLGAVGKYR  VRRKFLPRT  120
IWDGEETSLC  FKEKSRGVLR  EHYAHNPYP  PREKRELAEA  TGLTTTQVSN  WFKNRRQRDR  180
AAEAKERENT  ENNNSSSNKQ  NQLSPLEGGK  FLMSSESEEF  SPPQSPDONS  VLLLQGNMGG  240
ARSSNYSLPG  LTAQSPSEGL  QTHQHQLQDS  LLGPLTSSLV  DLGS

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SEQ ID NO:109 PFJ8 DNA SEQUENCE

Nucleic Acid Accession #: NM_005069

Coding sequence: 57-2060 (underlined sequences correspond to start and stop codons)

80

1 11 21 31 41 51
5 GGGGCTCCGC GGGCCTGGAG CACGGCCGGG TCTAATATGC CCGGAGCCGA GGGCGGATGA 60
AGGAGAAATC CAAGAATGCG GCCAAGACCA GGAGGGAGAA GGAAAATGGC GAGTTTTACG 120
AGCTTGCCAA GCTGCTCCCG CTGCCGTGGG CCATCACTTC GCAGCTGGAC AAAGCGTCCA 180
TCATCCGGCT CACCACGAGC TAAGTGAAGA TGCGCGCCGT CTTCGCCGAA GGTTTAGGAG 240
ACGGGTGGGG ACAGCCGAGC CGCGCCGGGC CCTGGACGG CGTCGCCAAG GAGCTGGGAT 300
CGCACTTGCT GCAGACTTTG GATGGATTGG TTTTGTGGT AGCATCTGAT GGCAAAATCA 360
10 TGTATATATC CGAGACCGCT TCTGTCCATT TAGGCTTATC CCAGGTGGAG CTCACGGGCA 420
ACAGTATTA TGAATACATC CATCCTCTG ACCACGATGA GATGACCGCT GTCTCAACG 480
CCCACGACC GCTGCACCAC CACCTGCTCC AAGAGTATGA GATAGAGAGG TGCTTCTTTC 540
TTGGAATGAA ATGTGTCTTG GCGAAAAGGA ACGCGGGCCT GACCTGCAGC GGATACAAGG 600
TCATCCACTG CAGTGGCTAC TTGAAGATCA GGCAGTATAT GCTGGACATG TCCTGTACG 660
15 ACTOCTCTA CCAGATTGTG GGGCTGTGG CCGTGGGCCA GTGCTGCA CCAGTGCCA 720
TCAACGAGAT CAAGCTGTAC AGTAACATGT TCATGTTTCA GGGCAGCCCT GACCTGAAGC 780
TGATATTCTT GGATTCCAGG GTGACCGAGG TGACGGGTTA CGAGCCGAG GACCTGATCG 840
AGAAGACCTT ATACCATCAC GTGCACGGCT GCGACGTGTT CCACTCCGC TACGCACACC 900
ACCTCTGTT GGTGAAGGGC CAGGTCAACA CCAAGTACTA CCGGTGCTG TCCAAGCGGG 960
20 GGGGTGCGT GTGGGTGCG AGCTACGCCA CCGTGGTGA CAACAGCCGC TGTCCCGGC 1020
CCCCTGCAT CGTGAGTGT AATTATGTAC TCAACGAGAT TGAATACAAG GAACTTCAGC 1080
TGTCCCTGGA GCAGGTGTCC ACTGCCAAGT CCCAGGACTC CTGGAGGACC GCCTGTGCTA 1140
CCTCACAAGA AACTAGGAAA TTAGTGAAGC CCAAAAATAC CAAGATGAAG ACAAAAGCTGA 1200
GAACAAAACC TTACCCCCA CAGCAATACA GCTGTTTCCA AATGGACAAA CTGGAATGCG 1260
25 GCCAGCTCGG AACTGGAGA GCGAGTCCCG CTGCAAGCGC TGCTGCTCCT CCAGAACTGC 1320
AGCCCCACTC AGAAAGCAGT GACCTTCTGT ACAAGCATC CTACAGCCGT CCTTCTCTCT 1380
ACCATACGG ACATTTCCT CTGGAATCTC ACGTCTTCA GAGCAAAAAG CCAATGTTGC 1440
CGGCCAAGTT CCGGCAGGCC CAAGGATCCG CTGTGTAGGT GGCACGCTTT TTCTGTAGCA 1500
CACTGCCAGC CAGCGGTGAA TGCCAGTGGC ATTATGCCAA CCCCCTAGTG CTAGCAGCT 1560
30 CGTCTCCAGC TAAAAATCTC CCAGAGCCAC CGGCGAACAC TGCTAGGCAC AGCTGTGTGC 1620
CAAGCTACGA AGCGCCGCGC GCGCCGCTGC GCAGGTTCGG CGAGGACACC GCGCCCGCGA 1680
GCTTCCGAG CTGCGGCCAC TACCGGAGG AGCCCGCGCT GGGCCCGGCC AAAGCCCGCC 1740
GCCAGGCGC CCGGAGCGG GCGCGCTGG CCGTGGCCCG CGCGGCACCC GAGTGTGCG 1800
35 CGCCCGGAC CCGGAGGCC CCGGCGCGC CGGCGCAGT GCGCTTCTG CTGCTCAACT 1860
AOCACCGCT GCTGGCCCGG CCGGAGCCG TGCGGGGGCG CGCACCCGCC GCCTCCGCC 1920
TGGCTCGC TCOCGGGGC CCGGAGGCG CGACCGCGC GCTGCGGCT CCGCACCCGA 1980
GGCCCGCGC CACTTCCCG CCGGCGCGC CCGTGGCGCA TCACTGGGC GCCTCGGTCA 2040
TCATCAACAA CCGGAGGTGA CCGCTGGCC GCGCGCGCA GGAGCTGGA CCGGCGCTCC 2100
CGGGCTCGC GCGCACCGA GCGCGGCAAA TGCGCACGAC CTACATTAAT TTATGCAGAG 2160
40 ACAGCTGTTT GAATGGACC CCGCGCCGA CTGCGGATT TCCACCGCG AGGCCCGCG 2220
CGCGGTGCC GAGGGCCGAG GAGCGCCCG GTCCGGGCG GTGACCGCCC GCCTCTGTCC 2280
TGCGAGGCC GGTGGGCCG AGTTGCTGG GGTGTGTTT CTCACTTG AAATCGGGCT 2340
TCACGGTCT TGCTGTGCC CCAACGTTCC ACAACAGTCC CGCTGGGGA TTGAAGCGGT 2400
TTCACTCCG AAATATCTC CACTTTCAG AGGGAAAAAC CACCTACCA CAGTCCGCTC 2460
45 TTCAAOTGT ACGGACAGC TGGGAGGGA CGCTGTGTC ACGAGCCCT TTATAGTCTT 2520
AGGTGAAGGC AGAAGTGATG ATTGTAAGTC CCATGAATAC ACAACTCCAC TGCTTTTAA 2580
AGTCATTCA GAGTCTCATT ATTTTGTGTT TTATTTAACC CTTCCTTCAA TACAAAAAGC 2640
CAACAAACCA AGACTAAGGG GTTGACCATG CAATTCCATT TTGTGTCTGT GAACATAGGT 2700
GTGCTTCCA AATACATTA CAAGCTCTTA CTTCGCCCTA ACCCTATGA ACTCTTGATA 2760
50 ACACCAAGAG TAGCACTTC AGAATATATT GAATAGGCAT TAAATGCAAA AATATATATG 2820
TAGCCAGACA GTTTATGAGA ATGACCTGT CAAGCTTCAT TATACGTGG CAAAATCCCT 2880
CTGGCCACA CAGATCTGTA ATCACTAGG CTGCTGTTT CTACAAATAG TGCTAATAAA 2940
GTAAATATG ACGTCAATA CCGAACACTG TCAATGACT GCACTTGTG AAGGAAAAAC 3000
ATGCTTAAG GGGTGAATG AAAATGATGT AGACATTTA AGCATTTCT ACACAGCGAG 3060
55 AAACTCTGT TACGTGTGTA ACAGGTAAC AGAAATCCT TCATAAGCA 3120
CCAGCAGTGT TAAAAAATG AGCTTCCATT AATTTTACT TTTATGGGT TTGCTTAA 3180
GATCTCAAC TGGAAAAATC CTGTCATGGC TCTGAACGTC ACAATGATT GAACCGCGT 3240
CCTTCAATTT TCTTCACT ATCAACACTG CAGCATTTT CTGCTTATC AAAATGGTTT 3300
ATTTAGGAA ACTTTTCCA CCTTCTGAA TGGAAAGAG TTTCACAAA TGTTTTAAAC 3360
60 TCATCGTCT AAAATCAAGT GCACTACAC CAACTGCTCT CAAAATGTA ACTGACTTTT 3420
TTTTTTTTT TTTTCCAA CCGTGTGAC TTAGTGAGGA CCGACACAA TCCCTACAGG 3480
GTGCTGTA GTGGGCTCA TGTAAAGAT CACAATTTG AAATTTAGGA CCGTGGGTCA 3540
TGCAGCGAG GGGCTGGATG GTAGGAAGGG ATGTGCCCG CTCTCCACGC ACTCAGCTAT 3600
AOCTATTCA CAGCTCCTG TGAGTGTGT CACAGGAAAT AAGCCGAGG TATTATTTT 3660
65 TTATGTTTAT GAGTCTGTA ATTAACCGT GATTCTTGA AGGTGTAGGT TTGATTACTA 3720
GGAGATACCA CCGACATTTT TCAATAAAGT ACTGCAAAAT GCTTTTGTG CTACCTTGT 3780
ATTAACTTT GGGCTGTAT TTAGTAAAAA TAAATCAAG CTATCGGAGC AGTTCAATAA 3840
CAAAGGTAC TGTGAGAAA AAAGACCTA TCATAGATTT ACAA

SEQ ID NO:110 PFJ8 Protein sequence;
Protein Accession #: NP_005060.1

75 1 11 21 31 41 51
MKEKSKNAK TRREKENGFE YELAKLLPL SAITSQDKA SIIRLTSSYL KMRVFPPEGL 60
GDAWQGPSRA GPLDGVAKEL GSHLLQTLTG FVFVVASDGG IMYISETASV HLGSLQVELT 120
GNSIYEIHP SDHDEMTAVL TAHQPLHHL LQYEIERSF FLRMKCVLAK RNAGLTCSGY 180
KVHCSGYLK IRQYMLDMSL YDSCYQVGL VAVGQSLPPS AITEKLYSN MFMFRASLDL 240

5 KLIFLDSRVTV ETVGYEPQDL IEKTLVHHVH GCDVFHLRYA HHLILLVKGQV TTKYYRLLSK 300
RGWVYVWQSY ATVVHNSRSS RPHCTVSVNY VLTEIEYKEL QLSLEQVSTA KSQDSWRTAL 360
STSQETRLKV KPNKTEMKTK LRTNPPYPPQ YSSPOMDKLE CGQLGNWRAS PPASAAAPPE 420
LQPHSESSDL LYTPSYSLPF SYHYGHFFLD SHVFSSKKPM LPAKFGQPQG SPCEVARFFL 480
STLPASGECQ WHYANPLVPS SSSPAKNPPE PPANTARHSL VPSYEAPAAA VRRFGEDTAP 540
PSFPGHYR EEPALGPAK ARQAARDGAR LALARAAPEC CAPPTPEAPG APAQLFFVLL 600
NYHRVLARRG PLGGAAPAS GLACAPGGPE AATGALRLRH PSPAATSPFG APLPHYLGA 660
VIITNGR

10

SEQ ID NO:111 PFJ7 DNA SEQUENCE

15 Nucleic Acid Accession #: NM_008549
Coding sequence: 1-1254 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
| | | | |
20 ATGAAOGGAC GCTGCATCTG CCGTCCCTG CCGTACTCAC CCGTCAGCTC CCGCAGTCC 60
TCGCTCGGC TGCCTCGGC GCCGACAGTG GAGTCTCAC ACGTCTCAT CACGGGTATG 120
CAGGACTGTG TGCAGCTGAA TCAGTATACC CTGAAGGATG AAATTGGAAG GGGCTCTAT 180
GGTGTGCTCA AGTTGGCTCA CAATGAAAT GACAATACCT ACTATGCAAT GAAGGTGCTG 240
TCCAAAAAGA AGCTGATCCG GCAGGCGGC TTCCACGTC GCGCTCCACC CCGAGGCACC 300
CGGCCAGCTC CTGGAGGCTG CATCCAGCCC AGGGGCCCA TTGAGCAGGT GTACCCAGGA 360
25 ATTGCCATCC TCAAGAGCT GGAACACCC AATGTGGTGA AGCTGGTGA GGTCTGGAT 420
GACCCCAATG AGGACCATCT GTACATGGTG TTGAACTGG TCAACCAAG GCGGTGATG 480
GAAGTGCCA CCGTCAACC ACTCTCTGAA GACCAAGGCC GTTCTACTT CCAGGATCTG 540
ATCAAGGCA TCGAGTACTT AACTACCAAG AAGATCATCC ACGTGACAT CAAACCTTCC 600
AACCTCTGG TCGGAGAGA TGGGCACATC AAGATCGCTG ACTTTGGTGT GAGCAATGAA 660
30 TTCAAGGGCA GTGACGGCT CCTCTCCAAC ACGTGGGCA GCGCCGCTT CATGGCACCC 720
GAGTGGCTCT CTGAGACCCG CAAGATCTTC TCTGGGAAGG CCTTGGATGT TTGGGCCATG 780
GGTGTGACAC TACTGCTT TGTCTTGGC CAGTGCCAT TCATGGACGA GCGGATCATG 840
TGTTTACACA GTAAATCAA GAGTCAGGCC CTGGAATTC CAGACAGCC CGACATAGCT 900
GAGGACTTGA AGGACCTGAT CACCGTATG CTGGACAAGA ACCTCGAGTC GAGGATCGTG 960
35 GTGCCGGAAG TCAAGCTGCA CCGCTGGGTC ACGAGGCATG GGGCGGAGCC GTTCCGCTCG 1020
GAGGATGAGA ACTGCACGCT GGTGAAGTG ACTGAAGAG AGGTCCAGAA CTCAGTCAA 1080
CACATTCCCA GCTTGGCAAC CGTGATCCTG GTGAAGACCA TGATACGTA ACGCTCCTT 1140
GGGAACCCAT TCGAGGGCAG CCGCGGGAG GAACGCTCAC TGTCAGGCC TGGAAACTTG 1200
40 CTCACCAAAA AACCAACCAG GGAATGTGAG TCCCTGTCTG AGCTCAAGAC CTAGAAAAATA 1260
AGTCCCTTCT CTGCTGTG CAAAGTAACG TAAGAGTTCC CTCACCGAG TGATGACAGA 1320
CGTCTTGTCT GTCAGCAC TCTCTCATA CACATAGCCA GCGCAGGTG ACCAGAACGT 1380
CCGAGGACAG ATGAGGCTT GTGTCTTAT GAGAGTGGGA GAACCTGGT GGCACCCCTG 1440
GTGACGGTGC TGTGGTGGT GGGGACCCCA CTGCTTTCC CACTGAGCAC ATCATGGCTA 1500
45 CCGTACTTGG TGGGAGTTCC ATTCACTAC TTCTGTTTCT TAAACATAGC TTTACTGAGG 1560
TACAATTAC ATACCATGTA ATCAACCCAC GGAAGTGTGA TGATTCAGTG GTTCTAATA 1620
CACACTTCTG CAGCCATTAC CACGCTCAAC TTAACGACAT TTTCATCAG CCAAGAAGAC 1680
ACCTCACTCT CCTAGCTGT CCGCATCCAA CTCCCCACC CCAGTAACCA CTCAGAAATG 1740
50 GTATGGATTG GCCTATCTG GACGTTTCTG ATAAATGGCG TCATACACTA AAAAAAAAAA 1800
AAAA

50

SEQ ID NO:112 PFJ7 Protein sequence:
Protein Accession #: NP_006540.1

55 1 11 21 31 41 51
| | | | |
60 MNGRCICPSL PYSPVSPQS SPRLPRRPTV ESHIVSITGM QDCVQLNQYT LKDEIGKGSY 60
GVVKLAYNEN DNTYYAMKVL SKKKLRQAG FFRPPFRGT RPAFGCIQF RGPBQVYQE 120
IAILKKLDHP NVVKLVEVLD DPNEDHLYMV FELVNQGPVM EVPTLKPLSE DQARFYQDL 180
IKGIEYLHYQ KIHRIKPS NLLVGEDGHI KIADQVSNE FKGS DALLSN TVGTPAFMAP 240
ESLSETRKIF SGKALDVWAM GVTLYCFVFG QCFMDERIM CLHSKIKSQA LEFPDQPDIA 300
65 EDLKDILTRM LDKNPESRIV VPEIKLHPVW TRHGAELPS EDENCTLVEV TEEEVENSVK 360
HPSLATVIL VKTMIRKRSF GNPFBSRRE ERSLSAPGNL LTKKPTRECE SLSELKT

65

SEQ ID NO:113 PFJ8 DNA SEQUENCE

70 Nucleic Acid Accession #: NM_021810
Coding sequence: 1-429 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
| | | | |
75 ATGAAACCTC TGATATGGAC ATGGTCAGAT GTTGAAGGCC AGAGGCCGGC TCTGCTCATC 60
TGACAGCTG CAGCAGGACC CACGAGGGA GTTAAGGGTT ATGGCAAGCC CTTTGAGCCA 120
AGAAAGTGA AAAACATACA CTCTACTCT GCTTACCCAG ATGCCACAAT GCACAGACAA 180
CTCTGGCTC CGGTGGAAGG AAGGATGGCA GAGACATTGA ATCAGAAACT CCATGTTGCC 240
AATGTGCTGG AAGATGACCC CGGCTACCTA CCTCACTCT ACAGCGAGGA AGGGGAGTGT 300
GGAGGGGCC CATCCCTCAG CTCTCTGGCC AGCTTGGAAC AGGAGTTGCA ACCTGATTG 360

CTGGACTCTT TGGGTTCAAA AGCGACTCCG TTTGAGGAAA TATATTGAGA GTCAGGTGTT 420
CCTTCTTAA

5 SEQ ID NO:114 PFJ6 Protein sequence
Protein Accession #: NP_068582.1

1 11 21 31 41 51
10 MKPLIWTWSD VEGQRPALLI CTAAAGPTQG VKGYGKPFEP RSVKNIHSTP AYPDATMHRQ 60
LLAPVEGRMA ETLNQKLHVA NVLEDDPGYL PHVYSEEGEC GGAPSLSSLA SLEQELQPD 120
LDSLGSKATP FEETYESGV PS

15 SEQ ID NO:115 PFJ5 DNA SEQUENCE

Nucleic Acid Accession #: NM_006361
Coding sequence: 131-985 (underlined sequences correspond to start and stop codons)

20 1 11 21 31 41 51
CGAATGCAGG CGACTTGGGA GCTGGGAGCG ATTTAAACG CTTTGGATTG CCGCGGCTG 60
GGTGGGGAGA GCGAGCTGGG TGCCCCCTAG ATTCCCGGCC CCGCACCTC ATGAGCGAC 120
CCTCGGCTCC ATGGAGCCCG GCAATTATGC CACCTTGGAT GGAGCCAAGG ATATCGAAGG 180
25 CTTGCTGGGA GCGGGAGGGG GCGGGAATCT GGTGCCCCAC TCCCTCTGA CCAGCCACCC 240
AGCGGCGCT ACGCTGATGC CTGCTGTCAA CTATGCCGCC TTGATCTGC CAGGCTCGGC 300
GGAGCCGCCA AAGCAATGCC ACCCATGCC TGGGGTGGCC CAGGGGACGT CCGCAGCTCC 360
CGTGCTTAT GGTACTTTG GAGGCGGGA TACTCTCTGC CGAGTGTCC GGAGCTCGCT 420
GAAACCTGT GCCAGGCAG CCACCTGGC CGGTACCC GCGGAGACTC CCACGGCCGG 480
30 GGAAGAGTAC CCAGTGGCC CCACTGAGTT TGCTTCTAT CCGGATATC CGGGAACCTA 540
CCACGCTAT GCCAGTTACC TGGACGTGC TGTGGTGAC ACTCTGGTG CTCTGGAGA 600
ACCGGCACAT GACTCCTGT TGCCTGTGGA CAGTTACAG TCTTGGGCTC TCGCTGGTGG 660
CTGGAACAGC CAGATGTGT GCCAGGAGA ACAGAACCCA CCAGGTCCCT TTTGGAAGGC 720
35 AGCATTGCA GACTCCAGC GGCAGCACCC TCTGACGCC TCGCCTTTC GTCCGGGCG 780
CAAGAAAGC ATTCCGTACA GCAAGGGGCA GTTGGGGAG CTGGAGCGGG AGTATGCGGC 840
TAACAAGTTC ATCAACAAG ACAAGAGCG CAAGATCTCG GCAGCCACCA GCCTCTCGGA 900
GCGCCAGATT ACCATCTGT TTAGAACCG CCGGGTCAAA GAGAAGAAGG TTCTCGCAA 960
GGTGAAGAAC AGCGCTACCC CTTAAGAGAT CTCCTTGCT GGTGGGAGG AGCGAAAGTG 1020
40 GGGGTGTCT GGGGAGACA GAAACCTGCC AAGCCAGGC TGGGGCCAAG GACTCTGCTG 1080
AGAGGCCCTC AGAGACAACA CCTTCCAG GCCACTGGCT GCTGGACTGT TCCTCAGGAG 1140
CGGCTCGGT ACCCAGTATG TGCAGGGAGA CGGAACCCA TGTGACAGC CCACTCCACC 1200
AGGGTTCCA AAGAACCTGG CCCAGTCATA ATCATTATC CTCACAGTGG CAATAATCAC 1260
GATAACCAT

45 SEQ ID NO:116 PFJ5 Protein sequence
Protein Accession #: NP_006352.1

50 1 11 21 31 41 51
MEPGNYATLD GAKDIEILLG AGGGRNLVAH SPLTSHAAP TLMPAVNYAP LDLPGSAEPP 60
KQCHPCGVP QGTSPAPVPY GYFGGGYYS RVSRSLLKPC AQAATLAAYP AETPTAGEEY 120
55 PSRPTAFY PGYPGTYHAM ASYLDVSVVQ TLGAPGEPRH DSLLPVDYQ SWALAGGWN 180
QMCCQGEQNP PGFFWKAFA DSSGQHPPDA CAFRRGRKKR IPYSKQLRE LEREYANKF 240
ITDKRRKIS AATSLSERQI TWFQNRVYK EKKVLAQVKN SATP

60 SEQ ID NO:117 PFJ4 DNA SEQUENCE

Nucleic Acid Accession #: NM_005628
Coding sequence: 591-2216 (underlined sequences correspond to start and stop codons)

65 1 11 21 31 41 51
GTAACCGCTA CTCCCGGACA CCAGACCACC GCCTTCGTA CACAGGGGCC CGCATCCAC 60
CTTCCCGGAC CTAAGAGCCT GGGTCCCTG TTTCCGGAG TCCGCTTCCC GGCCCCAGA 120
TTCTGGCATC CCAGCCCTCA GTGTCCAAGA CCCAGGCAGC CCGGGTCCC GCCTCCGGA 180
70 TCCAGGCTC CGGGATCTGC GCCACCAGAA CTAAGCTCC TGCAGACCTC CGCATCTGG 240
GGGCACTCAA CTCTCGGAG CCAAGGGGCC CAGTCCAC CCAGAGAAAC TCTCGTATTC 300
CCAGCTCTA GGGCAAGGA ACCCGGGCG TCCGAATCC CAGCTTCCG ACATCTGGCA 360
CACGGGGCAG AGCAGAGAAG CTCAGCGCCC AGCCTGGGA ATTTAAACAC TCCAGCTTC 420
AAGAGCCAAG GAACCTCAGT GCTGTGAAC CACAACCTA AGGAGCCCTC CAAAGTTCCA 480
GTCTCCAGT GCTGTACTC AACTCAGTCC TAGGAACGTC GGTCTCTGG AAGGAGCCCA 540
75 AGCGCTCCA GCCAGCTTC AGGCGCTAAG AAACCCCGGT GCTTCCATC ATGTGTGCGC 600
ATCTCTCTG AGACTCAAAG GGGCTCCAG CGGCGGAGCC CACCGCCAAC GGGGGCCTGG 660
CGCTGGCTC CATCGAGGAC CAAGGCGCG CAGCAGGGG CTACTGCGT TCCGGGACC 720
AGGTGCGCG CTGCTTCGA GCCAACCTG TGTGCTGCT GACAGTGTG GCGTGGTGG 780
CCGGCTGGC GCTGGGACTG GGGGTGTGG GGGCGGGGG TCGCTGGCG TTGGGCCCG 840

5 AGCGCTTGAG CGCCTTCGTC TTCCGGGGCG AGCTGCTGCT GCGTCTGCTG CGGATGATCA 900
 TCTTGGCGCT GGTGGTGTGC AGCTTGATCG GCGGCGCCGC CAGCCTGGAC CCCGGCGCGC 960
 TCGGCGGTCT GGGGCGCTGG GCGCTGCTCT TTTCTCTGTT CACCAGCTG CTGGCGTGG 1020
 CGCTCGGAGT GGGCTTGGCG CTGGCTCTGC AGCCGGGGCG GCGCTCCGCC GCCATCAACG 1080
 CCTCGTGGG AGCCGGGGGC AGTGCCGAAA ATGCCCCAG CAAGGAGGTG CTGGATTCTG 1140
 TCCTGGATCT TGGAGAAAT ATCTTCCCTT CCAACCTGGT GTCAGCAGGC TTTCGCTCAT 1200
 ACTTACACAT CTATGAAGAG AGGAATATCA CCGGAACAG GGTGAAGGTG CCGTGGGGC 1260
 AGGAGGTGGA GGGGATGAAC ATCTGGGCT TGGTAGTGT TTGCACTGTC TTGGTGTGG 1320
 CGCTCGGAAA GCTGGGGCCT GAAGGGGAGC TGCTTATCCG CTCTTCAAC TCCTTCAATG 1380
 10 AGGCCACCAT GGTCTGTGTC TCCTGGATCA TGTGGTACGC CCTGTGGGC ATCATGTTCC 1440
 TGGTGGCTGG CAAGATCGTG GAGATGGAGG ATGTGGGTTT ACTCTTTGCC CGCCTTGGCA 1500
 AGTACATCT GTGCTGCCCT CTGGGTCAAG CCATCCATGG GCTCTGGTA CTGCCCTCA 1560
 TCTACTTCT CTTCACCGC AAAAAACCTT ACCGCTTCT GTGGGGCATC GTGAAGCGC 1620
 TGGCCACTGC CTTTGGGAGC TCTTCCAGT CCGCCACGCT GCGCTGATG ATGAAGTGG 1680
 15 TGGAGGAGAA TAAGTGGTG GCGAAGCACA TCAGCCGTTT CATCTGCC ATCGGGCCA 1740
 CCGTCAACAT GGAAGGTGCC GCGCTCTCC AGTGCGTGGC CCGAGTGTTC ATTGCACAGC 1800
 TCAGCCAGCA GTCTTGGAC TTGTAAGA TCATCAACAT CCGGTCAAG GCCACAGCGT 1860
 CCAGGTGGG GGCAGCGGC ATCCCTGCTG GAGGTGTCT CACTTGGCC ATCATCTCG 1920
 AAGCAGTCAA CCTCCGGTC GACCATATCT CCTTGATCT GCGTGTGGA TGGTAGTGG 1980
 20 ACGGTCTG TACGTCTC AATGTAGAAG GTGACGCTT GGGGGCAGGA CTCCTCCAAA 2040
 ATTATGTGA CCGTACGGAG TCGAGAAGCA CAGAGCCTGA GTTGATACAA GTGAAGAGTG 2100
 AGCTGDCCT GGATCCGCTG CAGTCCCA CTGAGGAAGG AAACCCCTC CTCAAACACT 2160
 ATCGGGGCC CCGAGGGGAT GCGACGGTCG CCTCTGAGAA GGAATCAGT ATGTAACCC 2220
 CGGAGGGGAC TTCCCTGCC CTGCTGGGGG TGCTCTTGG ACACTGGATT ATGAGGAATG 2280
 25 GATAAATGGA TGAAGTAGG CTCTGGGGT TGCCTGCAC ACTCTGGGA GCGAGGGGCC 2340
 CCAGCACCT CCAGGACAGG AGATCTGGGA TGCTGGCTG CTGGAGTACA TGTGTTACA 2400
 AGGGTTACT CTCAAACCC CAGTTTCTA CTCATGTCC CAACTCAAG CTAGAAAAA 2460
 GCAAGATGA GAAATAATGT TCTGTGCGT CCGCACCGTG ACCTGCGTG CCTCCCTGT 2520
 CTCAGGGAGC AGGTACAGG TCAACATGG GAATTCTAG CCGCACTGG GGGATGTTAC 2580
 30 AACACATGC TGGTTATTT GCGGGCTGTA GTTGTGGGG GATGTGTGT TGCAGTGTG 2640
 TGTGTGTGT TGTGTGTGT TGTGTGTGT TCTGTGACC TCCTGTCCC ATGTGACGT 2700
 CCACCTGTC CCCAGATCCC CTATTCCTC CACAATAA GAAACACTCC CAGGACTCT 2760
 GGGGAGAGC TGAGGACAAA TACCTGCTGT CACTCCAGAG GACATTTTT TTAGCAATA 2820
 35 AATTGAGTGT CAACTATTTA AAAAAAAAAA AAAAAA

SEQ ID NO:118 PF14 Protein sequence

Protein Accession #: NP_005618.1

40 1 11 21 31 41 51
 | | | | |
 MVADPPRDSK GLAAAEPTAN GGLALASIED QGAAAGGYCG SRDQVRRCLR ANLLVLLTVV 60
 AVVAGVALGL GVSAGAGALA LQPERLSAFV FFGELLRL RLMLPLVVC SLIGGAASLD 120
 45 PGALGRIGAW ALLFLVTL LASALGVGLA LALQFGAASA ADASVGAAG SAENAPSKEV 180
 LDSFLDLARN IFFSNLVSA FRSYSTTYEB RNITOTRVKV PVQGEVGMN ILGLVVFIV 240
 FGVALRLGP EGELLIRFFN SFNEATMVLV SWIMWYAPV IMFLVAGKIV EMDVGLLEA 300
 RLGLYILCL LGHAHGLL LPLIYFLFR KNPYRFLWGI VTPLATFRT SSSSATFLM 360
 MKCVENNGV AKHISRFIL IGATVNMDDA ALFQCVAAVF IAQLSQSLD FVKITILVT 420
 50 ATASSVGAAG IPAGGVTLA ILEAVNLPV DHISLILAVD WLVDRCSTVL NVEGDALGAG 480
 LLQNYVDRT SRSTPELIQ VKSELPLDPL PVPTEEGNPL LKHYRGFAGD ATVASEKESV 540
 M

55 SEQ ID NO:119 PF13 DNA SEQUENCE

Nucleic Acid Accession #: NM_006708

Coding sequence: 88-642 (underlined sequences correspond to start and stop codons)

60 1 11 21 31 41 51
 | | | | |
 CTAGTTAAGG CGGCACAGGG CCGAGGCGTA GTGTGGGTGA CTCCTCCGTT CCTTGGGTCC 60
 CGTCTGCTGT GATACTGCAG TTCAGCCATG GCAGAACCGC AGCCCCGTC CGGCGGCCTC 120
 ACGGACGAGG CCGCCCTCAG TTGCTGCTCC GACGCGGAAC CCAGTACCAA GGATTTTCTA 180
 65 TTGCAGCAGA CCATGCTACG AGTGAAGGAT CTAAGAAGT CACTGGATT TTATACTAGA 240
 GTTCTTGGAA TGACGCTAAT CCAAAAATGT GATTTTCCA TTATGAAGT TCACTCTAC 300
 TTCTTGGCTT ATGAGGATAA AAATGACATC CCTAAAGAAA AAGATGAAAA AATAGCCTGG 360
 GCGCTCTCCA GAAAAGCTAC ACTTGAGCTG ACACACAATT GGGGCATGA AGATGATGCG 420
 ACCAGAGTT ACCACAATGG CAATTCAGAC CCTCGAGGAT TCGGTATAT TGAATTGCT 480
 70 GTTCTGTATG TATACAGTGC TTGTAAGAAG TTTGAAGAAC TGGGAGTCAA ATTTGTGAAG 540
 AAACCTGATG ATGGTAAAAA GAAAGGCTG GCATTTATTC AAGATCTGA TGGCTACTGG 600
 ATGAAATTT TGAATCTTAA CAAAATGGCA ACCTTAATGT AGTGTGTGA GAATTCCT 660
 TTGAGATTTC AGAAGAAAGG AAACAATGTG ATTCAAGATA TTACATACC AGAAGCATCT 720
 AGGACTGTG GATCACTGTC CCGATTCAA TTATTCTTCA GTCAATTTC CCTTCTATT 780
 75 TCAGCTGATC CTTTCACTT AACTGTTCAG TCATCTGGT TTTCAAGCAG TGCTTTATCT 840
 CATGTCTGT AATATAGTTG TGTAACTTTA TTTTATAGT AATAATTAGA ACAGTTCCT 900
 TCAGAGGCTG CATTTGCCCT TTCTGCCAC CTAATAATTA CTTCCTTCA AATTCGCTT 960
 TGAATCATCA TTTTAAAAA AAAATTAACA TTTTGTGT GTAGTTATCT TCTGGGGTTT 1020
 CAACTCTCA GAAACAAT TTTTCAAAAC GAAAAGGAAA GAACACTAGT GTCTTTTCA 1080
 TAAAGTACAA AGTGTATT TTACAAAAGA GTAGGTACT TTGAGAGCAA TTCAATCAT 1140

5 GCTGACAAGG ATACTGATAG AAAAAAGTAT TTCTTCTTAT TATAAAGTAC ATTTAAAGTT 1200
 CAAGGACTAA CCTTATTAT TTGGGAAAGG GGAGGAGGAA GGAAATGATA TGGTACOCAG 1260
 AACTGGGCT AGGCTGCAAC TTTATCTCAT TTAATACTCC CAGCTGTCAT GTGAGAAAGA 1320
 AAGCAGGCTA GGCATGTGAA ATCACTTTCA TGGATTATTA ATGGATTAA GAGGGCATCA 1380
 ATCAGCTCAA CTCAAGATT CATAATCAIT TTTAGTATTT AGATTGTGCC TCAAAGTTGT 1440
 AGTACCTCAC AATACCTCCA CTGGTTTCTT GTTGTAAAAA CCTTCAGTGA GTTTGACCAT 1500
 TGTGCTCTTG GCTCTTGGGC TGGAGTACCG TGGTGAGGGA GTAAACACTA GAAGTCTTTA 1560
 GTACAAAAC TCTCTAGGGA CAOCTGGTGA TTCTACACA AGTGATGTTT ATATTCTCA 1620
 TAAAGAGTCT TCOCTATCC AAGGTCTTCA TGATGCCAGT AGCCATATAT GATAAATTAT 1680
 GTTCAGTGAT AACTTAGTTA TCAGAAATCA GCTCAGTGGT CTCCCGGCC ATGATTACACA 1740
 TTTGATGAGT TTTAAAAAT CAAAGTGATT TTGAAAATCT CTAATGGCTC AGAAAAATAA 1800
 AACATCCAGT TTGTGGATGA CTATATTAG ATTCTCTAG ACTCTAGTGG AAGACCTTTG 1860
 GAAAGGCCAT GCAACCGTG CTGTACTGC TAGAAGCACT TTATGTTTCC TTTTGGGTG 1920
 15 AATGGATT ATGTAGTGC TTTAAACAAA TAGCAATACT TATAGACTGA AATAAAATGA 1980
 AACTTCAAAAT AAG

SEQ ID NO:120 PFJ3 Protein sequence

Protein Accession #: NP_006698.1

20 1 11 21 31 41 51
 MAEPQPSGG LIDEAALSCC SDADPSTKDF LLQQTMLRVK DPKKSLDFYT RVLGMTLIQK 60
 25 CDFPIMKFSL YFLAYEDKND IPKEKDEKIA WALSRKATLE LTHNWGTEDD ATQSYHNGNS 120
 DFRGFGHIGI AVPDVYSACK RFEEELGVKFKV KKPDDGKMKG LAFIQDPDGY WIEILNPNKM 180
 ATLM

30 Nucleic Acid Accession #: NM_002887
 Coding sequence: 70-729 (underlined sequences correspond to start and stop codons)

35 1 11 21 31 41 51
 CCGAGCCAG GTCTGTGCGT CCGGCGGACC GTCCGGGAGC GAACCGTGC TCCGCACTG 60
 GAGTCCGCGA TGGCTTCAGT GACAGATGGT AAACATGGAG TCAAAGATGC CTCTGACCAG 120
 AATTTGACT ACATGTTTAA ACTGCTTATC ATTGGCAACA GCAGTGTGG CAAGACCTCC 180
 10 TTCTCTTGC GCTATGCTGA TGACACGTC ACCCAGCCT TCGTTAGCAC CGTGGGCATC 240
 GACTTCAAGG TGAAGACAGT CTACCGTCAC GAGAAGCGGG TGAACCTGCA GATCTGGGAC 300
 ACAGCTGGGC AGGAGCGGTA CCGGACCATC ACAACAGCCT ATTACCGTGG GGCCATGGGC 360
 TTCAATCTGA TGTATGACAT CACCAATGAA GAGTCTTCA ATGCTGTCCA AGACTGGGCT 420
 ACTCAGATCA AGACCTACTC CTGGGACAAT GCACAAGTTA TTCTGGTGGG GAACAAGTGT 480
 15 GACATGGAAG AAGAGAGGGT TGTTCCTACT GAGAAGGGCC AGCTCCTTGC AGAGCAGCTT 540
 GGGTTTGAAT TCTTTGAAGC CAGTGCAAAG GAGAACATCA GTGTAAGGCA GGCCCTTTGAG 600
 CGCCTGTGGG ATGCCATTGG TGACAAGATG TCTGATTCGC TGGACACAGA CCGGTGGATG 660
 CTGGGCTCTC CCAAGAACAC GCGTCTCTCG GACACCCAC CGCTGCTGCA GCAGAAGTGC 720
 TCAATGCTAGC AAGGCCACCC TTCTGACCT CCGCTCATTG TGGCCCCACA CCAAGTCTG 780
 10 CTCTCTCTG TTACACACTG TCGCTCT

SEQ ID NO:122 PFJ2 Protein sequence

Protein Accession #: NP_002858.1

15 1 11 21 31 41 51
 MASVTDGKHG VKDASDQNFQ YMEKLLIGN SSVGKTSFLL RYADDITFPA FVSTVGIDFK 60
 VKTVYRHEKR VKLQIWDTAG QERYRTITTA YYRGAMGFL MYDITNEESF NAVQDWATQI 120
 10 KTVSWDNAQV ILVGNKDMB EERVVPTEKG QLLABQLGFD FFEASAKENI SVRQAFERLV 180
 DAICDKMSDS LDTDFPSMLGS SKNRLSDTP PLLQNCSC

5 Nucleic Acid Accession #: NM_001844
 Coding sequence: 158-4521 (underlined sequences correspond to start and stop codons)

0 1 11 21 31 41 51
 ACGCAGAGCG CTGCTGGGCT GCGGGGTCTC CCCTCTCTC CTCTGTCTCC AAGGGCCTCC 60
 TGCATGAGGG CGCGGTAGAG ACCCGGACCC GCGCGGTGCT CCTGCGGTTT CGCTGCGCTC 120
 CGCCCGGGCC CGGCTCAGCC AGGCCCGCG GTGAGCCATG ATTGCGCTCG GGGCTCCCA 180
 5 GTGCTGTG CTGCTGAGCG TGCTCGTCCG CGCTGTCTT CGGTGTGAGG GCCAGGATGT 240
 CCAGGAGCTT GGCAGCTGTG TGCAGGATGG GCAGAGGTAT AATGATAAGG ATGTGTGGAA 300
 GCGGAGGCC TGCCGATCT GTGTCTGTGA CACTGGGACT GTCTCTGCG ACGACATAAT 360
 CTGTGAAGAC GTGAAAGACT GCCTCAGCCC TGAGATCCCC TTCGGAGAGT GCTGCCCAT 420
 CTGCCAACT GACCTGCCA CTGCCAGTGG GCAACCAGGA CCAAAGGGAC AGAAAGGAGA 480
 ACCTGGAGAC ATCAAGGATA TTGTAGGACC CAAAGGACCT CTGGGCTCTC AGGGACCTGC 540

AGGGGAACAA GGACCCAGAG GGGATCGTGG TGACAAAGGT GAAAAAGGTG CCCTGGACC 600
 TGTGGGCAGA GATGGAGAAC CTGGGACCC TGGAAATCTT GGGCCCTG GTCTCCCGG 660
 CCCCCTGGT CCCCCTGGT TTTGGTGGAA CTTTGTCTGC CAGATGGCTG GAGGATTGA 720
 TGAAGAGGCT GGTGGCGCCC AGTTGGGAGT AATGCAAGGA CCAATGGGCC CCATGGGACC 780
 TCGAGGACCT CCAGGCCCTG CAGGTGCTCC TGGGCTCAA GGATTTCAG GCAATCTGG 840
 TGAACCTGGT GAACCTGGTG TCTCTGTCC CATGGGTCCC CGTGTCTC CTGTCCGCC 900
 TGGAAAGCCT GGTGATGATG GTGAAGCTGG AAAACCTGGA AAAGCTGGT AAAGGGGTCC 960
 GCCTGGTCT CAGGGTGCTC GTGGTTCCC AGGAACCCCA GGCTTCTC GTGTCAAAGG 1020
 TCACAGAGGT TATCCAGGCC TGGACGGTGC TAAGGGAGAG GCGGGTGCTC CTGGTGTGAA 1080
 GGGTGAGAGT GGTTCGCCGG GTGAGAACGG ATCTCCGGGC CCAATGGGTG CTCGTGGCT 1140
 GCCTGGTGA AGAGGACGGA CTGGCCCTGC TGGCGCTGCG GTGCGCCGAG GCAACGATGG 1200
 TCAGCCAGGC CCGCAGGTC CTCGGGTCC TGTGGTCTT GCTGGTGGT CTGGCTTCCC 1260
 TGGTGTCTT GGAGCCAAAG GTGAAGCCGG CCCCCTGGT GCGCTGGTC CTGAAGGTGC 1320
 TCAAGGTCT CGCGGTGAAC CTGGTACTC TGGTCCCTT GGGCTGCTG GTGCCCTCGG 1380
 TAACCTGGA ACAGATGAA TTCTGGAGC CAAAGGATCT GCTGGTCTC CTGGCATTGC 1440
 TGGTGTCTT GGCTTCCCTG GGCCACGGGG TCCTCTGGC CCTCAAGGTG CAAGTGTTC 1500
 TCTGGGCCC AAAGGTGAGA CCGGTGAACC TGGTATTCT GGCTTCAAAG GTGAACAAAG 1560
 CCCCAGGGA GAACCTGGCC CTGCTGGCCC CCAGGGAGCC CTGGACCCG CTGGTGAAGA 1620
 AGGCAAGAGA GGTGCCCGTG GAGAGCCTGG TGGCGTGGG CCAATCGTC CCGCTGGAGA 1680
 AAGAGGTCT CCGGAAACC GCGTTTCCC AGGTCAAGAT GGTCTGGCAG GTCCCAAGGG 1740
 AGCCCTGGA GAGCGAGGGC CAGTGGTCT TGTGGCCCC AAGGGAGCCA ACGGTGACCC 1800
 TGGCGTCTT GGAGAACCTG GCCTTCTCG AGCCCGGGT CTACTGGCC GCGCTGGTGA 1860
 TGTGTCTCT CAAGGCAAG TTGGCCCTTC TGGAGCCCT GGTGAAGATG GTGCTCTGG 1920
 ACCTCAGGT CTTAGGGGG CTGCTGGGCA GCCTGGTGC ATGGGTTTCC CTGGCCCAA 1980
 AGGTGCCAA GGTGAGCTG GCAAGCTGG TGAGAAGGA CTGCTGGTG CTCCTGTCT 2040
 GAGGGGTCTT CTTGGCAAG ATGGTGAGC AGGTGCTGCA GGACCCCTG GCGCTGTGG 2100
 ACCTGCTGT GAACGAGGCG AGCAGGGTGC TCTGGGCCA TCTGGGTTC AGGGAATTCC 2160
 TGGCCCTCT GGTCCGCCAG GTGAAGGTG AAAACAGGT GAACAGGGTG TTCCCGGTGA 2220
 AGCTGGAGC CTTGGCTCG TGGGTCCAG GGTGAACGA GGTTCACAG GTGAACGTGG 2280
 CTCTCCCGT GCGCAGGCC TCCAGGTCC CCGTGGCTC CCGGCACTC CTGGCACTGA 2340
 TGGTCCCAA GTGCTACTG GCCCAGCAG CCCCCTGGC GCACAGGGCC CTCAGGTCT 2400
 TCAGGGAAT CTTGGCGAGA GGGGAGCAGC TGGTATGCT GGGCCCAAAG GCGACAGGG 2460
 TGAGTGTGT GAGAAAGGCC CTGAGGGAGC CCTGGAAG GATGTTGGAC GAGGCTGAC 2520
 AGGTCCATT GGGCCCCCTG GCCCAGCTGG TGCTAACGC GAGAAGGGAG AAGTTGGACC 2580
 TCTGTGTCT GCAGGAAGTG CTGGTGTCT TGGCGCTCC GGTGAACGTG GAGAGACTGG 2640
 CCCCCCGGA CAGGCGGCTT TTGCTGGGCC TCTGGTGTG GATGGCCAG CTGGGGCAA 2700
 GGGTGAGCA GGAGAGGCCG GCCAGAAAG CGATGCTGT GCGCTGGTC CTAGGGGCC 2760
 CTCTGGAGC CTTGGGCTC AGGTCTTAC TGGAGTACT GTGCTAAAG GAGCCGAGG 2820
 TGCCCAAGC CCCCCGGAG CCACTGGATT CCTGGAGCT GCTGGCCGG TTGACCCCC 2880
 AGGTCCAA GTGAACCTG GACCCCTGG TCCCTTGGT CTTCTGGAA AAGATGTCT 2940
 CAAAGGTGT CAGTGAACCG GACGCCCCC TGGCCGAGT GGTGAACCG GCTCCAAGG 3000
 TCTGTCTGA CCCCCTGGC AGAAGGGAGA GCGTGGAGT GACGTTCCCT CTGGTGGCA 3060
 AGGTCCACA GGTCCCCAG GTCTGGTGG TCAGAGAGGC ATGCTGGTC TGCTGGGCA 3120
 AGTGGTGAG AGAGGATTCC CTGGCTGGC TGGCCCATG GGTGAGCCG GCAAGCAGG 3180
 TGCTCTGGA GCATCTGGAG ACAGAGGTCC TCTGGCCCC GTGGGTCTC CTGGCTGAC 3240
 GGGTCTGGA CAGTGAACCG GACGAGAGG AAGCCCGGT GCTGATGCC CCGCTGGCAG 3300
 AGATGGCGT GCTGGAGTCA AGGTGATCG TGGTGAAGT GGTGCTGGG GAGCTCTGG 3360
 AGCCCTGGG CCCCCTGGT CCGTGGCCC CGCTGGTCA ACTGGCAAG AAGGAGACAG 3420
 AGGAGAAGT GGTGCAAG GCGCATGGG ACCCTCAGG CCACTGGAG CCGGGGAAT 3480
 CCAGGTCTC CAAGGCCCA GAGGTGACA AGGAGAGGT GGAGAGCTG GCGAGAGAG 3540
 CTTGAAGGA CACCGTGGT TCACTGGTCT GCAGGGTCT CCGGCCCTC CTGGTCTTC 3600
 TGGAGACCA GGTCTCTG GTCTGTCTG TCTTCTGGC CTAAGAGTC CTCTGGGCC 3660
 CGTGGTCCC TCTGGCAAAG ATGGTGCTAA TGGAAATCT GCGCCATTG GCGCTCTGG 3720
 TCCCGTGA GCATCAGGG AAACCGGTCC TGTGGTCT CTTGGAATC CTGGGCCCC 3780
 TGGTCTCCA GTTCCCTCG CCGCTGGCAT CGACATGTC GCTTGTCTG GCTTAGGCC 3840
 GAGAGAGAAG GCGCCGACC CCGTGCAGT CATGCGGCC GACCAAGCAG CCGGTGGCT 3900
 GAGACAGCAT GACCCGAGG TGGATGCCAC ACTCAAGTCC CTCACAACC AGATTGAGAG 3960
 CATCCGACG CCGAGGGCT CCGCAAGAA CCGTCTGCG ACCTGACAG ACCTGAACT 4020
 CTGCCACCT GAGTGAAGA GTGGAGACT CTGGATTGAC CCAACCAAG GCTGCACCT 4080
 GGAAGCATG AAGTTTTCT GCAACATGA GACTGGCAG ACTTGGTCT ACCCAATCC 4140
 AGCAAACGT CCAAGAAAG ACTGGTGGAG CAGCAAGAG AAGGAGAAGA AACACATCTG 4200
 GTTTGAGAA ACCATCAATG GTGGCTTCA TTCACTAT GGAGATGACA ATCTGGCTCC 4260
 CAACACTGC AAGTCCAGA TGACCTTCT ACCTGCTG TCCACGGAAG GCTCCAGAA 4320
 CATCACTC CACTGCAAGA ACAGCATTGC CTATCTGGAC GAAGCAGCTG GCAACCTCAA 4380
 GAAGGCCCTG CTCATCCAG GCTCAATGA CCGTGAGATC CCGGCAGAG GCAATAGCAG 4440
 GTTCACTAC ACTGCTCGA AGGATGGCT CACGAAACAT ACCGTAAGT GGGCAAGAC 4500
 TGTATCGAG TACCGTTCAC AGAAGACCT ACCTCTCC ATCATGACA TTGACCCAT 4560
 GGACATAGG GGGCCGAGC AGGAATTCG TGTGGACATA GGGCGGTCT GCTTCTTGA 4620
 AAAACCTGA CCAAGAAACA ACACAATCC TTGCAAAACC AAAGGACCA AGTACTTTC 4680
 AATCTCAGT ACTTAGTAC TCTGACTGA ATGGCTGAC TGACCTGATG TCAATTATC 4740
 CCACTCTC ACAGTTCGA CTTTCTTCC CTCTTCTT AAGAGACCTG AACTGGGAG 4800
 ACTGAAAT AAGATCTCG TGTCTATT ATTTATGTC TTCTGTAAG ACCTCGGGT 4860
 CAAGGCAGG CAGGAAACT AACTGGTGT AGTCAAATG CCGCTGAGT ACTGCCCCA 4920
 GCGCAGCCA GAAGACCTC CTTAGGTGC CCGGCGCAG AACTGTGTG GTCTACACA 4980
 ATGGTCTAT TCTGTGCAA ACACCTCTG ATTTTTTAA ACATCAATTG ATATTAATAA 5040
 TGAAGAGAT ATTGGAAGT

Protein Accession #: NP_001835.2

1 11 21 31 41 51
 5 MIRLGAPQSL VLLTLLVAAY LRCQGGQDVQB AGSCVQDQQR YNDEKDVWKPE PCRICVCDTG 60
 TVLCDDIICE DVKDCLSPEI PFGECCPICP TDLATASQGP GPKGQKGEPP DIKDIVGPKG 120
 PPGPQGPAGE QGPRGDRGDK GEKGAPGPRG RDGEPGTPGN PGPPGPPGP GPPGLGNNFA 180
 AQMAGGFDEK AGGAQLGVQM GPMGPMGPRG PPGPAGAPGP QGFQGNPGEF GEPGVSGPMG 240
 10 PRGPPGPPGK PGDDGEAGKP GKAGERGPPG PQGARGFPPT PGLPGVKQHR GYPGLDQAKG 300
 EAGAPGVKGE SGSPGENGSP GFMGPRGLPG ERGRTGPAGA AGARGNDGQP GPAGPPGPVG 360
 PAGGPGFPGA PGAKGEAGPT GARGPEGAQG PRGEPGTPGS PGAGASGNP GTDGIPIGAKG 420
 SAGAPGIAGA PGFPGPRGPP GPQATGTLG PKGQTGEPI AGFKGEQGPK GEPGAPGPG 480
 APGPAGEBEG RGARGEPGV GPFGPPGERG APGNRGFPQG DGLAGPKQAP GERGPSGLAG 540
 PKGANGDPGR PGEPLPGAR GLTGRPGDAG PQGKVGPSGA PGEDGRPGPP GPQARGQPG 600
 15 VMGFPKPGA NGEPGKAGEK GLPGAPGLRG LPGKDGETGA AGPPGAPGA GERGEQGAPO 660
 PSFGQLPFP PGPPGEGGKP GDQGVFGEAG APGLVGPFRG RGFPGERGSP GAQGLQGPFG 720
 LPGTPTDGP KGASGPAGPP GAQGGPGLQG MPGERGAAGI AGPKGDRGDV GEKGEPGAPG 780
 KDGGRLTGP IGPFGPAGAN GEKGEVGPFG PAGESAGARGA PGERGETGPP GPAGFAGPPG 840
 ADGQPGAKGE QGEAGQKGA GAPGPQGPSG APGPQGPQGV TGPKGARGAQ GPPGATGFP 900
 20 AAGRVPKPGS NGEPGKAGEK GLPGAPGLRG LPGKDGETGA AGPPGAPGA GERGEQGAPO 960
 DDGPGAGEP PGPGLAGQR GIVGLPGQRG ERGFPGLPG SGEPGKQGP GASGDRGPPG 1020
 FVGPPGLTGP AGEPRGESP GADGPPGRDG AAGVKGDRGE TGAVGAFGAP GPPGSPGAP 1080
 PTGKQDRGE AGAQGPMGPS GPAGARGIQG PQGPRGDKGE AGEPRGERGLK GHRGFTLQGG 1140
 LPGPFGPSD QGASGPAGPS GPRGPPGPVG PSKDGANGI PGPGPPGPR GRSGETGAPG 1200
 25 PGNPPGPPG PGPPGPGIDM SAFAGLGPFE KGPDPLQYMR ADQAAGGLRQ HDAEVDATLK 1260
 SLNNQIESIR SPESGRKNPA RTCDLKLCH PEWKSGDYWI DPNQGTCLDA MKVFCNMTGT 1320
 ETCVYPNAN VPKNWVSSK SKEKKHIWFG ETINGGFHFS YGDDNLAPNT ANVQMTFLRL 1380
 LSTEGSQNT YHCKNSIAYL DEAGNLKKA LLIQGSNDVE IRAEGNSRFT YALKDGGCTK 1440
 30 HTGKWGKTVI EYRSQKTSRL PIDIAPMDI GGPEQEFVD IGPVCF

SEQ ID NO:125 PFH9 DNA SEQUENCE

166 Nucleic Acid Accession #: NM_005084
 Coding sequence: 162-1487 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 40 GCTGGTGGGA GGCTGCGAGT GCTGTCGGCG AGAAGCAGTC GGGTTTGGAG CGCTTGGGTC 60
 GCGTTGGTGC GCGGTGGAAC GCGCCAGGG ACCCAGTTC CCGGAGCAG CTCGCGCCG 120
 CGCTGAGAG ACTAAGCTGA AACTGCTGCT CAGCTCCAA GATGTTGCCA CCAAAATGTC 180
 ATGTGCTTTT CTGCTCTGC GGCTGCTGG CTGTGGTTTA TCCTTTTAC TGGCAATACA 240
 TAAATCTGT TGCAGCATGC AAATCATCAG CATGGGTCAA CAAAATACAA GTACTGATGG 300
 45 CTGCTGCAAG CTTTGGCCAA ACTAAATCC CCGGGGAAA TGGGCTTAT TCGTGTGTT 360
 GTACAGACTT AATGTTTGA CACTAATA AGGGCACCTT CTTCGTTTA TATTATCAT 420
 CCAAGATAA TGATGCTCT GACACCTTT GGATCCAAA TAAAGAATAT TTTTGGGTC 480
 TTAGCAATTT TCTTGAACA CACTGGCTTA TGGGCAACAT TTTGAGTTA CTCTTTGTT 540
 CAATGACAAC TCGTCAAAAC TGAATTCCT CTCTGAGGC TGGTGAATAA TATCCACTG 600
 50 TTGTTTTTTC TCATGCTCT GGGGCAATCA GGACACTTTA TTCTGCTATT GGCATTGACC 660
 TGGCATCTTA TGGGTTTAA GTTCTGCTG TAGAACACAG AGATAGATCT GCATCTGCA 720
 CTACTATTC CAAAGGACAA TCTGCTGCA AAATAGGGGA CAAGTCTTGG CTCTACCTTA 780
 GAACCTGAA ACAAGAGGAG GAGACACATA TACGAAATGA GCAGGTACGG CAAAGAGCAA 840
 AAGAATGTT CCAAGCTCT AGTCTGATC TTGACATTGA TCATGGAAG CCAAGTGAAGA 900
 55 ATGCATTAGA TTAAAGTTT GATATGGAAC AACTGAAGGA CTCTATTGAT AGGGAAGAAA 960
 TAGCAGTAAT TGGACATTCT TTTGGTGGAG CAACGGTTAT TCAGACTCTT AGTGAAGATC 1020
 AGAGATTGAG ATGTGGTATT GCCTGGATG CATGGATGTT TCCACTGGGT GATGAAGTAT 1080
 ATTCCAGAA TTCTCAGCC CTCTTTTTA TCAACTCTGA ATATTCCAA TATCTCTGTA 1140
 ATATCATAA AATGAAAAAA TGCTACTCAC CTGATAAAGA AAGAAAGATG ATTACAATCA 1200
 60 GGGGTTCACT CCACAGAAAT TTTGCTGACT TCATTTTGC AACTGGCAAA ATAATTGGAC 1260
 ACATGCTCAA ATTAAAGGGA GACATAGATT CAAATGTAGC TATTGATCTT AGCAACAAAG 1320
 CTTCATTAGC ATTCTTCAA AAGCATTAG GACTTCATAA AGATTTTAT CAGTGGGACT 1380
 GCTTGATTGA AGGAGATGAT GAGAATCTTA TTCCAGGGAC CAACATTAAC ACAACCAATC 1440
 AACACATCAT GTTACAGAAC TCTTCAGGAA TAGAGAAATA CAATTAGGAT TAAATAGGT 1500
 TTTT

SEQ ID NO:126 PFH9 Protein sequence:
 Protein Accession #: NP_005075.1

1 11 21 31 41 51
 70 MVFPKLVHVF CLOGCLAVVY PFDWQYINPV AHMKSSAWVN KIQVLMAAAS FGQTKIPRGN 60
 GPYSVGCTDL MFDHINKGTF LRLYYPSQDN DRLDLWIFN KEYFWGLSKP LGTHWLMGNI 120
 75 LRLFGSMIT PANWNSPLRP GEKYLTVFS HGLGAFRTLY SAIGDLASH GFIVAAVEHR 180
 DRASATYTF KDQSAAEIGD KSWLYLRLTK QEEETHIRNE QVRQRAKES QALSILDD 240
 HGKPVKNALD LKFDMEQLKD SIDREKIAVI GHSFGGATVI QTLSEDQFR CGIALDAWMF 300
 PLGDEVYSRI PQPLFEINSE YFQYPAHIK MKKCYSPDKE RKMITRGSV HQNFADTFE 360
 TKGKIGHMLK LKGDIDSNVA IDLSNKASLA FLQKHLGLHK DFDQWDCLJB GDDENLPGT 420
 NINTNQHM LQNSSGIEKY N

SEQ ID NO:127 PFH8 DNA SEQUENCE

5 Nucleic Acid Accession #: NM_015900
Coding sequence: 32-1402 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51

10 CACGAGCGGC ACGAGGATTT CCAGCTCAGC GATGCCCCA GGTCCCTGGG AGAGCTGCTT 60
CTGGGTGGGG GGCCTCATTT TGTGGCTCAG CGTTGGAAGT TCAGGGGATG CACCTCCTAC 120
CCACAGCCA AAGTGGCGTG ACTTCCAGAG CGCCAACCTT TTTGAAGGCA CCGATCTCAA 180
AGTCCAGTTT CTCTCTTTG TCCCTTCGAA TCTAGCTGT GGGCAGCTAG TAGAAGGAAG 240
CAGTGACCTC CAAAACCTCG GGTTCATGTC CACTCTGGGA ACCAACTAA TTATCCATGG 300
15 ATTCAAGGTT TTAGGAACAA AGCCTTCTCT GATTGACACA TTTATTAGAA CCCTTCTCGG 360
TGCAACGAAT GCTAATGTGA TTGCCGTGGA CTGGATTAT GGGTCTACAG GAGTCTACTT 420
CTCAGCTGTG AAAAATGTGA TTAAGTTGAG CCTGAGATC TCCCTTTTC TCAATAAACT 480
CCTGGTGTG GGTGTGTGG AATCTCAAT CCACATCATT GGTGTAGCC TGGGGGCCA 540
CGTTGGGGGC ATGTTGGGAC AGCTCTTCGG AGGCCAGCTG GGACAGATCA CAGGCTCGGA 600
20 CCCCCTGGA CTTGAGTACA CCAGGGCCAG TGTGGAAGAG CGCTTGGATG CTGGAGATGC 660
CCTCTTCGTG GAAGCCATCC ACACAGACAC CGACAATTG GGTATTTCGA TTCCCGTTGG 720
ACATGTGGAC TACTTCGTCA ACGGAGGCCA AGACCAACT GGTGCCCCA CCTCTTTTA 780
CGCAGTTAT AGTTATCTGA TCTGTATCA CATGAGGCT GTGCACCTCT ACATCAGCGC 840
25 CTTGAGAAAT TCTGTCCAC TGATGGCTT TCCCTGTGC AGCTACAAGG CCTTCTTGC 900
TGGACGCTGT CTGGATTGCT TTAACCTTT TCTGCTTTC TGCCCAAGGA TAGGACTGGT 960
GGAACAAGT GGTGTCAAGA TAGAGCCGCT CCCCAGGAA GTGAAAGTCT AACTCTGAC 1020
TACTTCACT GCTCCGACT GCATGCATCA CAGCCTCTG GAGTTTCACT TGAAGGAAC 1080
GAGAAACAAG GACACCAACA TCGAGTTAC CTCTCTAGC AGTAACATCA CCTCTTCATC 1140
30 TAAGATCAC ATACCTAAGC AGCAACGCTA TGGGAAAGGA ATCATAGCCC ATGCCACCC 1200
ACATGCCAG ATAAACCAAG TGAATTCAT GTTTCAGTCT TCAACCGAG TTTGAAAAA 1260
AGACCGGACT ACCATTATTG GGAAGTTCT CACTGDCCT TTGCTGTCA ATGACAGAGA 1320
AAAGATGCTC TGCTTACCTG AACCAGTGAA CTTACAAGCA AGTGTGACTG TTTCTGTGA 1380
CCTGAAGATA GCCTGTGTGT AGTTTAACT GGGCAGGACA CATCTCCCTG CATTTTTTTT 1440
35 TTTTTTTTT GAGAGAGAGG TGTGATGAGG GATGTGTGTG TGCAGCTTAT TGTAGACCAT 1500
TACTACTAAG GAGAAAAACA AAGCTCTTTC TTAATTTTCT CATAATCAGC TACCTGGAG 1560
GGGAGGGAGA ACTCATTTTA CAGAAGTTGG TTTCTTTGC CGATCTTATG TACATAOCCA 1620
TTTTAGCTTT CCCATGCATA CTAACTGCA CTGCTTTAT CTCTTGGGC ATTCGTACTT 1680
AGGATTCAT AGAAACATGT ACAGGGTAAA CAATTTTTA AAAATAAAAC TTATGGAGT 1740
40 AAAAAAAAAA AAAAAAAAAA

SEQ ID NO:128 PFH8 Protein sequence
Protein Accession #: NP_056884.1

45 1 11 21 31 41 51

MPFGPWESCF VVGGILWLVS VGSSGDAPPT PPKCADRQS ANLFEGTDLK VQFLFVPSN 60
PSCQQLVEGS SDLQNSGFNA TLGTLIHHG FRVLGKPSW IDTIFRTLLR ATNANVIAVD 120
50 WYGTGVYVF SAVKNVILKS LEISLFLNKL LVLGVSESSI HIGVSLGAH VGGMVQLPG 180
GQLGGITGLD PAGPEYTRAS VEERLDAGDA LFVEAIHDT DNLGIRFVG HVDYFVNGGQ 240
DQPCPTTFY AGYSYLICDH MRAVHLYISA LENSCLMAF PCASYKAFLA GRCLDCFNPF 300
LLSCPRTLV EQGVVKIEPL PKEVKVYLLT TSSAPYCMHH SLVEFHKLKEL RNKDTNIEVT 360
FLSSNTSSS KITPKQORY GKGIAHATP QCQINQVKFK PQSSNRVWKK DRTTHGKFC 420
55 TALLPVNDRE KMVCLPEPVN LQASVTVSCD LEIACV

SEQ ID NO:129 PFH7 DNA SEQUENCE

60 Nucleic Acid Accession #: NM_014384
Coding sequence: 89-1338 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51

65 CGTTGCCGGG TCGCAGGTGC CGCCAGTGC AGCGCAACGG AGGTCAAAGG CGTTCAGACT 60
CTTAGCTGAA CCGGAGCTG CGCGGGCTAT GCTGTGGAGC GGCTGCCGGC GTTTCGGGGC 120
GCGCTCGGC TGCCTGCCCG GCGGTCTCGG GGTCTCTGTC CAGACCGGCC AOCGGAGCTT 180
GACCTCTGTC ATCGACCTT CCAATGGACT TAATGAAGAG CAGAAAGAAAT TTCAAAAAGT 240
GGCTTTGAC TTGCTGTGCC GAGAGATGCC TCCAATATG GCAGAGTGGG ACCAGAAGGA 300
70 GCTGTTCCTA GTGGATGTGA TCGGAAAGGC AGCCAGCTA GGCTTCGGAG GGGTCTACAT 360
ACAAACAGAT GTGGGCGGGT CTGGGCTGTC ACGTCTTGAT ACCTCTGTCA TTTTGAAGC 420
CTTGGCTACA GGCTGCACCA GCACCAACAGC CTATATAAGC ATCCACAACA TGTGTGCTG 480
GATGATTGAT AGCTTCGGAA ATGAGGAACA GAGGCACAAA TTTTGGCCAC CGCTCTGTAC 540
75 CATGGAAGG TTTGCTTCT ACTGCCTCAC TGAACCAAGG AGTGGGAGTG ATGCTGCCTT 600
TCTTCTGACC TCCGTAAGA AACAGGGAGA TCATTACATC CTCAATGGCT CCAAGGCTT 660
CATCAGTGGT GCTGTGTGAGT CAGACATCTA TGTGTTCATG TGCGAAGACG GAGGACACAG 720
CCCCAAGGC ATCTCATGCA TAGTTGTGA GAAGGGGACC CCTGGCTCA GCTTTGGCAA 780
GAAGGAGAAA AAGTGGGGT GGAACCTCCA GCAACACGA GCTGTGATCT TCGAAGACTG 840
TGCTGTCCCT GTGGCCAACA GAATTGGGAG CGAGGGGCAG GGCTTCTCA TTGCGTGAG 900

5 AGGACTGAAC GGAGGGAGGA TCAATATTGC TTCTGCTCC CTGGGGGCTG CCCACGGCTC 960
 TGTATCTCT ACCCGAGACC ACCTCAATGT CCGGAAGCAG TTGGAGAGC CTCTGGCCAG 1020
 TAACCACTAC TTGCAATTC CACTGGCTGA TATGGCAACA AGGCTGGTGG CCGCGCGGCT 1080
 GATGGTCCGC AATGCAGCAG TGGCTCTGCA GGAGGAGAGG AAGGATGCAG TGGCCTTGTG 1140
 CTGCATGGCC AAGCTCTTTG CTACAGATGA ATGCTTTGCC ATCTGCAACC AGGCCCTTGA 1200
 GATGCAACGGG GGCTACGGCT ACCTGAAGGA TTACGCTGTT CAGCAGTACG TGCGGGGACTC 1260
 CAGGGTCCAC CAGATTCTAG AAGGTAGCAA TGAAGTGATG AGGATACTGA TCTCTAGAAG 1320
 CCGCTCTCAG GAGTAGAACC CACACTTGT CTGGCCTGGT GTTCAGTGGC ACTGCAGTCA 1380
 GTGTGATGTG GTGCCATGTG GGCCGCTCTA TTCAAAGGA ATCATGGATT AGACCCAAGG 1440
 10 GCTGAGCTCC TCTAGGGCAG GACCTGCACC CTGTGTGTTG GCACCAGCAT CGGGTCTTGG 1500
 ACTGGGGCAG AATCCCCAGT GGAACCGGAA GAGCTGGACT GATGAGAAAC ATCAGAAGAA 1560
 CACATACTAC CTGTCTTCC TAATGCCAGA AGGGTGACCA GTGAAGATTG AOCGTCAAAC 1620
 CATGAAAGTC CTCTCTGGA TCCACTTTAT CTTGATTAGT CTGCATTITA CTAGTTCACT 1680
 GGATCCCTCC TCTAGGGGCC TGGGGACTTT CACTGATGCT CTCTCTGATT CTAGAGCAAA 1740
 15 GGTGTGGGAA GGGGAAATGG AGGAATGCC TCTGTCTGT GTCTGTCTCT GTGCCACAGC 1800
 TACAGATGCA GAAAGTTTCT CTGGATAGCA CACCTCTGAA TGTAAATCAT GATAAAATGG 1860
 ATATTGGAA ACTTACTCTC AAGCTGTGAT GTAGGGTGTG TTCTACTTC TGGACTGCCT 1920
 CAATATCAAG GCGTGAAGCT TTGAATGTT GAATATTCGT TGGTTTTCAT GTTAAGACGC 1980
 20 CTGTGGTCCA GGAGTCTAT TCAGTGTTC TGTCTCTGAT AAACACTTTC AATATTTTTT 2040
 TGTGTTTTTG TTCTCTTTC TGAAGCTGTT OCTCTTTTA AATATTTTA ATCAGATTGA 2100
 TAAATCTAT CCTTCATCCA CCTCTGGTTC TACTATAGTT GATTTTTATT TTAATGTTT 2160
 AATTGATTT GATTAAACAC TTAAGTGGAT TTGGAATAA TAAACTCTC GTCCAATTG 2220
 GCTTTAAAA AAAAAAA

SEQ ID NO:130 PFH7 Protein sequence:
 Protein Accession #: NP_05198.1

30 1 11 21 31 41 51
 | | | | |
 MLWSGCRRFG ARLGCLPGL RVLVQTGHRSLTSCIDPSMG LNEEQKEFOK VAFDFAAREM 60
 APNMAEWDQK ELFPVDMRK AALQGRGGVY IQTDVGGSL SRLDTSVIF ALATGCTSTT 120
 35 AYISIHNMCA WMDSFNGEE QRHKFCPLC TMEKFASYCL TEPGSGSDAA SILTSKKQK 180
 DHYILNGSKA FEGAGESDI YVVMCRGTGP GPKGISCIIV EKGTFGLSPG KKEKKVGNWS 240
 QPTRAVIDED CAVPVANRIG SEGQGLIAV RGLNGGRINI ASCSLGAHA SVILTRDHLN 300
 VRKQFGEPLA SNQYLQFLA DMATRLVAAR LMVRNAVAL QEERKDAVAL CSMAKLFATD 360
 ECFACNQAL QMHGGYGYLK DYAVQYVRD SRVHQLEGS NEVMRILSR SLLQE

40

SEQ ID NO:131 PFH8 DNA SEQUENCE
 Nucleic Acid Accession #: NM_013989
 Coding sequence: 707-1105 (underlined sequences correspond to start and stop codons)

45 1 11 21 31 41 51
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 GCGTGCAGAG AGAGGCACCT TGCAACACAG ACAGATAGCA AGAAGGGAAA GACAGAGAGT 60
 50 GAGAAAAAAG AGGAGTCAGT CGCTCTGGG GAAGGGAGAG AGTGAGACTG GGAGAAAGAG 120
 AAGCACAGAA AGTGTGTGTA AAACGGAGTA AAGAAAGAAA AAAAAAAAC TACCTTAAA 180
 GCACATTAA AAAAAAATAA CTCTGGCAAT TCAAGAAAGA AACAGGCTAC GTTTAAAGAG 240
 CATAGAGACA ATGAAAGGCT AAAGAAAATT TAAAAATCTC TGCCACAGTC TCATAGGTGC 300
 TTGGAATGA AAGTAGAACT GCCTGTCTTT AACGGACTCT GACAGAGGTA ACTGGATTAG 360
 55 GGACGAGTAC GGCAGCTTTT TTTTTTTTTT TTTTTTTTTT TTTAACAATC TAAATCTGTA 420
 AAAAAAATAA AAAAAAATAA AAAAGGCAGC AGCTCCGAAT TGAATGAATT GATGGGCACA 480
 CTCCAAGTGC TGGGCTGGAG AGACTGGACT TAGTCTTGGC ATTCTGCTT CTTTGAAAGA 540
 GGAGACAATC TGGGCTTCTC TTTAATTAG TTTTTTTTCC CCTCTCCCC CAACCCCCAA 600
 CCTTCCCCCT TACCTCCCC AOCCTCTTA TCACCAOCCC CCTTTTAAAT AAGAGGGTGA 660
 60 AGGGGAACCA GAGCGCACAA GGGAACTGAC TCAGGAGGCA GAGAAGATGG GCATCTCTAG 720
 CGTAGACTTG CTGATCACAC TGCAAAATCT GCGAGTTTTT TTCTCAACT GCTCTCTCT 780
 GGCTCTCTAT GACTCGGTCA TTCTGCTCAA GCACGTGGTG CTGCTGTGTA GCGCTCCAA 840
 GTCCACTGCG GGAGAGTGGC GGCGCATGCT GACCTCAGAG GGACTGGGCT GCGTCTGGAA 900
 GAGCTTCTCT CTCGATGCTC ACAAACAGGT GAAATTGGGT GAGGATGGCC CCAATTCCAG 960
 65 TGTGGTGCA GTCTCCAGTA CAGAAGGAGG TGACAACAGT GGCATGGTA CCCAGGAGAA 1020
 GATAGCTGAG GGAGCCACAT GCCAATCTCT TGACTTTGCC AGCCTGAGC GCCACTAGT 1080
 GGTCAACTTT GGCTCAGCCA CTTCAGCTCC TTTCACGAGC CAGCTGCCAG CCTTCCGCAA 1140
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 CCAGAACCAG GAAGATCGAT GTGCAGCAGC CCAGCAGCTT CTGGAGCGTT TCTCTTGGC 1320
 70 GCGCCAGTGC CGAGTGTGG CTGACCGCAT GGACAATAAC GCCAACATAG CTTACGGGGT 1380
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 75 GCTTACTGAA AGACAGGAGT TTATCTATCG GAAGAATATG AATCTTAAC AGCTCCATAC 1680
 TTCTTTTACT ACTCAATGG CATTTGGGCTG AGTAAGTAAC CATATCACTC CTCTCTTAG 1740
 TAAAAAGCC FATGTGAAAA GATCCCAAGA TGGAGAGGAA GAAACGCTAA TTCAGCATGT 1800
 GTTCAATCTG CATTGAGAAG GAAGTGATAC ATCTGATGCA TGCTTTGAGA CCAGAAGAAA 1860
 AGACTTACCT GAATAATTAC TACATTAGGG AAGCTACTGT CTACGTTAAG ATAAAGGTTA 1920

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TIGCTTGGC TCTATTGGC ATGGATGGAG CCCAGTTGGA AAATTCOCOA ATATTACAAC 1980
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 ATATTGGTA TATTGTAGA TACCGAGAAT GATCCCTCAG TCTGAGAGGT TAGAATGATC 2160
 ATCTGTAATC TGAGGGTTAA TTCTAGGCA GGTGGAGAGA GTGGTAAAA AGAAATGAAA 2220
 TTGACAAGCT AGGAAAGAGG AGGCAGAAA ATTGGAAAA TTCACAGAGT TTCACCTTA 2280
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 AAAGACTTAT GTCTGGAAC TATCAAAAC TGACTTTAT TATTGCTTAG TGAATAACT 4620
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 TGCTGCATAA AATCTCAGGA GGGCAGGTTA GGAGACAGT ATGTATGGCC TTTGGGAAA 5100
 ATTCAAAGGG TGGGATTACA AGGGTGTTC TCAGGCATGC CCTATGGGC CCTATGTGA 5160
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 GGATCATAT ACCATTGAAA AAGGAAAAAT GTAGACTCTG ACTTCGGTCC CACTGAAGGA 5340
 TTAATGAAAA CCTTACTAG CATTTAGAGC TTTTCAGAAC ATCCCACTG TCAATGTGCT 5400
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 TTCCCTAAA TGGTATGGC AAAAGTCAGA GTTAAATAT ATATAGTTAG ATTGCAACT 5520
 CCTCCTCAC TCTAAAAATA GAATCCAAAC CCACCTTCA TATATGCTC CAGAATGGG 5580
 CTTAAGTACC AATCTCTGCT TTGCAATGG CACAATCTTG GTCATGCTC GAGGCTCTCT 5640
 AAGAAAAAG AGGATCTAGG ATGGGAGAGC TAGAAGGTTG CTAAGTGGGA AGAACAAGGC 5700
 CCTGAGGGGT TGGTCTACCA ATCTGGGAAG ATTTGAAAC AAACCTCTCG CAAGTGAAG 5760
 AAGGCTGAAG GCTGCTGCAA GTCATTGAGT GACTTTAGGA TGAGCAAAAC ATTGGGOCAC 5820
 TTCTAATGC CCTATGTGTA TAGTACCAGA AGCAAGGTCT CAGACTTAAC AGACCCAGCT 5880
 CTGTTCAGG GTGAGTCTGA ACCAATAGAA AGCAAAACAT TGCAGATATC CAACAAGAC 5940
 TGCTCATGCA AGTGGGGGCT GGCTACCGT CTTAGGCAGC AACAGCAGAG CTCAGGGAG 6000
 CTTATCAAT ATTTACTAG ACTTGAAGA CCGAGCAGAT GTTAAATGAA GTCATAATT 6060
 TGGCTCAAA OCTCCACTTC TCCCTCTCC CTCAAAAAGC CAACAGGTAA ACACATAAAT 6120
 GAAAGAAACC CACAGAAGGG GATGGGAAAT AAAAGAAAT CTCTCAAGAC TTCTCCAGGC 6180
 CCATGTCACT GTGAGTCTG GTTTTATGT GTATTAGGAT TGGGGGATGT GAAGAAATAA 6240
 GTATCCAGTA CTTTATAACC AAAGCAATTA AATGATATTG GGGTAGGGAA TGTGGCCAG 6300
 TTTTGTGTT TCTCCCTGAC ACATTGTCT CAGACCTCA CTAAGCCCA AGTAATGGG 6360
 CCGCCGGAAG AGGAGAGAC AGATGTGCCA GAGTTGACCC AGTGTGGGA TGATAACTAC 6420
 TGAGGAAAGA GTCATGACC TCAGTTAGTG GTTGGATGTA GTCACATTAG TTTGCTCTC 6480
 CCACTCTTT TCTCCCTGGC AAGGAGAAATA TGGGGGACAT GATGCTAAGA GCGCTGGGA 6540
 AATGTGGTGA GAATGCACGC GTGCATATGC TACACATATG TGCTTCTCAG TTGCAGAAA 6600
 TGAAGTCTT TGGGAGATTA TCAGTAGAAA GAGTGTATC ATATTGGTG TGAGTGTAT 6660

GTGTGCTTAT ACAATTGTGT CTGTATTTT AATAAACTTT GAATAAAAGA ATAAAAAAAA 6720
AAAAAAAAAAAA AAAAA

5 SEQ ID NO:132 PFH6 Protein sequence:
Protein Accession #: NP_054844.1

1 11 21 31 41 51
10 MGILSVDLLI TLQILPVFFS NCLFLALYDS VILLKHYVLL LSRKSTRGE WRRMLTSEGL 60
RCVWKSFLLD AYKQVKLGED APNSSVVHVS STEGGDMSGN GTQEKIAEGA TCHLLDFASP 120
ERPLVVNFQS ATXPFPTSQ LPAFRKLVEEF SSVADFLVY IDEAHPSDGW AIPGDSLSF 180
EVKKHQNQED RCAAQQLLE RFSLPPQCRV VADRMNNAN IAYGVAFERV CIVQRQKIA Y 240
15 LGKGPPSYN LQEVRIHWLEK NFSKRXXKTR LAG

20 SEQ ID NO:133 PFH5 DNA SEQUENCE
Nucleic Acid Accession #: NM_001141
Coding sequence: 72-2102 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
25 CAGGGGTGTC OCAGGGGGAG CCCCCTCTG CAGCCCTGTG CGCCGTAGAG AGCTGGACTT 60
AGGCTGGCAG CATGGCCGAG TTCAGGCTCA GGTGTCCAC CGGAGAAGCC TCGGGGCTG 120
GCACATGGGA CAAAGTGTCT GTTCAGCATCG TGGGGAACCG GGGAGAGAGC CCCCCTGTC 180
CCCTGGACAA TCTGGCAAAG GAGTTCACTG CGGGCGCTGA GGAGGACTTC CAGGTGACGC 240
TCCCGGAGGA CGTAGGCCGA GTGCTGCTGC TGGCGTGA CAAGGCGCC CAGTGTGTC 300
30 CCTGCTGGG GCCCTGGCC CCGGATGCTT GGTTCGCG CTGGTCCAG CTGACACCGC 360
CGCGGGGGG CCACCTCTC TTCCCTGCT ACCAGTGGCT GGAGGGGGG GGAACCTGG 420
TGCTGCAGGA GGTACAGCC AAGGTGTCT GGGCAGACA CCACCTGTG CTCCAGCAAC 480
AGCGCCAGGA GGAGCTTCAG GCCCGGCAGG AGATGTACCA GTGGAAGGCT TACAACCCAG 540
35 GTTGCCCTCA CTGCTGGAT GAAAAGACAG TGAAGACTT GGAGCTCAAT ATCAAACT 600
CCACAGCCAA GAATGCCAAC TTTATCTAC AAGCTGGCT TGCTTTTGA GAGATGAAAA 660
TCAAGGGGTT GCTGGAGCCG AAGGGGCTCT GGAGGAGTCT GAATGAGATG AAAAGGATCT 720
TCAACTTCCG GAGGACCCCA GCAGCTGAGC ACGCATTGA GCATGGCAG GAGGATGCT 780
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40 TCCCAAAGAA CTCCCGTC ACTGATGCCA TGTGGGCTC ATTGTGGGT CCTGGGACCA 900
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GCATCCAGAC CAATGTCTT AATGGGAAG CGCAGTTCT TCGGCCCCA ATGACCCCTG 1020
TATACCAAG CCAGGCTGC GGGCGCTGC TGCTCTGCT CATCCAGCT AGCCAGACCC 1080
CGGCCCAAA CAGCCCATC TTCTGCCA CTGATGACAA GTGGGACTGG TTGCTGGCA 1140
45 AGACTGGGT GGCATATGC GAGTTCTCT TCCATGAGG CCTCACGCAC CTGCTGCACT 1200
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50 GCTTCTGA GTTGATACAG AGGAACATGA AGCAGCTGAA CTATTCTCT CTGTGCTGC 1440
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CAAGTGATGA GTCTGTCCA GATGACAGAG AGCTCCAGG CTGGGTGAGA GAGATCTTCT 1620
CCAAGGGCT CTAACACAG GAGAGCTCA GTATCCCTC CTCACTGGAG AOCGGGAAG 1680
COCTGGTCA ATGTGTACC ATGGTATAT TCACTGCTC AGCCAAGCAT GCGGTGTCA 1740
55 GTGCAGGCA GTTTGACTC TGTGCTTGA TGCCAACTC GCCACCCAGC ATGCAGCTGC 1800
CACCAACCAC CTCGAAAGG CTGGCAACAT GCGAGGGCT CATAGCCACC CTCACCTG 1860
TCAATGCCAC ATGTGATGC ATCTTGTCT TCTGTTGCT GAGCAAGGAG CCTGGAGACC 1920
AAAGGCCCT GGGCACTAT CCGGATGAGC ACTTCACAG GAGGCCCCCT CGGCGGAGCA 1980
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60 GCTGTGCT GCTTACACC TACCTAGACC CTCCTCAT CGAGAACAGC GTCTCCATCT 2100
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65 TTTGAGGCT CCAAGCCTCA AAGTGCCGC AGAGCCACC TTGAGGGTTT TGCTAGTTGG 2400
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CATCCACTGA TTGACCTTA TGGTCAOCCA ACTCAAGGAC AGCAACCAAG AAGTGGCTGC 2520
CAAAGAGACT GGGCGCAGT GCTCATGCC ATAATCCAG CACTTTGGA GATGGAGCG 2580
70 GGAATCAT TTGAGTCAAG AAGTTCAAG CCAGCCTGGA CGACATAGCG AGACTCCACC 2640
TCTACCAAAA AATAAAAT AAAAAACAAA AAAAAAAAAA AAAAA

75 SEQ ID NO:134 PFH5 Protein sequence:
Protein Accession #: NP_001132.1

1 11 21 31 41 51
MAEFRVRVST GEAFGAGTWD KVSIVGTR GESPLPLDN LKLEFTAGAE EDFQVTLPED 60
VGRVLLRVH KAPVPLLG PLAPDAWFCR WRQLTPRGG HLLFCYQWL EGAGTLVLQB 120
GTAKVSWADH HPVLQQRQE ELQARQEMYQ WKAYNPGWPH CLDEKTVEDL ELNIKYSTAK 180

NANFYLAQGS AFAEMKIKGL LDRKGLWRSI NEMKRIFNFR RTPAAEHAFB HWQEDAFFAS 240
 QFLNGLNPVL RRCHYLPKN FVTDAMVAS LLGPGTSLQA ELEKSLFLV DHGLSGIQT 300
 NVINGKPOFS AAPMTLLYQS PGCGLPLPLA IQLSQTGPN SPIFLPTDDK WDWLLAKTWV 360
 RNAEFSFHEA LTHLLHSHLL PEVFTILATLR QLPCHPLFK LLIPHTRYTL HINTLARELL 420
 IVPGQVVDRS TGIHIEGFSE LIQRNMKQLN YSLLCLPEDI RTRGVEDIPG YYRDDGMQI 480
 WGAVERFVSE IIGYVYFDE SVQDDRELQA WVREIFSKGF LNQESSGIPS SLETREALVQ 540
 YVIMVIFTCS AKHAAVSAGQ FDSCAWMPNL PPSMQLPFFT SKOLATCEGF IATLPVFNAT 600
 CDVLALWLL SKEPGDQRPL GTYPDEHFE EAPRRSIATF QSRLAQISRG IQERNRGLVL 660
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SEQ ID NO:135 PFH4 DNA SEQUENCE

Nucleic Acid Accession #: NM_002742

Coding sequence: 236-2974 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
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 TTTTCCTCTCT GGGCTCTCTG AGAAAGAAAG TCTCTCTCTC GCGGCTGCAA AACTTTCTCT 180
 CTGCGCGCTC GCGCGCGCTC GCGCTCTCTC GCGCGCGCTC GCGCGCGCTC GAGCGATGAG 240
 GCGCGCTCTC GCGCGCGCTC GCGCGCTCTC GCGCGCTCTC GCGCGCGCTC GAGCGCGCTC 300
 AGCGCGCTCT GCGCGCTCTC GCGCGCTCTC GCGCGCTCTC GCGCGCTCTC GCGCGCTCTC 360
 GCGCGCGCTC GCGCGCGCTC TCTCTCTCTC TCTCTCTCTC TCTCTCTCTC TCTCTCTCTC 420
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 CTCTCTCTCT GCGCGCTCTC GCGCGCTCTC GCGCGCTCTC GCGCGCTCTC GCGCGCTCTC 960
 TCGAGAGAAAG AGGTCAAAAT CTCAATCATA CATTGGACGA CCAATTCACC TTGACAAGAT 1020
 TTTGATGCTT AAAGTTTAAAG TCTCTCTCTC TCTCTCTCTC TCTCTCTCTC TCTCTCTCTC 1080
 AGTGTGCTCT TACTCTCTCT AGCTCTCTCT GCGCGCTCTC GCGCGCTCTC GCGCGCTCTC 1140
 AGATTTCTCT TCTCTCTCTC TCTCTCTCTC TCTCTCTCTC TCTCTCTCTC TCTCTCTCTC 1200
 CGAAGTGACC ATTAATGGAG ATTGCTTAG CCGTGGGCA GAGTCTGATG TGTCTATGGA 1260
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 GCAAGATGCA GAGCGAGACC ACGAGGACGC CAACAGAAAC ATCAGTCCAT CAACAGGCAA 1440
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 GAGTATTCTA GATCTCTCTC GCGAGATTCA AGAAATGTTG GACATCAGCA CAGTATATCA 1980
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 ACTCAAGACA ATGCACTAG CTGTGCAAGA CTAAGTCTCT TTAAGCTTAA ATGCTTGA 3600
 AATGAAACTT GCCATATATA ACAGATACAT TTCTCTCTCT CTTATAATAC TCTGTTGATC 3660

TATGGAAAAAT CAGCTGCTCA GCAACCTTTC ACCTTTGTGT ATTTTTCAT AATAAAAAAT 3720
ATTTCTGTCA AAAAAAAAAA AA

5 SEQ ID NO:136 PFH4 Protein sequence;
Protein Accession #: NP_002733.1

10 1 11 21 31 41 51
MSAPPVLRPP SPLLPVAAAA AAAAAALVPG SGPGPAPFLA PVAAPVGGIS FHLQIGLSRE 60
PVLLQDSSG DYSLAHVREM ACSIVDQKFP ECGFYGMYYDK ILLFRHDPTS ENILQLVKAA 120
SDIQEGDLIE VVLSRSATFE DFQIRPHALF VHSYRAPAFD DHCGEMLWGL VRQGLKCEGC 180
15 GLNYHKRCFA KIPNNCSGVR RRRLSNVSLT GVSTIRTSSA ELSTAPDEP LLQKSPSESF 240
IGREKRSNSQ SYIGRPIHLD KILMSKVVP HTFVIHSYTR PTVCQYCKKL LKGLFRQGLQ 300
CKDCRFNCHK RCAPKVPNNC LGEVTINGDL LSPGAESDVV MEEGSDNDNS ERNSGLMDDM 360
EAMVQDAEM AMAEQNDSDG EMQDPDPDHE DANRTISPST SNNPLMRVV QSVKHTKRKS 420
STVMKEGWMV HYTSKDTLRK RHYWRDLSKC ITLFQNDTGS RYYKEIFLSE ILSLEPVKTS 480
20 ALPNGANPH CFEITANVV YVYGENVVNP SSPSPNNVL TSGVGADVAR MWEIAIQHAL 540
MPVPEGSSV GTGNLHRDI SVSISVNCQ IQENVDISTV YQIFDEVLG SQQGIVYGG 600
KHKRTGRDVA IKIDKLRFP TKQESQLRNE VAILQNLHHP GVVNLECMFE TPERVFFVME 660
KLHGDMLMI LSEKGRLEFE HITKFLITQI LVALRHLHFK NIVHCDLKPE NVLLASADPF 720
PQVKLDFGFI ARIIGKSFPR RSVVGTIPAYL APEVLRNKG YNRSLDMWSVG VHYVSLSGT 780
25 PFNEDEDIH DQIQNAAFMY PPNPWKEISH EADILNNLL QVKMRKRYSV DKTLSHPWLQ 840
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EMKALGERVS IL

30 SEQ ID NO:137 PFH3 DNA SEQUENCE
Nucleic Acid Accession #: X95425
Coding sequence: 712-3825 (underlined sequences correspond to start and stop codons)

35 1 11 21 31 41 51
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40 TTGCTTTTG CTGCTGCTC TCCTGTTTTT CATTCTCCAC ATTCTCTCAA TCCTCTTTCT 240
TTATCCTTAG CCACCTCTCT TTTTCTCTCC TTTTIAAAA AATCGGAGAT TCTGCTTAA 300
AATGATTGT CTCTCTTACC TTGCTCCATT TCAACACTGA AGGCTGCAAA GAACCTCAAC 360
TTTCCCTAG TGGTATTAA AAATCTCTCA TCCGTAAAAA GTCTTTTGA AAGGCAAGG 420
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45 ACTAATATTT CATTAACCC ACCAAAAGGG GGAGGGGAGA GGAGCCAGAA GCAAACTTCA 540
TCTGTCTAG ACGGATCCGT GGTTCCTACA TTGGAGGAG CCGCGTGTCA GAAGGCGTAG 600
GACCCCAAGG GGGGACAAGG AGGACTCCCG AGTCTCCCTT CTCGCTCTC CGAGACCGAA 660
GAGGTGGAAT GAGCCGCTCG GGACAGCGGC ACCGGAGGAG GCTCGGAGAA GATGCGGGGC 720
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50 ACCCCAGCGT CCTGGCCGG CTGCTACTCT GCACCTCGAG GGGCTCCCT CTGGAAGTGC 840
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55 TCAGAAATCT TCATAGAACT CAAATTTACC CTGCGGACT GCAACAGCT TCCTGGAGGA 1140
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AGAAACATCA AGGAAAACCA ATACATCAAA ATTGATAACA TTGCTGCCGA TGAAGCTTT 1260
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60 GTTCTGTGC GTGTATACTA TAAAAAATGC CCTTCTGTGG TACGACACTT GGCTGTCTTC 1440
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GTGTGCAGAT CTGGGTCTCT CAAAGCTCA CCTCACATCC AGAGCTGCGG CAAATGTCCA 1680
65 CCTCACAGT ATACCATGA GGAAGCTTCA ACCTCTGTG TCTGTGAAAA GGATTATTTT 1740
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GCCATCTCAA ATGTTAATGA AACTAGTGT TTTCTGGAAT GGATTCGCC TGCTGACACT 1860
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GTGTGTGAG AGTGTGGGG TCAATGCAG TACCTTCCC GGCAGGCGG CCTGAAAAAC 1980
70 ACTTGTGCA TGAATGTGGA TCTACTGCT CACACAACT ATACCTTGA GATTGAGGCA 2040
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ATCAAGCAT TTGAAAAAG CCAAGAGACC AGCTACACA TATCAAAAT TAAAGAGACA 2280
75 ACTATTACTT CAGAGGGCTT GAAACAGCT TCAGTTTATG TTTCCAAAT TCGAGCAGT 2340
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ATTTGTGTG CAGTGGTAT CGCGCTCTC CTCAGTGAA GTTGCTGCA ATGTGGCTGT 2520
GGGAGGGCTT CTTCCTGTG CGCTGTGCC CATCAATCC TAATATGCG GTGTGCTAC 2580
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 5 GAAGCAAGTA TCATGGGACA GTTTGATCAT CCTAACATCA TOCATTTAGA AGGTGTGGTG 2940
 ACCAAAAAGTA AACCAGTGAT GATCGTGACA GAGTATATGG AGAATGGCTC TTTAGATACA 3000
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 10 AGAAACATCT TAATCAACAG TAACTGTGTG TGCAAAAGTG CTGACTTTGG ACTTTCCCGG 3180
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 20 GATTGAGAC GGCTTGGAGT GACTCTTGTG GTTACCAGA AGAAGATCAT GAACAGCCTT 3780
 CAAGAAATGA AGGTGCAGCT GGTAAACGGA ATGGTGCCAT TGA~~ACT~~CTCA TGAAATGTC 3840
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 AAA

25

SEQ ID NO:138 PFH3 Protein sequence
 Protein Accession #: CAA64700.1

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1 11 21 31 41 51
 MRGSGPRGAG HRRPPSGGGD TPITPASLAG CYSAPRRAPL WTCLLCAAL RTLLASPSNE 60
 VNLLDSRTVM GDLGWIAFPK NGWEEIGVD ENYAPIHTYQ VCKVMEQNQN NWLLTSWISN 120
 EGASRIEFL KFTLRDCNSL PGGLGTCKET FNMYFESDD QNGRNIENQ YIKIDTIAAD 180
 35 ESFTELDLDG RVMKLNTEVR DVGLPSKKG F YLAFQDVGAC IALVSVRVYY KKCPSVVRHL 240
 AVFPDITIGA DSSQLLEVSG SCVNHSTDE PPKMHCSAEG EWLVPIGKCM CKAGYEEKNG 300
 TCQVCRPGFF KASPHIQSG KCPHSHYTHE EASTSCVCEK DYFRRESDFP TMACTRPFA 360
 PRNAISNVNE TSVFLEWIFF ADTGGRKDVS YYLACKKCNH HAGVCEECGG HVRYLPRQSG 420
 40 LKNTSVMVMD LLAHTNYTFE IEAVNGVSDL SPGARQYVSV NVTTNQAAPS PVINVKKGKI 480
 AKNSISLSWQ EPRDRNGILL EYEIKHFEKD QETSYYIIS KETTITAEGL KPASVYVFI 540
 RARTAAGYGV FSRREFEFTT PVFAASSDQS QIPVIAVSVT VGVILLAVVI GVLLSGSCCE 600
 CGCGRASSLC AVAHPILWR CGYSKAKQDP EEEKMHFHNG HIKLPVVRTY IDPHTYEDFN 660
 QAVHEFAKEI EASCHTIERV IGAGEFGEVC SGRLKLPGRK ELPVAIKTLK VGYTEKQRRD 720
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 PRWTAPEAI AFRKFTASD VWSYGIVMWE VVSYGERPYW EMTNQDVKA VEEGYRLPSP 900
 MDCPAALYQL MLDWQWKERN SRPKFDEIVN MLDELIRNPS SLKTLVNASC RVSNLLAEHS 960
 50 PLGSGAYRSV GEWLEAIKMG RYTEIFMENG YSSMDAVAQV TLEDLRLRGV TLVGHQKKIM 1020
 NSLQEMKVQL VNGMVPL

55

SEQ ID NO:139 PFH2 DNA SEQUENCE

Nucleic Acid Accession #: NM_016029
 Coding sequence: 78-1097 (underlined sequences correspond to start and stop codons)

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1 11 21 31 41 51
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 TGCTCTGCTC CTGTGTGAGC CTGCTGCGCT TCCTGAGGGC TGACGCGGAC CTGACGCTAC 180
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 65 TGACTGGAGC CTCGAGTGGA ATTGGTGAGG AGCTGGCTTA CCAAGTTGCT AAACATAGGAG 300
 TTTCTCTTGT GCTGTGAGCC AGAAGAGTGC ATGAGCTGGA AAGGGTGAAA AGAAGATGCC 360
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 TGGTCAACAA TGGTGGAAAT TCCACGCTT CTCTGTGCAT GGATACACAGC TTGGATGTCT 540
 70 ACAGAAAGCT AATAGAGCTT AACTACTTAG GGACGGTGTC CTTGACAAAA TGTGTTCTGC 600
 CTCACATGAT CGAGAGGGAAG CAAGGAAAGA TTGTTACTGT GAATAGCATC CTGGGTATCA 660
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 75 GCAATAAGTG AGACAGCTCC CACAAGATGA CAACCAATCG TTGTGTGGCG CTGATGTTAA 900
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 AGACAAAAAC TGACTGAAAA GAGCACTGT ACTTTTCAAG CCACTGGAGG GAGAAATGGA 1140
 AAACATGAAA ACAGCAATCT TCTTATGCTT CTGAATAATC AAAGACTAAT TTGTGATTTT 1200

ACTTTTAAAT AGATATGACT TTGCTTCCAA CATGGAATGA AATAAAAAAT AAATAATAAA 1260
AGATTGCCAT GAATCTTGCA AA

5

SEQ ID NO:140 PFH2 Protein sequence:
Protein Accession #: NP_057113.1

1 11 21 31 41 51
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10 MNWELLWLL VLCALLLV QLLRFLRADG DLTLLWAEWQ GRRPEWELTD MVVWVTGASS 60
GIGEELAYQL SKLGVSLVLS ARRVHELERY KRRCLENGNI KEKDILVPL DLTDTGSHEA 120
ATKAVLQEFGR IDILVNNNG MSQRSLCMDT SLDVYRKLIB LNYLGTVSLT KCVLFPHMER 180
15 KQGKIVTVNS ILGISVPLS IGYCASHAL RGFNGLRTE LATYPGIUS NICPGPVQSN 240
IVENSLAGEV TKTIGNNGDQ SHKMTTSRCV RLMLISMAND LKEVWISEQP FLVITYLWQY 300
MPTWAWWITN KMGKKRIENF KSGVDADSSY FKIFKTKHD

20

SEQ ID NO:141 PFH1 DNA SEQUENCE

Nucleic Acid Accession #: NM_021614
Coding sequence: 1-1740 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
| | | | |
25 ATGAGCAGCT GCAGGTACAA CGGGGGCGTC ATGGGGCGCG TCAGCAACTT GAGCGCGTCC 60
CGCGCGAACC TGACGAGAT GGACTCAGAG GCGCAGCCCC TGACGCCCC CGGTCTGTCT 120
GGAGGAGGTG CGGGCGCGTC CTCCCGTCT GCAGCGCTG CGCGCGCGCG CGCTGTTTCG 180
30 TCCTCAGCCC CGAGATCGT GTGTCTAAG CCGAGCACA ACACTCCAA CAACCTGGCG 240
CTCTATGAA CGGGCGCGG AGGCAGCACT GGAGGAGCG GCGCGGTGG CGGGAGCGGG 300
CAGGCGACA CGAGTGGCAC CAAGTCCAGC AAAAAGAAAA ACCAGAACAT CGGCTACAAG 360
CTGGGCCACC GCGCGCGCT GTTCGAAAAG CGCAAGCGGC TCAGCAGCTA CGCGCTCATC 420
TTGGCATGT TCGCATGCT GGTCTGCTC ATCGAGACCG AGCTGCTGT GGGCGCCTAC 480
35 GACAAGGGCT CGCTGTATTC CTTAGCTCTG AAATGCCCTA TCAGTCTCTC CACGATCATC 540
CTCTCTGGT TGATCATGCT GTACCAAGCC AGGGAATAC AGTTGTTTAT GGTGGACAAT 600
GGAGCAGATG ACTGGAGAAT AGCCATGACT TATGAGCGTA TTTCTTCAT CTGCTGGAA 660
ATACTGTTGT GTGCTATTCA TCCATAOCT GGAATTATA CATTACATG GACGGCCCGG 720
CTTGCCTTCT CCTATGCCCC ATCCACAACC ACCGCTGATG TGGATATTAT TTTATCTATA 780
40 CCAATGTTCT TAAAGTCTA TCTGATTGCC AGAGTCATGC TTTTACATAG CAAACTTTTC 840
ACTGATGCTT CCTCTAGAAG CATTGGAGCA CTTAATAAGA TAAACTTCAA TACACGTTTT 900
GTTATGAAGA CTTTAATGAC TATATGCCA GGAAGTGTAC TCTTGGTTTT TAGTATCTCA 960
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GTTACTAGCA ACTTCTTGG AGCGATGTGG TTGATATCAA TAACTTTCT CTCCATTGGT 1080
45 TATGGTGACA TGGTACCTAA CACATACTGT GGAAGAGGAG TCTGCTTACT TACTGGAATT 1140
ATGGGTGCTG GTTGCACAGC CTTGTTGTTA GCTGTAGTGG CAAGGAAGCT AGAAGTTACC 1200
AAGCAGAAAA AACACGTGCA CAATTTATG ATGGATACTC AGCTGACTAA AAGAGTAAAA 1260
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AAAAAGATAG ATCATGCAAA AGTAAGAAAA CATCAACGAA AATTCTGCA AGCTATTCT 1380
CAATTAAGAA GTGTAAAAAT GGAGCAGAGG AAAGTGAATG ACCAAGCAAA CACTTGGTG 1440
50 GACTTGGCAA AGACCCAGAA CATCATGTAT GATATGATT CTGACTTAAA CGAAAGGAGT 1500
GAAGACTTGG AQAAGAGGAT TGTACCTG GAAACAAAAC TAGAGACTTT GATTGGTAGC 1560
ATCACGCCCC TCCCTGGGCT CATAAGCCAG ACCATCAGGC AGCAGCAGAG AGATTTCATT 1620
GAGGCTCAGA TGGAGAGCTA CGACAAGCAC GTCACCTACA ATGCTGAGCG GTCCCGGTCC 1680
55 TCGTCCAGGA GCGCGCGGTC CTCTCCACA GCACCAACCA CTTATCAGA GAGTAGCTAG

60

SEQ ID NO:142 PFH1 Protein sequence:
Protein Accession #: NP_067627

1 11 21 31 41 51
| | | | |
60 MSSCRYNGGV MRPLSNLSA RRNLHMDSE AQPLQPPASV GGGGGASSPS AAAAAAAVS 60
SSAPEIVVSK PEHNNNNLA LYGTGGGGST GGGGGGGSGG HGSSSGTKSS KKKKNQNGYK 120
65 LGHRRALFEK RKRLSDYAL FGMFGIVMV IETELSWGAY DKASLYSLAL KCLSLSTII 180
LLGLIIVYHA REIQLFMYDN GADDWRIAMT YERIFFICLE ILVCAIPIP GNYTFTWTAR 240
LAFSYPSTT TADVDIISI PMFLRLYLIA RVMLLHSLKF TDASSRSIGA LNKINFNTRF 300
VMKLTMTICP GTVLLVFSIS LWIAAWTVR ACERYHDQDQ VTSNFGAMW LISITLSIG 360
YGDMPVNTYC GKGVCLLTGI MGAGCTALVV AVVARKLELT KAEKHVHNFM MDTQLTKRVK 420
70 NAAANVLRET WLTYKNTKLK KIDHAKVRK HQKFLQAIH QLSVKMEQR KLNDQANTLV 480
DLAKTQNMV DMISDLNERS EDFEKRIVTL ETKLETIGS IHALPLISQ TIRQQQRDFI 540
EAQMESYDKH VTYNASRSR SSSRRSSST APPTSSES

75

SEQ ID NO:143 PFG9 DNA SEQUENCE

Nucleic Acid Accession #: AL110139, coding region is FGENESH predicted
Coding sequence: 1-1896 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51

5
 10
 15
 20
 25
 30
 35

ATGGGCGGCG TGCGCTGCG CGCGCGCTC CTGCGGCTGC TGCTGCTGCG GCTCTGGCC 60
 GCTCCGCGCG CCGCGGCCAG CAGAGCGGAG TCCGTCTGCG CGCGGTGGCC CGAAACCGAG 120
 CGCGAGTGGC GCGCACCGCC CCGCGCGGGG CCGCGGAACA CCACCGGTT TGGGTCTGGG 180
 GCGGCGGGCG GCAGCGCGAG CTCAGCTCC AACAGCAGTG GCGACGCTT GGTGACCGC 240
 ATTTCCATCC TCTCCGCGA CTAACCAACC CTCAGGCGAG CCGTGATCGT GCGTTGCGC 300
 TTTACCACCC TCTCATGCG CTGCTGCTG CTGCGCGTCT TCAGGTGCGG AAAGAGGTTA 360
 AAGAAGACAC GCAAGTATGA TATCATCAC ACTCCAGCAG AGCGAGTGA AATGGCGCCA 420
 CTAATGAAG AGGATGATGA AGATGAGGAC TCCACAGTAT TCGACATCAA ATACAGAGTG 480
 TCTTGCGCG CTGCACTGAG ACGTCAGCTG CCAGGGTGGC AGAOGCTACT GACAGTTCT 540
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 TCAGCTGCAA CTGGGGTGT GAAGGACTGG ACCTGGAAGC CCTCTGCGT CGGAGGTGTT 720
 GAAACCAAAA CGAACGTTAT GTATAAAACC CCAGCTCCAT CCGTGGTGT AGGCATCTGC 780
 TCAGACTGTC ACTGGCAAGC TGTITTCAC GTCACCAAA TGGAGTTGCT TCTGCCACCC 840
 TTTGGGCATC CCTTAAAGT GCGGCTACT TCTACTCCC ATGGTTTTCG ACAACTGCAG 900
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 GCGAGGTGCT TGCCACTGTT CTTGGCAGAA ATGGCGGCTG CTGAAAGTGA CCTTCCAAAT 1020
 CCTTGGTGGC ACTTCAGCGC CACAGGCTCT CCAATAAAAA CCTTACAC ACAAAACCATG 1080
 AGTACCTGG GCTTGATGT TTTCTGTTG GCGGCGCAG GGGCACTT TGTGAAGAC 1140
 AGAGCAGTGA CTAAGTTCT CCAGGGTAGC TCTTCTCCA AACAGCTGG CTGGAAGCCA 1200
 GCGCTAGAGA GTGGGTTTCC CCATCATCTC AGGCTTCTCA GAGAGTGTCC TCGCTGAGC 1260
 ACCCATCTG TCAGGTGGC TCGTTTCTGAT GCGCGGGAC AAGCCAGCT GACGGGAGG 1320
 AGGTGTTTC GCGTGGCGG GCAGTCTCTG CATGGCGGAG GGTGAGCGGG TACCGCAACT 1380
 TGCTTTTGG TTTGAAGAT TCTGTTGAG CGCATCTC ACCTTGAOCT CTCTACAAA 1440
 ATCTGTCTCC CCGCTGTGCG CTGGAACAC CTACGGGAG CCAAGAGAAG CTCAGTGACT 1500
 GTCTTGGCT CATTTGAGCA GAGGCCACAA AAGGCAGCTG CTGCCACGG GGAGCTGTCT 1560
 AAAAGAGGGC CCACTGGGCA ATTGACGAGA CACACATGCC CTGGCTGGGG GATCACACAT 1620
 GCGAACCTGC AGACAATTCC AGATACCAA GGCCAGGAAG GCGCAGTGA GGATGTCACT 1680
 CACCTGGAG GAGACTTGA TGGGTGGCA AATTCTATT TGGAGGAAGA GGGTTTCCAG 1740
 GATGGCAGAT GCGAGAAAGT GGTCTGATG TCTGAGGAAG GCGCACCTAG TTTGACAGGA 1800
 TGTGAGAGGC TCACAGGTTT CCATCACTTC TCCAGCCATT CCAAGTCTTG GTCTCTCTT 1860
 TCCCCCGAC AGCCCTGTT TCTGTCCAGG CCCTGA

SEQ ID NO:144 PFG9 Protein sequence

Protein Accession #: none available, FGENESH predicted

40
 45
 50

1 11 21 31 41 51
 MRAPLPAFL LPLLLALLA APAARASRAE SVSAPWPEPE RESRPPPGPG PGNTRFGSG 60
 AAGSGSSSS NSSGDALVTR ISILLRDLPT LKAAVIVAF FTLIACLL LRVFRSGKRL 120
 KKTKYDIIT TPAERVEMAP LNEEDDEDED STVFDIKYRV SLPAALRRQL PGCQILLTVP 180
 VPPFELDID LPARCGRPD GGRPGKTCF PAWWHPVESW SAATWGVKDW TWKPSCVGGV 240
 ETKINVMYKT PAFSCVSGIC SDCHWQARFH VTMELLPLP FGHFFKVPPT STPHGFRQLQ 300
 LNLMEKLDSS ALRRNTRAPS ARCLPLVLA MAEAESDLPN PWWHFSATGS PIKLYTQTM 360
 STLGLDVFCC AGQRGTFCED RAVTKVLQGS SFSKQLRWKP ALESGFPHIL RLRECPPLS 420
 THPVRLARS ARGQASLTGR RVFRFRQSL HGGSGAGTAT CLLVLKILL RHPHLDLFYK 480
 ICLPCCAVEH LREAKRSSVT VLASFQSPQ KAAAHAHEPV KRGPSQLIR HPCFGWGITH 540
 ANLQITPDTQ QGEGPREDVT HPGDLDGVA NFYLEEBGFQ DGRQCKMVLN SEBGPPLSTQ 600
 CERLTGSHHF SSHSKSWFL SPQPLFLSR P

SEQ ID NO:145 PFG8 DNA SEQUENCE

Nucleic Acid Accession #: NM_013427

Coding sequence: 875-3783 (underlined sequences correspond to start and stop codons)

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 65
 70
 75

1 11 21 31 41 51
 GGCTGGGCTG CGAATAGCGT GTTCTCTCC GCGCGAACAC ACACACCGG CTTGGGGCT 60
 GTCTCTGAA GCTCCCTCT CCACGGAGAG CGCTGAGCGC CGCGGGAAT TCATCCAC 120
 CGTGGGCACG CAGTCTTTGG AGTCCCGGG CGCAGCACGC TCGGTGTGCC CACACTGCAG 180
 CAAGACAGAG ACCCGCGGG AACCTTGAGC TTGGAACAAC CTTGAGCCT CTGCAGTCGG 240
 AAGAGTGGGC GCAGCAGCCC AGCGGAGGCC AGCGCGCAA CCTCGGGCGC CGGGGCAAGG 300
 AGAGAGTGCA GGGAGGGGCA GCTCAGCGC CCGGCTCAGG AGCGGGAGGA AGTTCTCGCG 360
 GCGCGGGAG CGCGGTGGAC GCGCCTGGG CGCACGCCCA GGCAGCCTTC TCCCTGGCCC 420
 TCGGGACTGT CTTGGGCGG CAAGGAGGAG CTTGCTGGAG TCTTAGAGGC CATCCAGAGC 480
 CAGCGAGCAG GAGCGCTGCG TCTCCGCTC CAGCTAGGAA GGGGGAGTGG CGCTGGCAGG 540
 CTGGAGCTGG GAACCCAGCG AGCGCTGAC CTCTCTCTC CTCTCTCTGA CCTCTTTCG 600
 GTCTTGGCT CCGGAGGAAG GTTCTAGCGG CTGCAGGAGG TCCCCAGACC CATTTTCTA 660
 GAAGGCTGGT GATGATCTG CTGCTCTGC CGCGCGCGG GCACTTGGAG CGCAACGGCG 720
 GCGCGTGAAG TGGCTTTGC TCTCCACCG CTTGGGCAA CCGCGGGCA GCGCGCGCTG 780
 GCACTTTGC CTGATTCCT TCGGTTCC GACCAAAAG CACAGCGTC CAGGAGGGA 840
 GGAGGAGGTG GTCTCAGGT GCAGCCCCG CGAGATGTC GGCAGAGGC TGCTCCACAG 900
 CGTCTCTCC TGTCTGCG CCGCTTCAAG TAGCGCGGC TGGGCAAGG GCTTCTCAA 960
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 CGAGGCGGCG GCGAGGGCA GTGCGGGGG AGCCACGGCG GCGCGCTCT ACTCCCATC 1080
 ACTCCAGCC GAGAGTCTG GCGCTGCTT GCGCTCTCT TCCGGGGTC CGCGCCAG 1140
 GGCACACAG CTACCGCTC CTGGACTCT TTGCTGCTC TTCTCCACAC CCAGCACCCC 1200

GCAGGAGAAG TCACCATCCG GCAGCTTTCA CTTTACTAT GAGGTTCOC TGGGTGCGG 1260
 CGGCTCAAG AAGAGCATGG OCTGGGACCT GCCTTCTGT CTGGCCGGC CAGCCAGTAG 1320
 CCGAAGCGCT TCACGATCC TCTGTTTCAT CGGGGGAGGC CCCAATGGCA TCTTCGCTTC 1380
 5 TCTAGGAGG TGGCTCCAGC AGAGGAAGTT CCAGTCCCA CCGGACAGTC GCGGGCACCC 1440
 CTACGTGTG TGGAAATCCG AGGGTGATT CACCTGGAAC AGCATGTGAG GCGGCACTGT 1500
 GCGGCTGAGG TCAGTCCCA TCAGAGTCT CTCAGAGCTG GAGAGGGGCC GGCTGCAGGA 1560
 AGTGCCTTTT TATCAGTTGC AACAGGACTG TGACCTGAGC TGTCAGATCA CCATTCCCAA 1620
 AGATGGACAA AAGAGAAAAG AATCTTTAAG AAAGAAAAGT GATTCACTAG GAAAGGAGAA 1680
 10 AAACAAAGAC AAAGAATTCA TCCACAGGC ATTTGGAATG CCTTATCC AAGTCATTGC 1740
 GAATGACAGG GCCTATAAAC TCAAGCAGGA CTTCAGAGG GACGAGCAGA AAGATGCATC 1800
 TGACTTTGTG GCTTCCCTCC TCCATTGG AAATAAAAGA CAAACAAAG AACTCTCAAG 1860
 CAGTAATCA TCTCTCAGCT CAACCTCAGA AACACCGAAT GAGTCAACGT CCCAAACAC 1920
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 TCTGTATGAC AATCAGTCTC GACTACTAGA AGCTTTACAA CTTTCTTGC CTGCTGAGGC 2040
 15 TCAAAGTAA AAGGAAAAAG CCAGAGATAA GAAACTCAGT CTGAATCTA TTTACAGACA 2100
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 20 CATCAACT CTCTTGTGG AGCCGGAGGA ACAGCTGGGC ACCTTGACG TCTCATATA 2400
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 AGACAAAGAA TTTCTAGTTC AGAGTTCAGC CCGGCTGAG GAGAGCACCG CCATCATCGC 2640
 25 TGTGTGCAA AAGATGATTG AAAATTATGA AGCCCTGTT ATGTTTCCC CAGATCTCCA 2700
 GAACGAAGTG CTGATCAGCC TGTAGAGAC CGATCCTGAT GTGTTGGACT ATTTACTCAG 2760
 AAGAAGGCT TCCAAATCAT CAAGCCCTGA CATGCTCAG TCGGAAGTTT CCTTTTCCGT 2820
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 30 CCGGGGGGC TGGAGAAGC TTTACAGAGT GCCAGGGCAG TTTATGCTGG TGGGCCACTT 3000
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 AGGAATGACA GATTCTCTC GAGACATTT TGAAGCAGC TCCCTAAGAG CGGGGCGCTG 3180
 CTCCTTTCT CAAGGGAACC TGTCCCAAA TTGGCTCGG TGGCAGGGA GCGCCGAGA 3240
 35 GCTGGACAGC GACACGAGG GGGCTCGAG GACTCAGGCC GCAGCCGCC GACGAGGAGG 3300
 CAGGGCCAC OCTGCGGTG CGCGCGCTG CAGCACGCC CAOGTCCAGG TGGCAGGGAA 3360
 AGCGAGAGCG CCACCGGCCA GGTGCGGACA GTACTTGACC CTGAGCGGCG CCACGACCT 3420
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 40 ACCCATGGG AGTGGGAGG ATGACAAGG GCGCCGCTC CCATACCGG GCCCAGGGAA 3540
 GCGCGCGGA GCGGAGCCT GGTCCAGGG GCGCCGGA GCGTGGAGA CACCAAGGA 3600
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 45 GCGGAGAGC CTGGTCTGAG CCGGACCCA GCGAGGCC CCGTCCCGG AGCCCGCGC 3840
 CCTCCAGCC AGGGGGGACC GTGGGTGGT GGCCTGCA CACTTAATGT TCTTCTTCA 3900
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 50 AACTCTGCT TGGTATAGC TAACCGTATT TATGTGCTT CGGTTTGGC TATTGTGAT 4140
 TCTGTAACAG ATTATGTATA ATCATATAT ATATATTCAC AAAGAGAAAA CAAAAGGAAC 4200
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 55 CATATTTTA CATGAGAGT AGATACAAAA AGAAAAATCA CTGAATGCTT TTAGATATTG 4440
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 60 TTAAGAATCT ACACAGAATA TTCAAATTAT AGAACATGTT TTTCCCTT GCCCATAAT 4740
 CAGTATTGTC CAAATTACAT GCAATTCCT AAAAATAAAA TCACATTGGT AAAAGGCCTA 4800
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 65 AAAGTGATT ATAAAAAAG ATTTTITTT TTTAAACAT GCTACTCTTA ATTTTCATGT 5040
 TGGTGATGAA ATCCAGTG GTGTTTCTTA AGGTTCTATC TTGTGCCATG ATGAATAAAA 5100
 AGTTAAGCAA AAAAAAAAAA AAAAAAAAAA AAA

SEQ ID NO:146 PFG8 Protein sequence
 Protein Accession #: NP_038288.1

1 11 21 31 41 51
 MSAQSLHSHV FSCSSPASSS AASAKGFSKR KLRQTRSLDP ALIGOCGSDE AGAEGSARGA 60
 75 TAGRLYSFSL PAESLGRILA SSSRGPPRA TRLPPGPLC SSFSTPTQ EKSPSGSFH 120
 DYEVFLGRGG LKSMWDLV SVLAGPASSR SASSILCSSG GPNPFIASP RRWLQQRKFQ 180
 SPFDSRGHPY VVWKSEGDFT WNSMSGRSVR LRSVPIQSL ELERARLQEV PFYQLQDCD 240
 LSCQTFPKD GQKRKSLRK KLSLKGKKN KDKFIPQAF GMPLSQVIAN DRAYKLQDL 300
 QRDEQKQASD FVASLLPFGN KRQNKELSSS NSSLSSTSET PNESTSPNT EPAPRRRRR 360

5 AMSVDSITDL DDNQSRLLA LQLSLPAEAQ SKKEKARDKK LSLNPTYRQV PRLVDSQQH 420
 LEKHGLQTVG IFRVGSSKKR VRQLREEFDR GIDVSLSEEH SVHDVAALLK EFLRDMFDPL 480
 LTRELYTAH NTLLEPEEQ LGTLQLLIYL LPPCNDTLH RLLQFLSIVA RHADDNISKD 540
 GQEVTKNMT SLNLATIFGP NILHKQKSSD KEFSVQSSAR AEESTAHAV VQKMENYEA 600
 LFMVFPDLQN EVLISLLETD PDVVDYLLRR KASQSSSPDM LQSEVSFVG GRHSSTDSNK 660
 ASSGDISPYD NNSPVLERS LLAMQEDAAP GGSEKLYRVP GQFMLVGHLS SSKSRESSPG 720
 PRLGKDLSEE PFDIWTGTHS TLKSGSKDPG MTGSSGDIFE SSSLRAGPCS LSQGNLSPNW 780
 10 PRWQSPAEI DSDTQGAARR QAAAPATEGR AHPAVSRACS TPHVQVAGKA ERPTARSEQY 840
 LTLGSAHDL S ESELDVAGLQ SRATPQCQRP HSGSRDDKRP PFPYPGPKP AAAAAWIQGP 900
 PEGVETPDQ GGQAAREBQ VTQKKLSSAN SLPAGEQDSP RLGDAGWLDW QRERWQIWEL 960
 LSTDNPDALP ETLV

15 SEQ ID NO:147 PFG4 DNA SEQUENCE
 Nucleic Acid Accession #: NM_002202
 Coding sequence: 240-1289 (underlined sequences correspond to start and stop codons)

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 OCCCCGAGCC GCGCCGAGTC TGCCGCGGCC GCAGCGCCTC CGCTCCGCCA ACTCCGCCGG 60
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 25 GGCTGTTCAC CACTGTACA ACCACCATTT CACTGTGGAC ATTACTCCTT CTTACAGATA 240
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 30 AGTGACGAT CCGCTTCAGC AAGAACGACT TCGTGATGCG TGCCCGCTCC AAGGTGTATC 540
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 CGCTTCGGGA GGACGGTCTC TTTCGCGAG CAGACCCAGA TGTGTGGAG AGGGCCAGTC 660
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 40 CAGGAACTCC CATGGTGCTT GCCAGTCCAG AGAGACACGA CGGTGGCTTA CAGGCTAACC 1080
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 45 TGGAGAAAGT GGGAAATTAT AATGTGGAAC TCTGAAACAA AAGTATTTAA CGACCCAGTC 1380
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 50 ACTGCACATC TAGAGAAAA CAAAAATAGA AAATTTTCTA GTCCATCTTA ATCTGAATGG 1680
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 GTCTGTCAA GAACTTTTCC CCAAAAGATG TGTATAGTTA TTGGTTAAAA TGACTGTTTT 2100
 CTCTCTCTAT GGAATAAAAA AGGAAAAAAA AAAGGAAACT TTTTGTGTTT GCTCTGTCAT 2160
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 60 TTTGACATTT TTTGTTGCT GAAGTGAAAA AAAAGATAA AGGTGTACG GTGGTCTTTG 2280
 AATTATATG CTAATCTAT GTGTTTGTCT TTTTCTTAA ATATTATGT AAATCAAAGC 2340
 GCCATATGTA GAATTATATC TTCAGGACTA TTTCATAAT AAACATTGG CATAGAT

65 SEQ ID NO:148 PFG4 Protein sequence:
 Protein Accession #: NP_002193.1

70 1 11 21 31 41 51
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 MGDPPKKKRL ISLCVCGGNQ IHDQYILR VS PDLEWHAACL KCAECNQYLD ESCTCFVRDG 60
 KTYCKRDYR LYGKCAKCS IGFSKNDVFM RARSKVYHIE CFRVCVCSRQ LIPGDEFALR 120
 EDGLFCRADH DVVERASLGA GDPLSLHPA RPLQMAAEPI SARQPALRPH VHKQPEKTR 180
 VRTVLNEKQL HTLRTCAYAN PRPDALMKEQ LVEMTGLSPR VIRVWFQNR CKDKKRSIMM 240
 75 KQLQQQFPND KTNIQGMTGT PMVAASPERH DGGLQANPVE VQSYQPPWKV LSDFALQSDI 300
 DQPAFQQLVN FEEGGPGSNS TGSEVASMSS QLPDTPNSMV ASPIEA

SEQ ID NO:149 PFG2 DNA SEQUENCE

Nucleic Acid Accession #: NM_0011172

Coding sequence: 39-1103 (underlined sequences correspond to start and stop codons)

5 1 11 21 31 41 51
 GGGAGCTCT GCTTGGAGA TTCTCAGTGC TGGGATCAT GTCCTAAGG GGCAGCTCT 60
 CGCGTCTCT CCAGACGCGA GTGCATTCCA TCTGAAAGAA ATCGGTCCAC TCGTGGCTG 120
 TGATAGGAGC CCGTGTCTCA CAAGGGCAGA AAAGAAAAGG AGTGGAGCAT GGTCCCGCTG 180
 10 CCATAAGAGA AGCTGGCTTG ATGAAAAGGC TCTCCAGTTT GGGCTGCCAC CTAAAAGACT 240
 TTGGAGATTG GAGTTTACT CCAGTCCCA AAGATGATCT CTACAACAAC CTGATAGTGA 300
 ATCCAAGCTC AGTGGGTCTT GCCAACCAGG AACTGGCTGA GGTGGTTAGC AGAGCTGTGT 360
 CAGATGGCTA CAGCTGTGTC AACTGGGAG GAGACCACAG CTTGGCAATC GGTACCATTA 420
 GTGGCCATGC CCGACACTGC CCAGACCTTT GTGTGTCTG GGTGATGCC CATGCTGACA 480
 15 TCAACACACC CCTTACCCTT TCATCAGGAA ATCTCCATGG ACAGCCAGTT TCATTCTCC 540
 TCAGAGAACT ACAGGATAAG GTACCACAAC TCCCAGGATT TTCTGGATC AAACCTTGTA 600
 TCTCTCTGC AAGTATTGTG TATATTGGTC TGAGAGACGT GGACCTCTCT GAACATTTTA 660
 TTTTAAAGAA CTATAGATC CAGTATTTT CCATGAGAGA TATTGATCGA CTTGGTATCC 720
 AGAAGGTGAT GGAACGAACA TTGATCTGTC TGATTGGCAA GAGACAAAGA CCAATCCATT 780
 20 TGAGTTTGA TATTGATGCA TTTGACCCTA CACTGGCTCC AGCCACAGGA ACTCCTGTTG 840
 TCGGGGGACT AACCTATCGA GAAGCATGT ATATTGCTGA GGAAATACAC AATACAGGGT 900
 TGCTATCAGC ACTGGATCTT GTTGAAGTCA ATCCTCAGTT GGCCACCTCA GAGGAAGAGG 960
 CGAAGACTAC AGCTAACCTG CAGTAGATG TGATTGCTTC AAGCTTTGGT CAGACAAGAG 1020
 AAGGAGGGCA TATTGTCTAT GACCAACTTC CTACTCCAG TTCACCAGAT GAATCAGAAA 1080
 25 ATCAAGCAGC TGTGAGAATT TGGGAGACAC TGTGACTGTA CATGTTTCAC AACAGGCATT 1140
 CCAGAATTAT GAGGCATTGA GGGGATAGAT GAATACTAAA TGGTGTCTG GGTCAATACT 1200
 GCCTTAATGA GAACATTTAC ACATTCTCAC AATTGTAAGG TTTCCCTCT ATTTTGGTGA 1260
 CCAATACTAC TGTAATGTGA TTTGGTTTTT TGCAGTTCAC AGGGTATTAA TATGCTACAG 1320
 30 TACTATGTAA ATTTAAAGAA GTCATAAACA GCATTATTA CCTTGGTATA TCATACTGGT 1380
 CTGTGTGCTG TGTCTCTTC ACATTAAAGT GGTTTTTCAT CTTCTCTCC TCTCCACACA 1440
 GCCTGGCTAT ACAGTGCATC CTTGAAGTGT CAGCCACAG CAGCAATATG CTTATCTAT 1500
 CCACATCCTT AACATCATGC ATTCACAAGG TCAAAGTTCT GGTCCACAAA CCTTCCCTA 1560
 TAGAAGTTCA ATGGCTGCGA AAGAATTTGT AGTAAACCAG GCCTCCAGG ATGGCAGCT 1620
 35 CCAGTAAGAT GATAATGGAA AGCAGCAGCT TGTGGTTGT CACTCTACAA AGAGAAGCAA 1680
 AGTGGGGAGT AGTCAGAAAT TGGGATAACC TTCTTCTAA ACATTGGGG GTTAGACCTG 1740
 GGACCAACGGC TGGATCTCT GAGGCTGTAT GTTGATCAC ACAGCCACTT AGCAGGAAGT 1800
 ACTCATAAGG TTCTTAGCT GTCACTTAGG GATAACACTG TCTACCTCAC AGAAATGTTA 1860
 AACTGAGACA ATAAAACCA AAGCAT

SEQ ID NO:150 PFG2 Protein sequence:

Protein Accession #: NP_001163.1

45 1 11 21 31 41 51
 MSLRGSLRL LQTRVHSILK KSVHSVAVIG APFSQGQKRK GVEHGPAAIR EAGLMKRLSS 60
 LGCHLKDFGD LSFTPVKDD LYNLIVNPR SVGLANQELA EVVSRAVSDG YSCVTLGGDH 120
 SLAIGTISGH ARHCPDLCVV WYDAHADINT PLTTSSGNLH GQFVSFLRE LQDKVPQLPG 180
 50 FSWIKFICSS ASIVYGLRD VDPPEHILK NYDIQYFSMR DIDRLGIQKV MERTFDLLIG 240
 KRQRPHLSF DIDAFDPTLA PATGTPVVG LTYREGMYIA EEIHNTGLS ALDLVEVNPQ 300
 LATSEEEAKT TANLADVIVA SFGQTREGG HIVYDQLPTP SSPDESENQA RVRI

SEQ ID NO:151 PFG1 DNA SEQUENCE

Nucleic Acid Accession #: NM_017906

Coding sequence: 80-1255 (underlined sequences correspond to start and stop codons)

60 1 11 21 31 41 51
 AATTATATAT TTTACTCTA TGTCTCTA CATGTTTTT TCTTCCGTG GCTGGCGGAA 60
 GAGGCACGTG CGCTGCTGAA TGAAGCTG CGCTGTTGC TACGAGCAGG TCCTCTTTGG 120
 GTTGCCTGTA CACCGGAGC CCAAGGCTTG CGGCGACCAC GAGCAATGGA CTCTTGTGGC 180
 65 TGACTTCACT CACCATGCTC AACTGCTC CTTGTCAGCA GTAGCTGTAA ATAGTGGTTT 240
 TGTGGTCACT GGGAGCAAAG ATGAAACAAT TCACATTTAT GACATGAAAA AGAAGATTGA 300
 GCATGGGGCT CTAGTGCATC ACAGTGGTAC AATAACTTGC CTGAAATCTT ATGGCAACAG 360
 GCATTTAATC AGTGGACCGG AAGATGGACT CATCTGATC TGGGATGCAA AGAAATGGGA 420
 ATGCTGGAAG TCAATTAAGG CTCACAAAGG ACAGGTGACC TTCTTCTTA TTCACCCATC 480
 70 TGGCAAGTTG GCGCTGCGG TTGGTACAGA TAAACTTTA AGAACGTGGA ATCTTGTAAG 540
 AGGAAGATCA GCATTCTAA AAAATATAAA ACAAAATGCT CACATAGTAG AATGTTCCCC 600
 AAGAGGAGAG CAGTATGTAG TTATCATACA GAATAAAATA GACATCTATC AGCTTGACAC 660
 TGCATCCATT AGTGGACCA TCACAAATGA AAAGAGAATT TCTCTGTGA AATTCTTTC 720
 AGAGTCTGTC CTGTCAGTGG CTGGAGATGA AGAAGTTATA AGGTTTTTGG ACTGTGATTC 780
 75 ACTAGTGTGC CTCTGCGAAT TTAAGCTCA TGAACACAGG GTAAAGGACA TGTTCAAGTT 840
 TGAATTTCCA GAGCATCATG TTATTGTTT AGCATGGAGT GATGGTTTCA TCAAAATGTG 900
 GAAGCTTAAG CAGGATAAGA AAGTTCCCTC ATCTTACTC TGTGAAATAA AACTAATGC 960
 CAGGCTGACG TGTCTGGAG TGTGGCTAGA CAAAGTGGCA GACATGAAAA GCCTTCTCC 1020
 AGCTGCAGAG CTTCTCTCTG TAAGTAAAGA ACAGTCCAAA ATTGGCAAAA AGGAGCCTGG 1080
 TGACACAGTG CACAAAGAAG AAAAGCGGTC AAAACCTAAC ACAAGAAAA GCGGTTTAAC 1140

AGGTGACAGT AAGAAAGCAA CAAAAGAAAG TGGCCTGATA TCAOCCAAGA AGAGGAAAAAT 1200
 GGTAGAAATG TTGGAAGAAA AGAGGAAAAA GAAGAAAAATA AAAACAATGC AGTGAATCAC 1260
 AGATGTCTCC TGAAAGAACT CTTTGTAGATG AAATCATCTT ACTCAAAATGT ACCTTAATTT 1320
 TTTTITTTTC CTGAGTAAAA GCAAGAAATT TCTTCCTTTG GAAAAAATAT ATATATTAAA 1380
 5 AAACCACTTT TAGATGGTTT TTTTAAAAA AAAAAAAAAA ACTGGTAAAA TTACTTTTGG 1440
 CAGACAGTGT TTTATGAATT ATGTATCATG TTGATATATA ATATGTTAAT GTGTTCATGA 1500
 ATTTTACTT TGTACAAAGC AAATAAAGAT CTTTCTCAAA AAAAAAAAAA AAAA

10

SEQ ID NO:152 PFG1 Protein sequence
 Protein Accession #: NP_060376.1

1 11 21 31 41 51
 MELVAGCYEQ VLFQFAVHPE PKACGDHEQW TLVADFTTHA HTASLSAVAV NSRFVVTGSK 60
 DETIHYDMK KKIEHGALVH HSGTTTCLKF YGNRHLISGA EDGLICIWDA KKWECLKSIK 120
 AHKQGVTFLS IHPGSKLALS VGTDKTLRTW NLVEGRSAFI KNKQNAHIV EWSFRGEQYV 180
 20 VIQNKIDYI QLDYASISGT ITNEKRISVV KFLSESVLAV AGDEEVIRFF DCDSLVLCLCE 240
 FKAHENRVKD MFSFEIPEHH VTSASSDGF IKMWKLKQDK KVPFLLCEI NTNARLTCLG 300
 VWLDKVDAMK SLPPAAEPPS VSKEQSKIGK KEPGDTVHKE EKRSPKNTTK RGLTGDSKKA 360
 TKESGLISTK KRKMVEMLEK KRKKKKIKTM Q

25

SEQ ID NO:153 PFD6 DNA SEQUENCE

Nucleic Acid Accession #: NM_014668
 Coding sequence: 110-2853 (underlined sequences correspond to start and stop codons)

30 1 11 21 31 41 51
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 AATCGAGGAT GTGGAGTGGG GACCCAGACG TTAATGGAG CTGGAGGGTC TGCTTGCAT 180
 35 CCGTATCTTC AGTGGGATGG ACCCGCATGG GGAGTCCTTG CCGAGGTCTT TGAGGTACTG 240
 TGACCTGCGA TTGATAAACT CCTCTGCTT GGTGAGAACA GCCTGGAGC AGGAGCTGGG 300
 CCTGGCTGCC TACTTTGTGA GCAACGAGGT TCCCTGGAG AAGGGGGCTA GGAACGAGGC 360
 CTGGAGAGAT GATGCTGAGA AGCTGAGCAG CACAGACAAC GAGGATGAGG AGCTGGGGAC 420
 AGAAGGCTCT ACCTCGGAGA AGAGAAGCCC CATGAAAAGG GAGAGGTCCC GCTCCACGGA 480
 40 CTCAGCATCC TCATCCCTCT CCTCCAAGGC TTCCGGTTCA GGGCTCGGTG GCGAGTCCCT 540
 GGCTCAGGCC ACAGCACTCC CCCAGGGAGA GCATGOCAGG TGGCCCCAGC CCGTGGCCCC 600
 CCGAGAGGAG GGCAGAGCCC CTGGTGAGAA ACAGAGGCCG CCGGCAAGTC AGGGGCCACC 660
 CTCGGCCATC AGCAGGCACA GTCCGGGGCC GACGCCCCAG CCGACTGTA GCTCAGGAC 720
 CGGCAGAGAG AGCGTCCAGG TGTCGGTCACT CTGTCGTGTC TCCAGCTGT CTCTCTCTC 780
 45 GGGCTCATCC TACTCATCCG TGGCGCCCGC TGCCGGCAGC TGGGTCTGTC AGGCCTCCCA 840
 GTGCTCTCTG ACCAAGGCGT GCGGCCAGCC ACCATTGTCT TTCTGCGCA AGCTGTGTA 900
 CGACATGGTT GTGTCCACTG ACAGCAGTGG CTTGCCAAG GCGCCCTCCC TCCTGCCCTC 960
 CCGCTGGGTC ATGTGGGCCA GCTCTTTCCG CCGCTGTCTC AGCAAGACCA TGACATCCAC 1020
 CGAGCAGTCC CTCTACTACC GGCAGTGGAC GGTGCCCGCG CCCAGGCCA TGGACTACGG 1080
 50 CAACCGCGCC GAGGGCCCGG TGGACGGCTT CCAACCCCGC AGGCTGCTGC TCAGCGGCC 1140
 CCTCAGATC GGAAGACAG GTGCTAOCCT GCAGTCTCTC AGTGTCTGT CCAGGATGCT 1200
 TGTTCGGCTC ACAGAAGTGG ATGTCTATGA CGAGGAGGAG ATCAATATCA ACCTCAGAGA 1260
 AGAATCTGAC TGGCATTATC TCCAGCTTAG CGAACCCTGG CCAGACCTGG AGCTGTTCAA 1320
 GAAGTTGCC TTTGACTACA TCATTCACGA CCGAAGTAT GAAGATGCCA GCTGATTG 1380
 55 TTGCACATC CAGGGTATAA AGAGTGAAGA CAGAGGGATG TCCCGGAAGC CGGAGGAOCT 1440
 TTATGTGCGG CGTCAGACGG CACGGATGAG ACTGTCCAAG TACCGAGGT ACAACACCTA 1500
 CCACCCTGT GAGCAGTGGC ACCAGTACAT GGGCTTCCAC CCGGCTACC AGCTGTATGA 1560
 GTCAACCTG CACGCCCTTG CTTCTCTTA CTCCATGCTA GGAGAGGAGA TCCAGCTGCA 1620
 60 CTTTCATATC CCAAGTCCA AGGAGCACCA CTTTGTCTTC AGCAACCTG GAGGOCAGCT 1680
 GGAGAGCATG CGACTACCCG TGTGACAGA CAAGAGOCAT GAATATATAA AAAGTCCGAC 1740
 ATTCACTCCA ACCACCGGC GTACGAACA TGGGCTCTTT AATCTGTACC ACGCATGGA 1800
 CGGTGCCAGC CATTTGCAGG TGCTGGTGT CAAGGAATAC GAGATGGCAA TTTATAAGAA 1860
 ATATTGGGCC AACCACATCA TGCTGGTGT CCGCAGTATC TTCAACAGTG CTGGAGTTGG 1920
 65 TGCTGCTCAT TTCTCATCA AGGAGCTGTC CTACCATAAC CTGGAGCTCG AGCGGAACCG 1980
 GCAGGAGGAG CTGGGAATCA AGCCGACGA CATCTGGCT TTCAATTGTA TCTCTGATGA 2040
 CTCTGCGTG ATGTGGAACG TGTGGATGT CAACTCTGCT GGGAGAGAA GCAGGGAGTT 2100
 CTCTGCTG GAAAGGAACG TGTCTTTGAA GCACATCATG CAGCACATG AGCGGGCCCC 2160
 CGACATCATG TGTGCGGCC TGCTGGGCT GCGGAAGTGG TCCAGCAAG CCGGGGCCAG 2220
 70 CGAGGTGCAA GAGCGCTTCT CCGCTGCCA CGTGCAACAC TTATCATOC TGAACGTGGA 2280
 CCTGAACCCG AAGCTGCACT ACAACAGAA CCGGTTCTGT TGTGACGATG TAGACTTCAA 2340
 CCTCGGGTG CACAGCGCGG GCTCTCTGCT CTGCGGTTT AACCGCTTCA CGGTGATGAA 2400
 GAAGCAGATG GTGGTGGGG GCCACAGGTC CTCCACATC ACATCCAAGG TGTCTGATAA 2460
 CTCTGCGCG GTCTGCGCG CCGAGTACAT CTGTGCCCG GACAGCAAGC ACAOGTTCT 2520
 75 CGCAGCGGCC GCGCAGCTCC TGCTGGAGAA GTTCTGTCAG CACCACAGCC AOCTCTTCT 2580
 CCGCTGTCC CTGAAGAACC ATGACACCC AGTGCTGTCT GTCAGTGT ACCTGAACCT 2640
 GGGATCTCAG ATTCTGTTT GCTATGTGAG CTCAGGCC CACTCTTAA ACATCAGCTG 2700
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 CTTTTGAAA AAGTTTCATT TTCTGAAAGG TGGAGCTGT TGTGTCATCT GTCAGGACCG 2820
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GCGCGATGAG TTCCAGACCG CCAATGCCAG GGAAGACCGG CCGCTCTTTT TTCTGACGGG 2940
 ACGACACATC TGAGGAAGAC AGCGGCGAGT TTTCTGAAGA GATGAGTGTCT CAGAGCCCTC 3000
 ATGCTGTGTA GGCTAAAGGG AGGCGTGGAA CGGTGGGGCG TTGACTGGA ATGGACCCCA 3060
 GGGACTGTCC AGGTGCAGCC CCTCTAGTA CACATGGGCG CCGGAGGCGG TGGTCTCTGG 3120
 AGCCAGGAAG ACTCGCAGT GGTGAGAAT GAAAACCTGA GACTOCCAAG TTCTGGGCCA 3180
 GCGCATGTCT CTGGGCTGTT TTAAGCCCA TTTCAGGAG AACAAAGATT TACTTCTGT 3240
 CCGCCATTC GTGTCTTCC ATGGACAAAC CTGATTTTTT TCTCTTAGTT CTAAAGAATC 3300
 TTGGGTATT TTGTAGCGGT GCCAGTATT CAGTAGATGG GATTTCAGCC AAGTAGGTTC 3360
 CCTGTAAAC TCTACAAAG CAATATTOCA AAGGAACATT TAACTGTAA AGGCTGGAGA 3420
 CAAGAAAAAA TAAGTAGATC GTTTAATAA CAATTATTTA ATTGCCTATA AGTTTGTGT 3480
 TTCAGAGGCT AGCCCAAAGG CATCAAAATT AATAAAGTTA AACAAATTGA TTTACTTCAG 3540
 AGCAAAATG ATCTATTAA AATAATATAG GGTAAATACC CTACCTCTTA GAAAGGGCAA 3600
 AAATGCAAG AAGCTTTCTT TAAACTAAA AGGGTTTTTT GGGGGGGGAG TTGGCGGGGA 3660
 GGAAATAAGG CTAACAGAGG TTGAOCTAAA ATTAGCCTTA CAAAGGAGAA AGGACCACAT 3720
 TGCTTACTTG AAACAGACAA TGAACAACAA CAAAGTGATA TATAAAATAG TTGATGAGAA 3780
 CTAGACTTAT GACTGTAGTT TACTAGAGTT TAGTTTTAG TTGCTGAAGT AGTCTATTTT 3840
 CTCTTACTAA TGTTTGGTTC CTCAGGGAAG AATCTCACTT GACTAGAGAG GAGGTGGGAA 3900
 CAGAAGAGAG AAGGAGGCGG GGAGATGTAT TTCTTAGGGC TCACCCCTTC ACAGACTGAC 3960
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 TCTTACCAT TCTCTGCTCT CAGCTCCCG AGTAGCTGGG ACTACAGCGG CCCACCACCA 4140
 CGCCCGGCTA ATTTTTGTA TTTTTTAGTA GAGACGGGT TTCAACATGT TAGCCAGGAT 4200
 GGTCCTGATC TCTGACCTC GTGATCCGC CGCCTGGCC TOCCAAGTG CTGGGATTAC 4260
 AGGCGTGAGC CACCGTGCCT GCCCAGAAAT GGTTTTTAA GCCACAGTG AGAGGCCACC 4320
 CATTGCCCGG CGCCTGGACA GTGATCATCT TGTTCATCTT GTTCAGTCTT TCTTGTGTG 4380
 ATTGGAATTA TTCTGCTCT TTGAAAGATG AGAAGGTTGA GATGCAAGA GTCTACCTTT 4440
 CCAAGTTCTC ACTGTGGAA AGAGCTAGAA GCACAGTCA AAGTCTGGC TTCTGGACTC 4500
 TGCACTGAGG GTCTCCCTTC TCCACTTG CTACCTCAA TGCCCACTG TTTTGAAGT 4560
 GGCCATAAC TTGAAGGAAA AGTTTAAAGA CAGTCAATT TAATCATCAG AATGCATTCT 4620
 TTTTTTTT GAGACGGAG TTCACTCTT GCTGCCAGG CTGGAGTGCA ATGGTGAAT 4680
 GATCTCGCT CACTGCAACC TCTGCTCTT GGGTTCAAGT GATTCTCCAG CTTACGCTC 4740
 CCGAGTAGCT GGGATTATG GCGCCCAACA CCATGCCAG CTAATTTTGT TATTTTTTTT 4800
 TTTTAGTAG GATGGGGTTC GCGCAGGTTG GCCAGGCTG TCTTGTGAAC TCTGGGCTC 4860
 AGGTGATCTG CCCACCTCAT CTTCCAAAAG TGCTGGGATT ACAGGCATGA GCCACTGCGC 4920
 CTGGCCTCAG AATGCATTCT TACACATCTA TCCTAGACAT TTATAAGCAC TCTAATGGAT 4980
 AACAAATCAA GAAATAATGA TTGAAAAGA TGATGCCGAA GAGTTGATGT CAATCTTTT 5040
 TTCTAAGAA AAAAAAGTCC CGAGTATTA ATATTAGAT CAATGTTAT AAAATGATTA 5100
 CTTGTATCT CTATTATCT CTATTITGA ATAAAACTG ACCTTCTTA ATCATATACT 5160
 TGCTTTTGT AATAGCAGC TTTGTGTCA TTCTCCAC TTTATTAGT AATTAAAT 5220
 GGAAAAACC CTCAACTAA TATTCTGT TGTTCAGTC TTATAATAA AACTATAAT 5280
 GCATG

45 SEQ ID NO:154 PFD6 Protein sequence:
 Protein Accession #: NP_055483.1

1 11 21 31 41 51
 50 MWQKIEDVFW RPQTYLELG LPCLIFSGM DPHGESLPRS LRYCDLRLN SSCLVRTALE 60
 QELGLAAYFV SNEVPLEKGA RNEALESDBE KLSSTDNEDE ELGTGEGTSE KRSPMKRERS 120
 RSHDSASSSL SSKASGALG GESSAQPTAL PQGEHARSPO PRGPAEGRRA PGEKQRPAS 180
 QGPPSAISRH SPGPTPQDC SLRTGQRSVQ VSVTSSCQL SSSSGSSSS VAPAAGTWVL 240
 55 QASQSLTKA CRQPTVFLP KLYDMVVST DSSGLPKAAS LLPSPVMWA SSFRPLSKT 300
 MSTEQSLYY RQWTVPSPH MDYGNRAEGR VDGPHPRLL LSGPPQIGKT GAYLQFLSVL 360
 SRMLVRLTEV DYDEEENI NLRRESDWHY LQLSDPWPDL ELFKLPFDY IHDPKYEDA 420
 SLICSHYQGI KSEDRGMSRK PEDLYVRRQT ARMRLSKYAA YNTYHHCBC HQYMGHPRY 480
 QLYESTLHAF ARSYSMLGEB IQLHFIPKS KEHIFVFSQP GGQLESMLRP LVTDKSEHYI 540
 60 KSPITPTTG RHEHGLFNLY HAMDGASHLH VLVVKEYEMA IYKYYWPNHI MLVLSIFNS 600
 AGVGAHFIL KELSYHNLEL ERNRQEELGI KPQDIWPFIV ISDDSCVMWN VVDVNSAGER 660
 SREFSWERN VSLKHIMQHI EAAPDIMHYA LLGLRKWSSK TRASEVQEPF SRCHVNFII 720
 LNVDLTONVQ YNQNRFLCDD VDFNLRVHSA GLLLCRFNRF SVMKKQIVVG GHRSFHTSK 780
 VSDNSAAVVP AQYICAPDSK HTFLAAPAL LLEKFLQHHS HLFPLSLKN HDHPVLSVDC 840
 65 YLNLGSQSV CYVSSRPHSL NISCDLLFS GLLYLCDSF VGASFLKKEH FLKGATLCVI 900
 CQDRSSLRQT VVRLELEDEW QFRLRDEFQT ANAREDRPLF FLTGRHI

70 Nucleic Acid Accession #: NM_000522
 Coding sequence: 1-1187 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 75 ATGACAGCT CCGTGTCTCT CCACCCCCGC TGGATCGAGC CCACCGTCAT GTTCTCTAC 60
 GACACCGCG GCGCGCTGGT GCGCGACGAG CTCAACAAGA ACATGGAAGG GCGCGCGCG 120
 GCTGCAGCAG CGGCTGCAGC GCGCGCGGCT GCGCGGGCGG GGGCGGGGGG CTTCCCCAC 180
 CCGCGCGCTG CGGCGGCAGG GGCACCTTC TCGGTGGCGG CCGCGCGCGG GCGTGGCGG 240
 GCGCGCGCGG CCAACCAAGT CGGCAACTGT ATGGGCGACC CCGCGCGCTT GCGCGCAGGA 300
 GCGCGGTCCG CTACAGCAG CCGCCCCGGG GAGGCGCCCG CCGTGGCTGC CCGCGCTGCT 360

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GCCGCGGCTG CCGCTGCAGC CGCCGCGGCC GCCGCGCGGT CGTCTCGGG AGGTCCCGGC 420
 CCGGCGGGGC OGGGGCGGC AGAGGCGGCC AAGCAATGCA GCGCTGCTC GGCAGCGGG 480
 CAGAGCTCGT CCGGGCCCGC GGCGCTGCC TATGGCTACT TGGCAGCGG CTACTACCG 540
 TGGGCGGCA TGGGCGCGC CCGCAACGCC ATCAAGTGT GCGCCAGCC CCGCTCGGC 600
 GCCGCGCGC CCGCTTGGC GGACAAGTAC ATGGATACCG CCGGCCAGC TGGGAGGAG 660
 TTCAGCTCC GCGCTAAGGA GTTCGCTTC TAACCACAGG GCTACGCAGC CGGGCCTTAC 720
 CACCACATC AGCCATGCC TGGCTACCTG GATATGCCAG TGGTCCGGG CCTCGGGGC 780
 CCGGCGAGT CCGGCCAGC ACCCTTGGT CTTCATGG AAAGTACCA GCGCTGGGC 840
 CTGCCAACG GCTGGAACGG CCAATGTAC TGCCCAAG AGCAGGCGCA GCGTCCAC 900
 CTCTGGAAGT CCACTCTGC CGACGTGGT TCCATCCCT CGGATGCCAG CTCCTATAGG 960
 AGGGGAGAA AGAAGCGGT GCCTTATAC AAGGTGCAAT TAAAGAAGT TGAACGGAA 1020
 TACGCCAGC ATAAATTCAT TACTAAGGAC AAACGGAGG GATATCAGC CACGACGAAT 1080
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SEQ ID NO:156 PFC6 Protein sequence
 Protein Accession #: NP_000513.1

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1 11 21 31 41 51
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 MTASVLLHPR WIEPTVMFLY DNGGGLVADE LNKNMEGAAA AAAAAAAAAA AGAGGGGPH 60
 PAAAAAGGNF SVAAAAA AAAANQCRNL MAHPAPLAPG AASAYSSAPG EAPPSAAAA 120
 AAAAAA AAASSSGGPG PAGPAAAEAA KQCSFCAAA QSSSGPALP YGYFGSYYP 180
 CARMGFPPSA IKSCFPFSA AAAAAFADKY MDTAGPAEE FSSRAKEFAF YHQGYAAGPY 240
 HHHQPMPOYL DMPVVPGLGG PGESRHEPLG LPMESYQFWA LPNGWNGQMY CPKEQAQPPH 300
 LWKSTLPDVV SHPSDASSYR RGRKRVPYT KVQLKELERE YATNKFTKD KRRRISATTN 360
 LSRQVTTWF QNRRVKEKEV INKLKITS

SEQ ID NO:157 PFA3 DNA SEQUENCE

Nucleic Acid Accession #: AW102723
 Coding sequence: 523-2576 (underlined sequences correspond to start and stop codons)

35
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1 11 21 31 41 51
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 TTCTTACTT TTCTGCGC TAGAGCAGCG AGCAGCCTGG AACAGACCA GCGGAGGAC 180
 ACCTGTGGG GAGGAGGCG CTGGAGGAGC TTAGAGACCC CAGCCGGCG TGATCTCAC 240
 ATGTGCGGAT TTGCAGGCG CGCCCTGGAG CTGCTAGAGA TCGGAAGCA CAGCCCGAG 300
 GTGTGGAAG CCACCAAGAC TGCGGCTCTT GGAGAAAGCG TGAGCAGGG GCGACCGCG 360
 TCTCGGCTC GTCTGCACC TGTGCTGCA GCTGCTGAC AGTGACAATG ACATCCAGT 420
 TACCACTGC CTGAATTGA TAGTGGCTC TGTGTGTCAG TCTATATAA GAACTACAGC 480
 TCATCAGGAG GAGATCGCAG CAGGTAAGA GACACCAACA CATTGTTCTG CAAGAAGCTC 540
 AAGGATCTCA AGATCACAGG AGAGTGTCT TTCTCTTAC TGGCACCAGG TCAAGTTCT 600
 AACGATCTT CAGAGGAGC AGCAGGAAGC TCAGAGAGCT GCAAGCAAC CGTGCCATC 660
 TGTCAAGACA TTCTGAGAA GAACATACAA GAAAGTCTT CTCAAGAAA AACCAAGTCG 720
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 AAATCTTTGG AAAGAGAAGA CTTTGAAGAA ACAATTGCA AGCAAGCAGT GCAGCAGAGT 900
 CCAGTGGAGT TATCAAGAA TCTCTGGTG AAGAGGTTT TAAATATGT TACGAGGAAG 960
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 CCTTCTGAAA CAGAGCAGC ATTGCCAAGA AGCAGGAAA AGGGGAGCT TGAGGAGGCC 1080
 TCCATTCTAT GCTGGATAA GGAGGATGAT TTCTACATG TTTACTACT CTTCCTAAG 1140
 AGAAACACCT CCTGATTCT TCCGGCAGC ATAAAGGCG CTGCTCACT ATTATATGAA 1200
 ACGGAAGTGG AAGTGTGTT AATGCTTCC TGCTTCATA ATGATGTCAG CGAGTTTGTG 1260
 AATCAGCCCT ACTGTGTGA CTCGTTTCA ATGAAAAGCA CCAAGCCATC CCTGTCCCC 1320
 AGCAAAACCC AGTCTCGCT GGTGATTCCT ACATCGCTAT TCTGCAAGAC ATTTCATT 1380
 CATTTCATG TTGACAAAGA TATGACAATT CTGCAATTG GCAATGGCAT CAGAAGGCTG 1440
 ATGAACAGGA GAGACTTCA AGGAAAGCCT AATTTGAAT ACTTGAAT TCTGACTCCA 1500
 AAAATCAAC AGACCTTAG CCGGATCATG ACTATGTTGA ATATGCAGT TGTGTACGA 1560
 GTGAGGAGAT GGGACAACCT TGTGAAGAAA TCTCAAGGG TATGGACCT CAAAGGCCAA 1620
 ATGATCTACA TTGTTGAATC CAGTGCATC TTGTTTTGG GGTCAACCTG TGTGACAGA 1680
 TTAGAAGATT TTACAGGACG AGGGCTCTAC CTCTCAGACA TCCCAATTCA CAATGCACTG 1740
 AGGGATGTGG TCTTAATAGG GGAACAAGCC CGAGCTCAAG ATGGCCTGAA GAAGAGGCTG 1800
 GGAAGCTGA AGGCTACCT TGAGCAAGCC CACCAAGGCC TGGAGGAGGA GAAGAAAAAG 1860
 ACAGTAAAGC TCTGTGCTC CATATTCC TGTGAGGTTG CTAGCAGCT GTGGCAAGGG 1920
 CAAGTTGTGC AAGCAAGAA GTTCAGTAAT GTCAACATGC TCTTCTAGA CATGTTGGG 1980
 TTACTGCCA TGTCTGCCA GTGCTACCG CTGCAAGTCA TCAACATGCT CAATGCACTG 2040
 TACACTGCTG TGACACAGCA GTGTGAGAG CTGGATGCT ACAAGGTGGA GACCATTCG 2100
 ATGCCATTG TGTGGCTGG GGGATTACAC AAAGAGAGTG ATACTCATGC TGTTAGATA 2160
 GCGCTGAGG CCTGTAAGAT GATGGAGCTC TGTATGAAG TTATGTCTCC CCATGGAGAA 2220
 CCTATCAAGA TCGCAATTGG ACTGCACTCT GATCAGTTT TGTGCGGT CATTGGAAT 2280
 AAAAGGCCG GTTACTGCT TTTGGAAC AATGTCAC TGGCTAACA ATTGAGTCC 2340
 TGCAGTGTAC CAGAAAAAT CAATGTCAGC CCAACAATT ACAGATTACT CAAAGACTGT 2400
 CCTGTTTGG TGTTAACCC TCGATCAAGG GAGGAACCT CACCAAACT CCTAGTGAA 2460
 ATCCCGGAA TCTGCCATTT TCTGGATGCT TACCAACAAG GAACAAACT AAAACCATGC 2520

TTCCAAAAGA AAGATGTGGA AGATGCAAGC CAATTTTTTA GGCAAAGCAT CAGGAATAGA 2580
 TTAGCAACCT ATATACTAT TTATAAGTCT TTGGGGTTTG ACTCATTGAA GATGTGTAGA 2640
 GCCTCTGAAA GCACTTTAGG GATTGTAGAT GGCTAACAAG CAGTATTAAT ATTTTCAGGAG 2700
 CCAAGTCACA ATCTTTCTCC TGTTTAACAT GACAAAATGT ACTCACTTCA GTACTTCAGC 2760
 TCTTCAAGAA AAAAAAAAAA ACCTTAAAAA GCTACTTTTG TGGGAGTATT TCTATTATAT 2820
 AACCAGCACT TACTACCTGT ACTCAAAAT CAGCACTTGG TACATATATC AGATAATTGT 2880
 AGTCAATTGT ACAAATGTAT GGAGTCACT GCAATCTCAT ATCTGCTGG AATGCCATGG 2940
 TTATTAAGT GTGTTTGTGA TAGTTGTCGT CAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 3000
 AAAA

SEQ ID NO:158 PFA3 Protein sequence
 Protein Accession #: NP_000847.1

1 11 21 31 41 51
 MPCTKLKDLK ITGECPSLL APGQVPNESS EEAAGSSSEC KATVPICQDI PEKNIQESLP 60
 QRKTSRSRVY LHTLAESICK LIFPEFERLN VALQRTLAKH KIKESRSKLE REDFEKTIAE 120
 QAVQQSPVEL SKNLLVKRFL KYVTRKMKTS LGWLEAPLKI FKQLQYPSSET EOPLRSRKK 180
 GQLEDASILC LDKEDDLHV YFFFKRTTS LILPGIHKAA AHVLYETEVE VSLMPPCFHN 240
 DCSEFVNQPY LLYSVHMKST KPSLSPSKPQ SSLVIPTSLF CKTFPFHFMF DKDMTILQFG 300
 NGIRRLMNRD DFQGKPNFEY FEILTPIKIQ TFGIMTMLN MQFVVRVRW DNSVKKSSRV 360
 MDLKGQMIYI VESSAILFLG SPCVDRLDF TGRGLYLSDI PIHNLRDVV LIGEQARAQD 420
 GLKKRLGKLL ATLEQAQHAL EEEKKKTVDL LCSIFPCEVA QQLWQGVVQ AKKFSNVMTL 480
 FSDIVGFTAI CSQCSPLQVI TMLNALYTRF DQCGELDVY KVEIAMPV WLGLHKESD 540
 THAVQIALMA LKMMELSDV MSPHGEPIKM RIGLHSGSVF AGVVGVMKMP YCLFGNNVTL 600
 ANKFESCSVP RKINVSPTTY RLLKDCPGFV FTPRSREELP PNFSEIPGI CHFLDAYQQG 660
 TNSKPCFQKK DVEDASQFFR QSRNRLATY IFYKSLGFD SLKMCRASES TLGIVDG

SEQ ID NO:159 PFA1 DNA SEQUENCE

Nucleic Acid Accession #: NM_004362
 Coding sequence: 102-1834 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 CGCGGGCGGG ACTGGTCTGA AGAGACGCGG GGACAAAGTG GCAACGACTT GGACATCTGA 60
 GCTGTCACTG CCGAAACACG GCGCAAGAG AGATAATCAA TATGCACTTC CAAGCCTTTT 120
 GGCTATGTTT GGGTCTCTG TTAATCTCAA TTAATGCAGA ATTTATGGAT GATGATGTTG 180
 AGACGGAAAG CTTTGAAGAA AATTCAGAAG AAATGATGT TAATGAAAGT GAACCTTTCCT 240
 CAGAGATTAA ATATAAGACA CCTCAACCTA TAGGAGAAGT ATATTTTGCA GAAACTTTTG 300
 ATAGTGAAGG GTTGGCTGGA TGGGTCTTAT CAAAAGCAAA GAAAGATGAC ATGGATGAGG 360
 AAATTTCAAT ATACGATGGA AGATGGGAAA TTGAAGAGTT GAAAGAAAAC CAGGTACCTG 420
 GTGACAGAGG ACTGGTATTA AAATCTAGAG CAAAGCATCA TGCAATATCT GCTGTATTAG 480
 CAAAACCATT CATTTTGTCT GATAAACCTT TGATAGTTCA ATATGAAGTA AATTTTCAAG 540
 ATGGTATTGA TTGTTGAGGT GCATACATTA AACTCTAGC AGACACTGAT GATTGTATTG 600
 TGGAAGAACT TTATGATAAA ACATCCTATA TCATTATGTT TGGACCAGAT AAATGTGGAG 660
 AAGATTATA ACTTCATTTT ATCTTCAGAC ATAAACATCC CAAAAGTGA GTTTTCGAAG 720
 AGAAACATGC CAAACCTCCA GATGTAGAAC TTAAGAAAGT CTTTACAGAC AGGAAGACTC 780
 ATCTTTATAC OCTTGTGCT GATCCAGATG ACACATTTGA GGTGTTAGTT GATCAAAACG 840
 TTGTAACAAA AGGAAGCCTC CTAGAGGATG TGGTTOCTCC TATCAAACTT CCAAAAGAAA 900
 TTGAAGATCC CAATGATAAA AAACCTGAGG AATGGGATGA AAGAGCAAAA ATTCTGATC 960
 CTCTGCCGT CAAACAGAAA GACTGGGATG AAAGTGAACC TGCCCAATA GAAGATTCAA 1020
 GTGTTGTAA ACCTGCTGGC TGGCTTGATG ATGAACCAAA ATTTATCCCT GATCCTAATG 1080
 CTGAAAACCC TGATGACTGG AATGAAGACA CGGATGGAGA ATGGGAGGCA CCTCAGATTG 1140
 TTAATCCAGC ATGTGGGATT GGGTGTGGTG AGTGGAAGAC TCOCATGATA GATAACCCAA 1200
 AATCAAAAGG AGTATGGAGA CCTCCACTGG TCGATAATCC TAACTATCAG GGAATCTGGA 1260
 GTCTCGAAA AATTCCTAAT CCAGATTATT TCGAAGATGA TCATCCATT CTCTGACTT 1320
 CTTCAGTGC TCTTGGTTTA GAGCTTTGGT CTATGACCTC TGATATCTAC TTGATAATT 1380
 TTATTATCTG TTGCGAAAAG GAAGTAGCAG ATCACTGGGC TGCAGATGGT TGGAGATGGA 1440
 AAATAATGAT AGCAATGCT AATAAGCCTG GTGTATTAAT ACAGTTAATG GCAGCTGCTG 1500
 AAGGCCACCC ATGGCTTTGG TTGATTTATC TTGTGACAGC AGGAGTGCCA ATAGCATTAA 1560
 TTAATTCATT TTGTTGGCCA AGAAAAAGTA AGAAAAACA TAAAGATACA GAGTATAAAA 1620
 AAACCGACAT ATGTATACCA CAACAAAAG GAGTACTAGA GCAAGAGAA AAGGAAGAGA 1680
 AAGCAGCCTT GGAAAAACCA ATGGACCTGG AAGAGGAAAA AAAGCAAAAT GATGGTGAAA 1740
 TGCTTGAAAA AGAAGAGGAA AGTGAACCTG AGGAAAAGAG TGAAGAGAA ATTGAAATCA 1800
 TAGAAGGCA AGAAGAAAGT AATCAATCAA ATAAGTCTGG GTCAGAGGAT GAGATGAAA 1860
 AAGCAGATGA GAGCAGAGGA TCTGGAGATG GGCGGATAAA GTCAGTACCG AAAAGAAAGAG 1920
 TAGGAAAGGA CTAACTAGA TTGAAATATT TTAATTTCC GAGAGGATGT TTGGCATTGT 1980
 AAAAAACAG ATGCGAGACC TGAACCTTAA TCAGTCTGCA CATCCGTTT CTAATATCA 2040
 GCAACATTAT ATCTTTCAG ACATTTATTT TAGTCTCTCA TTTCGAGGA AAAAGAGCA 2100
 ACTTTGAAGT TACCTCATCT TTGAATTAG AATAAAAGTG GCACATTACA TATCGGATCT 2160
 AAGAGATTAA TACGATTAGA AGTTACACAG TTTTAGTTGT TTGGAGATAG TTTTGGTTT 2220
 TACAGAAACA AATAATATGT AGCAGCTTCA TTGCTATTGG AAAAATCAGT TATTGGAATT 2280
 TCCACTTAAA TGGCTATCA ACAATATAAC TGGTAGTTCT ATAATAAAA TGAGCATATG 2340
 TTCTGTGTG AAGAGCTAAA TGCAATAAAG TTTCTGTATG GTTGTGTGAT TCTATCAACA 2400
 ATTGAAAGTG TTGTATATGA CACACATTTA OCTAGTTTGT GTCAAATTAT AGTTACAGTG 2460
 AGTTGTTTGC TAAATTATA GATTCCTTAA AGGACATGOC TTGTCATAA AATCACTGGA 2520

TTATATTGCA GCATATTTTA CATTGAATA CAAGGATAAT GGGTTTTATC AAAACAAAAT 2580
 GATGTACAGA TTTTITTTCA AGTTTTATA GTTGCTTAT GCCAGAGTGG TTTACCCAT 2640
 TCACAAAATT TCTTATGCAT ACATTGCTAT TGAAAAATAA ATTTAAATAT TTTTCATCC 2700
 TGAAAAAAA

SEQ ID NO:160 PFA1 Protein sequence
 Protein Accession #: NP_004353.1

1 11 21 31 41 51
 MHFQAFWLCL GLLFISINAE FMDDDVETED FEENSEEDV NESELSSEIK YKTPQPIGEV 60
 YFAETFDSEGR LAGWVLSKAK KDDMDDEISI YDGRWEIEEL KENQVPGDRG LVLKSRKHH 120
 AISAVLAKPF IFADKPLIVQ YEVNFQDGD CGGAYIKLLA DTDDLLENF YDKTSYIMF 180
 GPDKCGEDYK LHFIFRHKHP KTGVFEEKHA KPPDVLKKF FTDRKTHLYT LVMNPDFTF 240
 VLVDTQTVNNK GLLLEDVVPF IKPPKEIEDP NDKKPEEWDE RAKIPDSAV KPEDWDESEP 300
 AQIEDSSVVK PAGWLDDEPK FIPDPNAEKP DDWNEDTGE WEAPQILNPA CRIGCGEWP 360
 PMDNPKYKG VWRPFLVDNP NYQGIWSPRK IPNPDYFEDD HPFLTSFSA LGLELWSMTS 420
 DIYFNFNFC SEKEVADHWA ADGWRWKIMI ANANKPGVLK QLMAAAEGHP WLWLIYLVTA 480
 GPVIALTSF CWPVRKVKKH KDTEYKTDI CIPQTKGVLE QEEKEEKAAL EKPMDLSEK 540
 KQNDGEMLEK EEESEPEEKS EEEIEIEQ EESNQSNKSG SEDEMKEADE STGSGDGP 600
 SVRKRRVRKD

SEQ ID NO:161 PEZ9 DNA SEQUENCE

Nucleic Acid Accession #: NM_005932
 Coding sequence: 75-2216 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 GGGAGCGCG CGCTCCAGC GAAAGCAGCA GGGCAGGGAT CTGCGTTGGA GGAAGGGACT 60
 GCTCTGGTGC TAGAATGCTG TGGCTCGGAA GGCTGGGCGG CTGGGAGGCC AGAGCAGCAG 120
 CTCTGCCGCC CGCGCGGGCG GGCGCGGGAA GCCTCGAAGC CGGATCCGG GCGCGAAGGG 180
 TCAGCACCAG CTGGTCTCCG GTGGGCGCGG CCTTCAATGT CAAGCCCGAG GGCAGCGCCT 240
 TGGACCTGTT CGCGGAGCGG GCGGCTCTTT TTGGAGTTCC TGAGCTGAGT GCGCCAGAAG 300
 GATTTCATAT TGCACAAGAA AAAGCCTTGA GAAAGACAGA ATTGCTTGTG GACCGTGCAT 360
 GTTCCACCCC ACGTGGGCCC CAGACCGTGC TGATCTTGA TGAGCTCTCG GATTCCCTAT 420
 GCAGAGTGGC CGACTTGGCT GATTTTGTGA AAATCGCTCA CCTGAGCCA GCATTCAGAG 480
 AAGCTGCGGA AGAAGCTTGT AGAAGTATTG GCACCATGGT AGAGAAGTTG AACACAAATG 540
 TGGATTATA TCAAAGTTTG CAAAATTTAC TAGCTGATAA AAAACTTGTG GATTCCTTG 600
 ATCCGAAAC AAGCGAGTG GCTGAAGTGT TTATGTTTGA TTTGAAAT AGTGGAAATG 660
 ATCTAGACAA ACAAAGCGT AAAAGAGCAG TGAACCTCAA TGTAAATC TTGGATTGTA 720
 GTAGTACATT TCTTATGGGA ACCAATTTT CCAACAAGAT TGAGAAGCAT CTCTTACCAG 780
 AACACATCG TGTAACTTT ACATCTGCTG GGCATCATAT CATAATTGAT GGTCTCCACG 840
 CAGAATCACC AGATGACTTG GTGCGAGAAG CTGCTTAA AATTTTCTT TATCCCAATG 900
 CTGGTCAATT GAAATGTTTA GAAGAATTGC TCAGCAGCAG AGATCTTCTG GCAAAGTTGG 960
 TGGGGTATTC CAGTTTTCT CACAGGGCTC TCAGGAAGC GATAGCTAAA AATCCAGAGA 1020
 CTGTCTGCA GTTCTGTGAA AACTATCTG ACAACTTTC TGAAGAAGT CTGAAAGATT 1080
 TTGAGATGAT ACGAGGGATG AAAATGAAAC TGAATGCTCA AAATCCGAA GTAAATGCC 1140
 GGGACCCGCC TTACTACAGT GGTGTGATC GTGCAGAAAG GTATAATATT GAGCCAGGCC 1200
 TATATTGCC GTTTTCTCT CTGGAGCAT GCATGGAAGG CCGTAATATT TTGCTTAAAC 1260
 GACTGTGGG GATTTCATTA TATGAGAGC AGCCTGCAA AGGAGAGGTG TGGAGCGAAG 1320
 ATGCGGAAA ACTGGCTGT GTTCATGAAT CTGAAGGATT GTTGGGTAC ATTTACTGTG 1380
 ATTTTITTC GCGAGCAGAC AAACCACATC AGGATTGCCA TTCACTATC CGTGGAGGCA 1440
 GACTAAAGGA AGATGGAGAC TATCAACTCC CACTGTAGT TCTTATGCTG AATCTTCCOC 1500
 GTTCTCAAG GAGTTCTCCA ACTTGTCTAA CTCTGGCAT GATGGAAAA CTTTCCATG 1560
 AAATGGGACA TGCCATGCAT TCAATGCTAG GACGTACTCG TTACCAACAC GTCACTGGGA 1620
 CCAGGTGCC TACTGATTT GCTGAGGTTT CTCTATTCT GATGGAGTAC TTTGCAAATG 1680
 ATTATCGAGT AGTTAACCAA TTGOCAGAC ATTATCAGAC TGGACAGCCA CTGCCAAAA 1740
 ATATGGTGT TCGTCTTGT GAATCTAAAA AGGTTTGTG TGCAGCTGAT ATGCAACTTC 1800
 AGGTCTTTTA TGCCACTCTG GATCAAAATC ACCATGGGAA GCATCCCTG AGGAAATCAA 1860
 CCACAGACAT TCCTAAGGAA ACACAAGAGA AATCTATGG CTAACCATAT GTTCCAAATA 1920
 CTGCTGCA GCTGCGATT AGCCACCTCG TGGGTATGG TGCTAGATAT TACTCTTACC 1980
 TCATGTCCAG AGCGGTGCGC TCCATGGTTT GGAAGGAGTG TTTCTACAG GATCCTTTCA 2040
 ACAGGGCTGC CGGGAGGCGC TATCGCAGG AGATGCTGOC CCACGGTGA GGCAGGGAGC 2100
 CCATGCTCAT GGTGAAGGT ATGCTTCAGA AGTGTCTTC TGTGATGAC TTGTAAGTG 2160
 CCTGCTTC CGACTTGGAT CTGACTTCG AAATTTCTT CATGGATTCT GAATAAAGA 2220
 AACACTCTAC CCTCTAATC AAGGTCATGT AGTAATGACT TTGTATAAA TGCTACAGCT 2280
 GTGAGAGCTT GTTCTGATT GTTTCATTGT TCGTCTGT AATTCTGAAA AACTTTAAAC 2340
 TGGTAGAAT TGAATAAAT AATTTGTTT AATTAATAAA AAAAAAAAAA AA

SEQ ID NO:162 PEZ9 Protein sequence
 Protein Accession #: NP_005923.1

1 11 21 31 41 51
 MLCVGRIGGL GARAAALPFR RAGRGSLAEG IRARRVSTSW SPVGAAFNVK PQGSRLDLFG 60
 ERARLFGVPE LSAPEGFHIA QEKALRKTEL LVDRACSTPP GPQTVLIFDB LSDSLCRVAD 120

5 LADFKIAHP EPAFREAAEE ACSIGTMVE KLTNVDLYQ SIQKLLADKK LVDSLDPETR 180
 RVAELFMDF EISGHLDDKQ KRKRAVDLNV KILDLSTFL MGTNFPNKIE KHLLEPHRR 240
 NFTSAGDHI IDGLHAESPD DLVREAAKYI FLYPNAGQLK CLEELSSRD LLAKLVGYST 300
 10 FSHRALQGTI ARNPETVMQF LEKLSDKLSE RTLKDFEMIR GMKMKLNAQN SEVMPWDPPY 360
 YSGVIAERY NIEPSLYCFP FSLGACMEGL NILLNRLLGI SLYAEQPAKG EVWSEDVRKL 420
 AVVHESEGLL GYTYCDFFQR ADKPHQDCHF TRGGRLLKED GDYQLPLVVL MLNLPSSRS 480
 SPTLLTPGMM ENLFHEMGHA MHSMLGRTRY QHVTGTRCPT DFAEVPILM BYFANDYRVV 540
 NQFARHYQTG QPLPKNMVSR LCESKKVCAA ADMQLQVFYA TLDQHYHGKH PLRNSTDIL 600
 15 KETQEKFYGL PYVPTAWQL RFSHLVGYGA RYYSYLSMRA VASMVWKECF LQDPFNRAAG 660
 ERYRREMLAH GGGREPMLMV EGMLQKCPV DDFVSALVSD LDLDFFETFLM DSE

SEQ ID NO:163 PEZ8 DNA SEQUENCE

15 Nucleic Acid Accession #: AF103907
 Coding sequence: none (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 20 ACAGAAAGAAA TAGCAAGTGC CGAGAAGCTG GCATCAGAAA AACAGAGGGG AGATTGTGT 60
 GGCTGCAGCC GAGGGAGACC AGGAAGATCT GCATGGTGGG AAGGACCTGA TGATACAGAG 120
 GAATTACAAC ACATATACTT AGTGTTTCAA TGAACACCAA GATAATAAG TGAAGAGCTA 180
 GTCCGCTGTG AGTCTCTCA GTGACACAGG GCTGGATCAC CATCGACGGC ACTTCTGAG 240
 25 TACTCAGTGC AGCAAAGAAA GACTACAGAC ATCTCAATGG CAGGGGTGAG AAATAAGAAA 300
 GGCTGCTGAC TTACCATCT GAGGCCACAC ATCTGCTGAA ATGGAGATAA TTAACATCAC 360
 TAGAAACAGC AAGATGACAA TATAATGTCT AAGTAGTGAC ATGTTTTCG ACATTTCOCAG 420
 CCCCCTTAAA TATCCACACA CACAGGAAGC ACAAAGGAA GCACAGAGAT CCGTGGGAGA 480
 AATGCCCGGC CGCATCTTG GGTATCGAT GAGCCTCGCC CTGTGCTGG TCCGCTTGT 540
 30 GAGGGAAGGA CATTAGAAAA TGAATTGATG TGTTCCTTAA AGGATGGGCA GGAAACAGA 600
 TCCTGTTGTG GATATTATT TGAACGGGAT TACAGATTTG AAATGAAGTC ACAAAGTGAG 660
 CATTACCAAT GAGAGGAAAA CAGAOGAGAA AATCTTGATG GCTTCACAAG ACATGCAACA 720
 AACAAATGG AATACTGTGA TGACATGAGG CAGCCAAGCT GGGGAGGAGA TAACCACGGG 780
 GCAGAGGGTC AGGATCTTGG CCTGCTGCC TAAACTGTGC GTTCATAACC AAATCATTTC 840
 35 ATATTCTTAA CCTCAAAAC AAAGCTGTG TAATATCTGA TCTCTACGGT TCCTTCTGGG 900
 CCCAACATTC TCATATATC CAGCCACACT CATTTTAAAT ATTAGTTC CAGATCTGTA 960
 CTGTGACCTT TCTACACTGT AGAATAACAT TACTCATTIT GTTCAAAGAC CCTCTGTGTT 1020
 GCTGCTAAT ATGTAGCTGA CTGTTTTTCC TAAGGAGTGT TCTGGCCAG GGGATCTGTG 1080
 AACAGGCTGG GAAGCATCTC AAGATCTTTC CAGGGTTATA CTTACTAGCA CACAGCATGA 1140
 40 TCATTACGGA GTGAATTATC TAATCAACAT CATCCTCAGT GTCTTTGCC ATACTGAAAT 1200
 TCATTTCCTA CTTTGTGACC CATTTCTAAG ACCTCAAAAT GTCATTCAT TAATATCACA 1260
 GGATTAACCT TTTTITTTAA COTGGAAGAA TTCAATGTGA CATGCAGCTA TGGGAATTTA 1320
 ATTACATATT TGTITTTCCA GTGCAAGAT GACTAAGTCC TTATCCCTC CCTTTGTTT 1380
 GATTITTTTT CCAGTATATA GTTAAATGC TTAGCCTGT ACTGAGGCTG TATACAGCAC 1440
 45 AGCCTCTCCC CATCCCTCCA GCCTTATCTG TCATCAACAT CAACCCCTCC CATACCACT 1500
 AAACAAATTC TAACATGTAA TTCTTGAAC ATGTCAGGAC ATACATTAT CCTCTGCT 1560
 GAGAAGCTCT TCCTGTCTC TTAATCTAG AATGATGTAA AGTTTGAAT AAGTGTACTA 1620
 TCTTACTTCA TGCAAAGAAG GGACACATAT GAGATTCATC ATCAGATGAG ACAGCAAATA 1680
 CTAAAGAGTG AATTGTGATA TAAGAGTTTA GATAAATA TAAGATGCAA GAGCCACAGA 1740
 50 GGGAATGTTT ATGGGGCAGC TTGTGAAGCC TGGGATGTGA AGCAAAGGCA GGGAACCTCA 1800
 TAGTATCTTA TATAATGATC TTCAATTCTC TATCTCTATC ACAATATCCA ACAAGCTTTT 1860
 CACAGAATTC ATGCAGTGCA AATCCCAAAA GGTAACCTTT ATCCATTTCA TGGTGAGTGC 1920
 GCTTTAGAAAT TTGGCAAAAT CACTCTGCTC ACTTATCTCA ACTTGAGAT GTGTTGTGCC 1980
 TTGTAGTTAA TTGAAGAATA TAGGGCACTC TTGTGAGCCA CTTTGGGTT CACTCTGGC 2040
 55 AATAAAGAAT TTACAAAGAG CTAATCAGGA CCAAGTGTGA AGAGCTCTGT GTGTGTGTGT 2100
 GTGTGTGTGT GAGTGTACAT GCCAAAGTGT GCCTCTCTCT CTGACCCAT TATTTCAGAC 2160
 TTAACAACAG CATGTTTCA AATGGCACTA TGAGCTGCCA ATGATGTATC ACCACCATAT 2220
 CTCATTATTC TCAGTAAAT GTGATAATAA TGTCATCTGT TAACATAAAA AAAGTTTGAC 2280
 TTCACAAAAG CAGCTGGAAA TGGACAACCA CAATATGCAT AAATCTAACT OCTACCATCA 2340
 60 GCTACACACT GCTTGACATA TATTGTTAGA AGCACTGCC ATTTGTGGGT TCTCTAAGC 2400
 AAAATACTTG CATTAGTCT CAGCTGGGGC TGTGCATCAG GCGGTTTGAG AAATATTCAA 2460
 TTCTCAGCAG AAGCCAGAAT TTGAATTCCC TCATCTTTTA GGAATCATTT ACCAGGTTTG 2520
 GAGAGGATTC AGACAGCTCA GGTGCTTCA CTAATGTCTC TGAACCTCTG TCCCTCTTTG 2580
 TGTTCATGGA TAGTCAATA AATAATGTTA TCTTTGAAC TATGCTCATA GGAGAGAATA 2640
 65 TAAGAACTCT GAGTGATATC AACATTAGGG ATTCAAAGAA ATATTAGATT TAAGCTCACA 2700
 CTGGTCAAAA GGAACCAAGA TACAAAGAAC TCTGAGCTGT CATGCTGCC ATCTCTGTGA 2760
 GCCACAACCA ACAGCAGGAC CCAACGCATG TCTGAGATCC TTAATCAAG GAAACCACTG 2820
 TCATGAGTTG AATCTCTCTA TTATGGATGC TAGCTTCTGG CCATCTCTGG CTCTCTCTTT 2880
 GACACATATT AGCTCTAGC CTTTGTCTCC ACGACTTTTA TCTTTCTCC AACACATGCG 2940
 70 TTACCAATCC TCTCTCTGCT CTGTGCTTT GGACTTCCC ACAAGAATT CAACGACTCT 3000
 CAAGTCTTT CTTCATCTCC CACCCTAAC CTGAATGCT AGACCTTAT TTTTATTAAT 3060
 TTCCAATAGA TGCTGCTAT GGGCTATATT GCTTTAGATG AACATTAGAT ATTTAAAGCT 3120
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 75 TATATTACTG ATGTCTAGCA ACAGCATGGT CCGCAATGTA GCCATGCAAA TGAGAAACCC 3240
 AGTGGCTCTT TGTGTACAT GCATGCAAGA CTGCTGAAGC CAGAAGGATG ACTGATTACG 3300
 CCTCATGGT GGAGGGGACC ACTCTGGGC CTCTGTGATT GTCAGGAGCA AGACCTGAGA 3360
 TGCTCCCTGC CTTCAGTGT CTCTGCATCT CCGCTTTCTA ATGAAGATCC ATAGAATTTG 3420
 CTACATTGGA GAATTCGAAT TAGGAACCTA CATGTTTAT CTGCGCTATC AATTTTITAA 3480
 ACTTGCTGAA AATTAAAGTT TTCAAAAATC TGTCTGTGA AATTACTTTT TCTTACAGTG 3540
 TCTTGGCATA CTATATCAAC TTGATTCCTT TGTTACAAC TTCTTACTC TTTTATCACC 3600

5 AAAGTGGCTT TTATTCTCTT TATTATTATT ATTTCTTTT ACTACTATAT TACGTTGTTA 3660
 TTATTTTGTT CTCTATAGTA TCAATTTATT TGATTAGTT TCAATTTATT TTTATTGCTG 3720
 ACTTTTAAAA TAAGTGATTG GGGGGGTGGG AGAACAGGGG AGGGAGAGCA TTAGGACAAA 3780
 TACCTAATGC ATGTGGGACT TAAACCTAG ATGATGGGTT GATAGGTGCA GCAAACCACT 3840
 ATGGCACACG TATACCTGTG TAACAAOCT ACACATCTCTG CACATGTATC CCAGAACGTA 3900
 AAGTAAAAAT TAAAAAAG TGA

10 PEZB Protein sequence:
 Protein Accession #: none

SEQ ID NO:164 PEZB DNA SEQUENCE

15 Nucleic Acid Accession #: AB028945
 Coding sequence: 1-3785 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 ATGATGATGA ACGTCCCGG CGGAGGAGCG GCCGCGGTGA TGATGACGGG CTACAATAAT 60
 GGTGCGTGTG CCGGGAATTC TCTCTACAGT GACTGCATTA TTGAGGAGAA GACGTTGGTC 120
 20 CTGCAGAAAA AAGACAATGA GGGCTTTGGA TTGTGCTTC GAGGGGCCAA AGCTGACACA 180
 CCATTGAAG AATTACACAC AACACCGGCT TTCCAGCCC TACAGTACCT GGAGTCCGTG 240
 GATGAAGGTG GGTGCGGTG GCAAGCCGGA CTAAGGACCG GGGACTTCTT GATTGAGGTT 300
 AACAAATGAG ATGTTGTCAA AGTCGGCCAC AGGCAGGTGG TGAACATGAT CCGGCAGGGA 360
 25 GGGAAATCAC TGTCTCTAA GTTGGTCACG GTGACCAGGA ATCTGACCC CGACGACACC 420
 GCCAGGAAGA AAGTCCCCC GCCTCAAAG CGGGCACCGA CCACAGCCCT CACCTGCGC 480
 TCCAACTCCA TAACAGAGGA GCTGGAGGAG CTCGTGGATA AAGATAAAAC CAGGAGAGTA 540
 GTCCCGGCTT CCAAGCCCTC CCGGCTGCT GAGAACATGG CTGTGGAAC GAGGGTGGCG 600
 ACCATCAAG AGCGGCCAG CAGCGGTGC TTCCCGCGG GCTCAGACAT GAACTCTGTG 660
 30 TACGAACGCC AAGGAATCGC CTGATGACG CCCACTGTT CTGGGAGCCC AAAAGCCCGG 720
 TTTCTGGGCA TCCCTCGAGG TACGATGCGA AGGCAGAAAT CAATAGACAG CAGAATCTTT 780
 CTATCAGGAA TAACAGAGGA AGAGCGGCAG TTTCTGGCTC CTCCAATGCT GAAATTCAAC 840
 AGAAGCTGT CATGCGCGA CACCTCTGAG GACATCCCC CTCCACCGCA GTCTGTGCC 900
 CCGTCCCCAC CACCTCTC CCAACCACT TACAACCTGC CCAAGTCCC AACTCCAAGA 960
 35 GTCTACGGGA CGATTAAGCC TCGTTCAAT CAGAATTCTG CCGCCAAGGT GTCCCCCGCC 1020
 ACCAGGTCCG ACACCGTGGC CACCATGATG AGGAGAGAAG GGATGTACTT CAGGAGAGAG 1080
 CTGGACCGCT ACTCTCTGGA CTCTGAAGAC CTCTACAGTC GGAATGCCCG CCGCAAGCC 1140
 AACTTCGCGA ACAAGAGAGG CCAGATGCGA GAAACCCAT ACTCAGAGGT GGGGAAGATC 1200
 GCCAGCAAAG CCGTCTACGT CCGGCCAAG CCGGCAGCG GGAAGGGGAT GCTGGTGAAG 1260
 40 CAGTCCAACG TGGAGGACAG CCGGAGAAG ACGTGCTCCA TCCCTATCCC GACCATCATC 1320
 GTGAAGGAGC CGTCCACCAG CAGCAGCGGC AAGAGCAGCC AGGGCAGCAG CATGGAGATC 1380
 GTACCCGAG CCGCGGAGC ACGAGGCCAG CTGCGGCTG ACGAAAGCCT GACCGTCAGC 1440
 AGCCCTTTG CCGCGCCAT CCGCGGAGCC GTCCGCGAC GTGAGAAGCG GCTGGAAGCC 1500
 AGGAGGAAC TCCCGGCTT CCTCTCACA GACCTGGGG ATGAGGATGT GGCCTGGGG 1560
 45 CCACCCGCCC CCAGGAGCGG GCGCTCCATG TTCCCGAGG AGGGGGATT TGTGACGAG 1620
 GACAGCGCTG AGCAGCTGTC ATCCCCATG CCGAGTGCCA CGCCAGGGA GCGGAAAC 1680
 CATTTCTAG GTGGCGCGA GGCCAGTGT CCGGGTGAGG CTGGGAGGCC GCTGAATTCC 1740
 ACGTCCAAG CCAGGGGCC CGAGAGCAGC CCAGCAGTGC CTTCCGCGAG CAGCGGCACA 1800
 GCGGGCCCG GGAATTATGT CCAOCCACT ACAGGGCGGC TGCTTGATCC CAGCTCCCG 1860
 50 CTGGCCCTGG CACTCTCCG AAGGGACCGA GCCATGAAG AGTCTCAACA GGGACCCAAA 1920
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5 SEQ ID NO:165 PEZ6 Protein sequence
 Protein Accession #: BAA82874.1

1 11 21 31 41 51
 10 MMNNVPGGGA AAVMMTGYNV GRCPRNSLYS DCHEEKTVV LQKKDNEGFG FVLRGAKADT 60
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 15 FLGIPRGITMR RQKSIDSRIF LSGITEERO FLAPPMLKFT RLSLMDPTSE DIPPPQSV 300
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 20 SPFAAALAGA VRDREKRLA RRNSPAFLST DLGDEDVGLG FPAPRTRPSM FPEGDFADE 540
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SEQ ID NO:166 PEZ4 DNA SEQUENCE

35 Nucleic Acid Accession #: NM_000024
 Coding sequence: 220-1461 (underlined sequences correspond to start and stop codons)

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75 SEQ ID NO:167 PEZ4 Protein sequence
 Protein Accession #: NP_000015.1

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 NLRKEVYIL LNWIGVYNSG FNPLYCRSP DFLRIAFQELL CLRRSSLKAY GNGYSSNGNT 360
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SEQ ID NO:168 PEZ1 DNA SEQUENCE

15 Nucleic Acid Accession #: NM_004457
 Coding sequence: 143-2305 (underlined sequences correspond to start and stop codons)

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SEQ ID NO:169 PEZ1 Protein sequence
Protein Accession #: NP_004448.1

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1 11 21 31 41 51
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MYNFQLVTLV ATLLGGPAIVH ALNETEVTNI ITSKEQLQTK LKDIVSLVPR LRHIITVDGK 240
15 PPTWSDFFPKO IIVHTMAAVE ALGAKSMEN QPHSKPLPSD IAVIMYTSQS TGLPKGVMS 300
HSNIIAGITG MAERIEPLGE EDVYIGYLP L AHVLELSAEL VCLSHGCRIG YSSPQTLADQ 360
SSKIKKGSKG DTSMLKPTLM AAVPEIMDRI YKNVMNKKVSE MSSPQRLFI LAYNYKMEQI 420
SKGRNPLCD SFVFRKVRSL LGGNIRLLC GGAPLSATTQ RFMNICRCP VGGQYGLTES 480
20 AGAGTISEVW DYNTRGVGAR LVCCEIKLN WEEGGYFNTD KPHPRGEILI GGQSVYTMGY 540
KNEAKTKADF SEDENGQRWL CTGDIGEFEP DGCLKIIRK KDLVKLQAGE YVSLGKVEAA 600
LKNLPLVDNI CAYANSYHSY VIGFVVPNQK ELTELARKKG LKGTWEEELN SCEMENEVLK 660
VLSEAAISAS LEKFEIPVKI RLSFEPWTPS TGLVTDFAKL KRKELKTHYQ ADIERMYGRK

25

SEQ ID NO:170 PCQ7 DNA SEQUENCE
Nucleic Acid Accession #: none found
Coding sequence: 38-1075 (underlined sequence corresponds to start and stop codon)

30

1 11 21 31 41 51
AGCAACGACG CCGGGCAGCG GGAGCGGCGG CCGCGCCATG TGGCTGCTGG GGCCGCTGTG 60
CCTGCTGCTG AGCAGCGCCG CGGAGAGCCA GCTGCTCCCC GGGAACTACT TCACCAATGA 120
GTGCAACATA CCAGGCAACT TCATGTGACG CAATGGACGG TGCATCCCGG GCGCCTGGCA 180
GTGTGACGGG CTGCTTGACT GCTTCGACAA GAGTGATGAG AAGGAGTGCC CCAAGGCTAA 240
35 GTGCAAAATG GGCACCAACT TCTTCCCTGG TGCCAGCGGC ATCCATTGCA TCATTGGTCG 300
CTTCCCGTGC AATGGGTTTG AGGACTGTGC CGATGGCAGC GATGAAGAGA ACTGCACAGC 360
AARCCCTCTG CTTTGTCTCA CCGCCCGCTA CCACCTGCAAG AACGGCTCTT GTATTGACAA 420
GAGCTTCATC TGGGATGGAC AGAATAACTG TCAAGACAAC AGTGATGAGG AAAGCTGTGA 480
AAGTTCACAA GAATCCCGCA GTGGGAGGT GTTTGTGACT TCAGAGAACC AACTTGTGTA 540
40 TTACCCACAG ATCACTCATG CCATCATCGG CAGCTCCGTC ATTTTGTGTC TGGTGGTGGC 600
CCTGCTGGCA CTGGCTTTGC ACCACACAGG GAAGCGGAAC AACCTCATGA CGCTGCCCGT 660
GCACCGCTCG CTGCTGCTGC CGGCTGGTGG GTCTGAGACC ACCCCACACA 720
CTGCAACGTC ACCTACACAG TCAATAATGG CATCCAGTAT GTGGCCAGCC AGGCGGAGCA 780
GAATGCGTGC GAAGTAGGCT CCCCACCTTC CTACTCCGAG GCGTTGCTGG ACCAGAGGCC 840
45 TGCGTGGTAT GACCTTCCTC CACCGCCCTA CTCTTCTGAC ACGGAATCTC TGAACCAAGC 900
CGACCTGCCC CCTTACCGCT CCGGTGCCGG GAGTGCCAAC AGTGCCAGCT CCCAGGCAGC 960
CAGCAGCTGC CTGAGCGTGG AAGACACCG CCACAGCCCG GGGCAGCCTG GCCCCAGAGA 1020
GGGCACTGCT GAGCCCGAGG ACTCTGAGCC CAGCCAGGCG ACTGAAGAGG TATAAGTCCC 1080
AGTTATCTCA GAGTCCATAT GGGTAAATCT GCTCTGACTT GTTGCCATTC TAACAATTTG 1140
50 TGCTCATGGG AAGCTCTTTA AGCACTGTGA AGGATGTCTC AAGTTACAGT TTGGGATATT 1200
AACTATCTCT GCATTCCTCT CCTCCCCAG ACTTCAGAGA TGTTTTCTG GCGTCTCAGT 1260
TGACATGATC TGTGTGCTGT CTTTCTGTGC AGGTCACTCT TCCCTTGGGA CCAGAGATCA 1320
CACCTCATAT TTTCACATTA TCTGTCTTCT GTTGAGAGAA CAGCATATAA AACAGTATTG 1380
AATAGGCTTG GGAAGAGACA ATGTTTCTGT GCTATATTGG ATGCTCAGAA GTGCAGGAGA 1440
55 CGCTGAGACC AATCTCTCTT GCTGGGTAGT TAACCTATAG CATTTGGGGA TTTGGGTTAG 1500
ATGATCTAAC CAGGAGGCCA TCACTGGATG GTCAACCCCC CAAAAAATT CCATTTGAGC 1560
ATCAAAAACCT GCTTTGCACA ATCCTATTTG ATGCCCCCAG TTCAGCAGAG TCAGTGCCCA 1620
AAGAAAACCT TGGACGTGAG TAACACCCCT CAGCAGTCGC AACGTTATTT TGGTTTGTG 1680
AAGGACTCTG AAACCATCTA CCTGTATATA ATCTGGCTT TAGAAATTTG CCCAAGAAATG 1740
60 CTCAATCTGA GAGCTTTCTT CAGCAGCATA TATCATCAGC CTCATCTTAA AATAGGACAG 1800
GAGCCCTCTC CATGAGTTTA TCCAAGTTCT CAGCTCTTAA AATGCAGGCT GCCAAGACCC 1860
TACACCTGCC CTGGCTCTAC AGCCACTTAC CTGGTTTCTG GACTGTCAAC CTCCCAGCTG 1920
ACCTGCCCTT AGCCAGGAGG TAGAGACCTA ACTTGAGTTG GCGCCAAAGT TGAACCTGGC 1980
GTATGTCCTT GTGGCCCAAC CCCAGCCTGT CTGTCTCATT CATGCAGGCT CAACACTGGC 2040
65 CTCCAAAGTT CCCTTAACAC TTGCAAGTC CTTTCTTACT GTGCATTGAG ACTTGAGGAC 2100
ACTGTTTCTT ATCACAGGTG AGAGCCATGT TCAATACCTC CAGCAAGCTC TCTTGGCTCC 2160
CTGCACTGTG CAGCTCTCTC TTCCCAAGGT CCCAATACCA GCACCTCTAG TTAGAGTTAG 2220
GGTCAGGGTG AGGCTCTCTC CAACATCCCA GTAGTTTCTC CTCTGAGACA CATGGGCAAG 2280
AGACAATTTG GAGTCAAGAT TTTCCATTTG GATCTATTTT AATCTTTTTA GAAATGCATT 2340
70 TGAACAGTGT TGTTTGTTTT TTCCCTTCTA GTTAAGGGAC TATTTATATG TGTATAGGAA 2400
AGCTGTCTCT TTTTGTGTTT TTCTTTTAA C AAGTCCAAA GAAAGATGCA AAAGGAGATC 2460
ACACCCCTGC CCGGCTGAGC CCGGTGATAA CAAGTCACTC CAGACTAACC TGTGTGCCAG 2520
ACATTTGTGC ATTGTTGACAT TTTGAGGTTA TTATTATACA AGTTCTTGAA GGAAGCAGAA 2580
75 AGAGGGACTC CTCTCTCCCT CCGTGTATAG TCTCTATGTT TGTGCTAGTT TTTCTTTTTT 2640
TTCTCTGTGT CAGTCTCAGC ACAGGGCCCG CCTCCCTGCA GGAATAAGGG GTAAAACGTT 2700
AGGTGTTGTT TGGCAAGAAA CCACACTGAC TGATGAGGGG TAAAATGSGA CCAGGTAGAG 2760
CCACTCCGGG CAGCTGTAC CCAATCAGAA CTCTTTTCGG CAGCTGAAGA AATGTTCACT 2820
AACCCTTTTG ACCTAATTA AARACAGAGC TGCAGGAAGT GGGCTAAAG TGGCATTCTG 2880
TGATCTGTGT CTGTGAGACT TCTTTCTTTT TTTTAAACCA ATCCAAAGGA TGTTCAGAAA 2940

5 AAGCTAGCCA CTGGTATTTT GTTTTGTGTTA AAAAAAAAAA GAAAGAAAGA AAGAAAGAAA 3000
 AACGGAAAGG AACCTAGCTG CCTGTATCTT TCATTTTAA AATAGCACTT GAGTTATTTT 3060
 CTGAGTAATC CAATAAGAA CTTTTGATGA CAGCCAGAAT GTGTAGAAC TCTGGCTGAA 3120
 CATTTTCATCT CCCTGTAGTC AGAAGGGCTT TATTTCTCCC TTTGATGGG CCCCTCTCTC 3180
 TTTCTGGTGC TCTGGAAGTT GTTTAGAGGA AAGAATCTTA ATTTTAATTA ATTGGCAGT 3240
 GAGTTAATCT CACTCGCTTT TCTGCTTCCA GGCATCTTAG GAAAAACAA TGGTTTATGT 3300
 AGATAAGGGA TGCTTACTAA TGCTTTTTTA AAACAACAG GGACATTTT ATTATAGATT 3360
 TGATTTTTTT AAGGAATGTT TTTAAAAATA TATAAATAGG ACACCAAAGC GGCAGGTTT 3420
 10 TTTTGGGGG GAGGGGGTTT GTTTTCCAAC TCAAGATGCG ACATTAGTGG CCAGCAATAT 3480
 TTTTAACTC ATTCCAACCA GGAAGCTTTT TTATACATTG CCTAATCTA CGCCAACCAG 3540
 AAAATAGTCT CATCTCTTTT TTTCTCAAAT GAGATCCGTG TTTTATTTTA GCATTAAAT 3600
 AGTTACACTG TGATGACTGG CCTATTACCT GACTCAGCTC CCTCTACCTT GAAATTGACA 3660
 TTTTAAAAA ATGCAACTAA GTGGTTAATA GTGTGTGACG CTCAAAGTTA ATGTAAACTG 3720
 15 GAAAGGTGT GTGTCTGTGC TTTTGTGTTT TTGGTTAGCG TTGGTTTGT TTTTAAATTT 3780
 TTATCTTTC TAATAAATTT GCAGTTTCAT TCTTCTGTT TTGTCAAAG GWTCTAMARM 3840
 AAMMRAAAC AWYWTGGGG GGGCTGGGC CTCGGAATAA GTTTTAAACA CCACTTCGGG 3900
 TGGGGGGGG ICDGQNCQD NSDEBCESS QEPGSGQVFF TSENQLVYYP LITYALIGSS 3960
 GAAACCTCG CCAAGAAAAA GGTGGGAGA ATTCTCCACA CCAGAAAAA ACCGCGCGG 4020
 20 GGAACCCGA GAGTGTGCG TAAACCACAC CCGAAGAGAG AACTCAGAAG CACACAAGCG 4080
 GGACTCAACC AGGAGGACCC AAGGGAACCC GATAGAGTAC G

25 SEQ ID NO:171 PCQ7 Protein sequence:
 Protein Accession #: none found

30 1 11 21 31 41 51
 MLLGLPLCLL LSSAAESQLL PGNPINECN IPGNFMCNSG RCIPQAWQCD GLPDCFDKSD 60
 EKBCPKAKSK CGPTFFPCAS GIHCIIIRFR CNGFEDCPDG SDEENCTANP LLCSTARYEC 120
 KNLCLDKSP ICDGQNCQD NSDEBCESS QEPGSGQVFF TSENQLVYYP LITYALIGSS 180
 VIFVLVALL ALVLHQRKR NNLMTLPVHR LQHPVLLSRL VVLDHPHRCN VTYNVMNGIQ 240
 35 YVASQAEQNA SEVGSPSPYS EALLDQRPAN YDLPPFPYSS DTESLNQADL PPYRSRSGSA 300
 NSASSQAASS LLSVEDTSHS PGQPGPQEGT ABPRDSEPSQ GTEBV

40 SEQ ID NO:172 PEL3 DNA SEQUENCE
 Nucleic Acid Accession #: NM_005858.1
 Coding sequence: 57-1535 (underlined sequences correspond to start and stop codons)

45 1 11 21 31 41 51
 GTCATATTGA ACATTCCAGA TACCTATCAT TACTCGATGC TGTTGATAAC AGCAAGATGG 60
 CTTTGAATC AGGGTCACCA CCAGCTATTG GACCTTACTA TGAAAACCAT GGATACCAAC 120
 CGGAAAAACC CTATCCCGCA CAGCCCACTG TGGTCCCCAC TGCTACGAG GTGCATCCGG 180
 CTCAGTACTA CCGTCCCGCC GTGCCCACTG ACGCCCCGAG GGTCTCTGAG CAGGCTTCCA 240
 ACCCGCTGCT TCGCAGCAGG CCAAAATCCC CATCCGGGAC AGTGTGCACC TCAAGACTA 300
 50 AGAAGCACT GTGCATACC TTGACCTGG GACCTTCCT CGTGGGAGCT GCGCTGGCGG 360
 CTGGGCTACT CTGGAAGTTC ATGGGCAGCA AGTGTCCCAA CTCTGGGATA GAGTGGAGCT 420
 CTTAGGACTC CTGCATCAAC CCTCTAATC GGTGTGATGG CGTGTACACG TGCCCCGGCG 480
 GGGAGGACGA GAATCGGTGT GTTCGCCCTCT ACAGACCAAA CTTCATCTCT CAGATGTACT 540
 CATCTCAGAG GAAGTCTCTG CACCCGTGTG GCCAAGACGA CTGGAACGAG AACTACGGGC 600
 GGGCGGCTG CAGGGACATG GGCTATAAGA ATAATTTTTC CTCTAGCCAA GGAATAGTGG 660
 55 ATGACAGCG ATCCACAGC TTTATGAAAC TGAACACAAG TGCCGGCAAT GTCGATATCT 720
 ATAAAAAAT GTACACAGT GATGCCGTGT CTTCAAAAGC AGTGGTTTCT TTACGCTGTT 780
 TAGCCCTCGG GGTCAACTTG AACTCAAGCC GCCAGAGCAG GATCGTGGCG GGTGAGAGCG 840
 CGCTCCCGGG GGCTTGGGCC TGGCAGGTCA GCCTGCACGT CCAGAACGTC CACGTGTGCG 900
 60 GAGGCTCCAT CATCACCCC GAGTGGATCG TGACAGCCGC CCACTGCGTG GAAAAACCTC 960
 TTAACAATCC ATGGCATTTG ACGGCATTG CGGGATTTT GAGACANTCT TTCATGTCTT 1020
 ATGGAGCCGG ATACCAAGTA CAAAAGTGA TTTCTCATCC AAATTATGAC TCCAAGACCA 1080
 AGAACAATGA CATTCGGCTG ATGAAGCTGC AGAAGCCTCT GACTTTCAAC GACCTAGTGA 1140
 AACCAATGTG TCTGCCCAAC CCAGGCATGA TGCTGCAGCC AGAACAGCTC TGCTGGATTT 1200
 CCGGGTGGGG GGCCACCGAG GAGAAAGGGA AGACCTCAGA AGTGTGAAC GCTGCCAAGG 1260
 65 TGCTTCTCAT TGAGACACAG AGATGCAACA GCAGATATGT CTATGACAAC CTGATCACAC 1320
 CAGCCATGAT CTGTGCCGGC TTCTGCAAGG GGAACGTGGA TTCTTGCCAG GGTGACAGT 1380
 GAGGGCTCTC GGTCACTTCG AACACAATA TCTGGTGGCT GATAGGGGAT ACAAGCTGGG 1440
 GTTCTGGCTG TGCCAAAGCT TACAGACCAG GAGTGTACGG GAATGTGATG GTATTACGG 1500
 70 ACTGGATTTA TGCACAATG AAGGCAACG GCTAATCCAC ATGGTCTTCG TCCTTGACGT 1560
 CGTTTACAA GAAACAATG GGGCTGGTTT TGCTTCCCGG TGCATGATTT ACTCTTAGAG 1620
 ATGATTGAGA GGTCACTTCA TTTTATTAA ACAATGAAC TGTCTGGCTT TGGCACTCTC 1680
 TGCCATACGT TGCAAGCTGC AGTGGCTCCC CTGCCAGCC TGCTCTCCCT AACCCCTTGT 1740
 75 CCGCAAGGCG TGATGGCCGG CTGGTTGTGG GCACTGGGGG TCAATTGTGG AAGGAAGAGG 1800
 GTTGGAGGCT GCGCCCACTG AGATCTTCTT GCTGAGTCTT TTCCAGGGGC CAATTTTGG 1860
 TGAGCATGGA GCTGTCACTT CTCAGCTGCT GGATGACTTG AGATGAAAAA GGAGAGACAT 1920
 GGAAGGGGAG ACAGCCAGGT GGCACCTGCA CGCGCTGCCC TCTGGGGCCA CTTGGTAGTG 1980
 TCCCAGGCT ACTTCACAAG GGGATTTTGC TGATGGGTTT TTAGAGCCTT AGCAGCCCTG 2040
 GATGTGTGCC AGAATAAAG GGAACAGCC TTCTATGGGT GTCACTGTGT AGTCACTTGT 2100
 AAGGGGAACA GAAACATTTT TGTTCTTATG GGTGAGAAAT ATAGACAGTG CCCTTGGTGC 2160

5 GAGGGAAGCA ATTGAAAAGG AACTTGCCCT GAGCACTCCT GGTGCAGGTC TCCACCTGCA 2220
 CATTGGGTGG GGCCTCTGGG AGGAGAGACT AGCCTTCCTC CTCATCCTCC CTGACCCCTGC 2280
 TCCTAGCACC CTGGAGAGTG AATGCCCTTT GGTCCCTGGC AGGGCGCCAA GTTTGGCACC 2340
 ATGTCGGCCT CTTCAGGCCT GATAGTCATT GGAATTTGAG GTCCATGGGG GAAATCAAGG 2400
 ATGCTCAGTT TAAGGTACAC TGTTTCCATG TTATGTTTCT ACACATTGAT GGTGGTGACC 2460
 CTGAGTTCAA AGCCATCTTT

10 SEQ ID NO:173 PEL3 Protein sequence

Protein Accession #: NP_005647.1

15 1 11 21 31 41 51
 MALNSGSPPA IGFYYENHGY QPENFYPAQP TVVPTVYEVH PAQYYPSEVP QYAPRVLTQA 60
 SMFVVCQPK SPSGTCTSK TKKALCITLT LGTFVLGAAL AAGLLWKFMG SKCSNSGLEC 120
 DSSGTCINPS NWCQGVSHCP GGEDENRCVR LYGNPFLQM YSSQRKSWHP VCQDDWNNENY 180
 GRAACRDMGY KNNFYSSQGI VDDSGSTSPH KLNTSAGNVD IYKLIYHSDA CSSKAVVSLR 240
 CLACGVNLNS SRQSRIVGGE SALPGAWFWQ VSLHVQNVHV CGGSIITPEW IVTAHCVSK 300
 20 PLNNPWHWTA FAGILRQSPH FYGAGYQVQK VLSHPNVDK TKNNDIALMK LQKPLTPNDL 360
 VKFVCLNPNP MMLQPEQLCM ISGWGATEEK GKTSEVLNAA KVLIIETQRC NSRYVYDNL 420
 TPAMICAGFL QGNVDSQGD SGGPLVTSNN NIWMLIGDTS NGSCKAKAYR PGVYGNVMVF 480
 TDWIYRQMKK NG

SEQ ID NO:174 PBJ4 DNA SEQUENCE

Nucleic Acid Accession #:

AI694767

Coding sequence:

130-1086 (underlined sequences correspond to start and stop codons)

30 1 11 21 31 41 51
 CAGAGAGGCT GTATTTCAGT GCAGCCTGCC AGACCTCTTC TGGAGGAAGA CTGGACAAAG 60
 GGGGTACACAC ATTCTCTCCA TACGGTTGAG CCTCTACCTG CCTGGTGCTG GTCACAGTTC 120
 35 AGCTTCTTCA TGATGGTGGG TCCCAATGGC AATGAATCCA GTGCTACATA CTTCATCCTA 180
 ATAGGCCTCC CTGGTTTAGA AGAGGCTCAG TCTGCTTGG CCTTCCCAT TGTCTCCCTC 240
 TACCTTATTG CTGTGCTAGG TAACCTGACA ATCATCTACA TTGTGCGGAC TGACACACAGC 300
 CTGCATGAGC CCATGTATAT ATTTCTTTGC ATGCTTTTCA GCATTGACAT CCTCATCTCC 360
 ACCTCATCCA TGCCCAAAAT GCTGGCCATC TTCTGGTTCA ATTCCACTAC CATCCAGTTT 420
 40 GATGCTGTGC TGCTACAGAT GTTTGCCATC CACTCCTTAT CTGGCATGGA ATCCACAGTG 480
 CTGCTGGCCA TGGCTTTTGA CCGCTATGTG GCCATCTGTC ACCCACTGCG CCATGCCACA 540
 GTACTTACGT TGCTCTGTGT CACCAAAATT GGTGTGGCTG CTGTGGTGGC GGGGGCTGCA 600
 CTGATGGCAC CCTTCTCTGT CTTCATCAAG CAGCTGCCCT TCTGCCGCTC CAATATCCTT 660
 TCCATCTCCT TCCCTCTACA CCAAGATGTC ATGAAGCTGG CCTGTGATGA TATCCGGGTC 720
 45 AAGTCTGTCT ATGGCCTTAT CGTCATCATC TCCGCCATTG GCCTGGACTC ACTTCTCATC 780
 TCCTTCTCAT ATCTGCTTAT TCTTAAGACT GTGTTGGGCT TGACACGTGA AGCCAGGGCC 840
 AAGCCATTTC GCACTTGGCT CTCTCATGTG TGTGCTGTGT TCATATTCTA TGTACCTTTC 900
 ATTGGATTGT CCAATGGTGA TCGCTTTAGC AAGCGGCGTG ACTCTCCACT GCCCGTCACT 960
 TTGGCCAATA TCTATCTGCT GGTCTCTCCT GTGCTCAACC CAATTGTCTA TGGAGTGAAG 1020
 50 ACAAGGAGAA TTGCACAGCG CATCCTTCGA CTTTTCCATG TGGCCACACA CGCTTCAGAG 1080
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 GTTACATTTT TGGAGACAG TATTGAGAAA AAAAATTTC TTAATAAAAA TACAACCTAG 1200
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 55 TTTTCTATTT ACCATGCAGT CCAAACTTAA ACTGCTTCTA CTGATGGTTT ACAGCAATCT 1380
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 TAAACACAGA ATATAATAAA ATGAGATAAT CTAGCTTAAA ACTATAACTT CCTCTTCAGA 1500
 ACTOCCAAAC ACATGGGATC TCAGAAAAAT ACTGTCTTCA AAATGACTTC TACAGAGAAG 1560
 AATAATTTT TCCTCTGGAC ACTAGCACTT AAGGGGAAGA TTGGAAGTAA AGCCTTGAAA 1620
 60 AGAGTACATT TACCTAGCTT AATGAAAGTT GACACACTGT TCTGAGAGTT TTCACAGCAT 1680
 ATGGACCTTG TTTTTCCTAT TTAATTTTCT TATCAACCTT TTAATTAGGC AAAGATATTA 1740
 TTAGTACCCT CATGTAGCC ATGGGAAAA TGAATTTTCA TGGGGATCAG TGAATTAAAT 1800
 GGGGTATAC AAGTATAAAA ATTAATAAAA AAGACTTCA TGCCCAATCT CATATGATGT 1860
 GGAAGAAGCT TTAAGAGAG CAACAGGGTA GTGGGTTAGA GATTTCAGA GTCTTACATT 1920
 65 TTCTARAGGA GGTATTTAAT TTCTTCTCAC TCATCCAGTG TTGTATTAG GAATTTCCTG 1980
 GCACAGAAAC TCATGGCTTT AATCCACTA GCTATTGCTT ATTGTCTGG TCCAAATGCG 2040
 AATTACCTGT GTCTTGGAAAG AAGTGATTTC TAGGTTCCACC ATTTAGGAAG ATTCTTATTC 2100
 AGAAAGCTGT CATAGGGCTT ATAGCAAGTT ATTTATTTTT AAAAGTTCCA TAGGTGTTTC 2160
 TGATAGGCAG TGAGCTTAGG GAGCCACAG TTATGATGGG AAGTATGGA TGGCAGGTGT 2220
 70 TGAAGATAAC ATTGGCCTTT TGAATGTGAC TCGTAGCTGG AAAGTAGAGG AATCTTCAGG 2280
 ACCATGCTTT ATTTGGGGCT TTGTGCAGTA TGGAACAGGG ACTTTGAGAC CGGGAAGCA 2340
 ATCTGACTTA GGCATGGGAA TCAGGCATTT TTGCTTCTGA GGGGCTATTA CCAAGGGTTA 2400
 ATAGGTTTCA TCTTCAACAG GATATGACAA CAGTCTTAAC CAAGAAACT AAATTACATA 2460
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 75 CCTGATATGG ATTCTATINA CATGCTTTCA TCCCTTTTGT TAATGGATAT CATATTGGA 2580
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 AAAGTGCTTA GAACATAATA GTGCTTATGC TTGACACGGG TTAATTTTCA TCAAACTTGA 2760
 TTCTTCTCT GTGTAACACA TAGCCAGGCA ATTTTCCAGC CTCTCTTGA TTTGGGTATTA 2820
 80 TTAATTTTGA GCCATTACTT CCAATGTGAG TGGAAAGTGA ATGTGCAATT TTTATACCTG 2880
 GCTCATAAAA CCTTCCCATG TGCAGCCTTT CATGTTGACA TTAATATGTA CTTGGGAAGC 2940

TATGTGTAC ACAGAGTTAA TTAACCGAA AGGCCTGGNA ATTTTGTGNN AANNAACTG 3000
 TGGCCNAG GCCCNCAACC CTTTTNNNA ATTTGGCAAN NTCCACTTT GTANTTTGGT 3060
 AAGGAGCCA GTTGATAAG TGAATAATAA AGTACTATTG TGTC

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Protein Accession #: SEQ ID NO:175 PBJ4 PROTEIN SEQUENCE
 not available, cloned at Eos

1 11 21 31 41 51
 MVDPNHNESS ATYFILIGLP GLEBAQFWLA FFLCSLYLIA VLGNLTITYI VRTESLSHEP 60
 MYIFLCMLSG IDILISTSSM PKMLAIFWFN STTIQFDACL LQNFALHSLS GMESTVLLAM 120
 APDRYVAICH PLRHATVLT PLRTKIGVAA VVRGAALMAP LRVFIKQLPF CRSNILSHSY 180
 CLHQDVAKLA CDDIRNVVY GLIVTISAIG LDSLLISFSY LLILKTVLGL TREBAQAKAFG 240
 TCVSHVCAPF LPVVPFGLS MVHRFSKRRD SPLPVILANI YLLVFPVLNP IVYGVKTKEI 300
 RQRILRLPHV ATHASEP

Nucleic Acid Accession #: SEQ ID NO:176 PM72 DNA SEQUENCE
 Coding sequence: NM_004624.1
 57-1544 (underlined sequences correspond to start and stop codons)

TCGGAGCCTG CGGAGGGTGG TGGTGGTGGT GGTGGTGGCC CTCGCCCGCC TCACTCATGC 60
 CTCCTCCTCC TCCTCTCTCG CTCAGGCGCC TCGGTGGCGG TTGGTGGCGG GTTACGCGGC 120
 TGGTGGTGGC GGGCGCCCGG GCTCGCTCTC GGGGAGCGCG GGGCGGATCT CGCGCGCGAG 180
 GCGGCGGCGG CCGAGGTGGG GTCGCGCGGC GGAGGCGGCT CGAGCTTCGT GCTGCGCGCT 240
 CGCTCTTGGG CTCTCTCGTG CAGGAGGAGT GTGACTATGT GCAGATGATC GAGGTGCAGC 300
 ACAAGCACTG CCGTGGAGGAG GCCAGCTGG AGAATGAGAC AATAGGCTGC AGCAAGATGT 360
 GGGACAACCT CACTGTCTGG CCAGCCACCC CTCGGGGCCA GGTAGTTGTC TTGGCTGTTC 420
 CCCTCATCTT CAAGCTCTTC TCCTCCATTC AAGGCCGCAA TGTAAAGCCG AGCTGCACCG 480
 ACGAAGGCTG GACGACCTG GAGCCTGGCC CGTACCCCAT TGCTGTGGT TTGGATGACA 540
 AGGACGCGAG TTGTGATGAG CAGCAGACCA TGTCTACGGT TTCTGTGAAG ACCGCTTACA 600
 CCATGCGCTA CGGCTGTGCC CTCGCCACCC TTCTGGTGGC CACAGCTATC CTGAGCCTGT 660
 TCAGGAAGCT CCATGACAG CGGAAGTACA TCCACATGCA CCTCTTCATA TCCTTCATCC 720
 TGAGGCTGTC CGCTGTCTTC ATCAAAGACT TGGCCCTCTT CGACAGCGGG GAGTCGGACC 780
 AGTGCTCCGA GGGCTCGGTG GGCTGTAAGG CAGCCATGGT CTTTTPCCAA TATGTGTGTA 840
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 CCTCTCTCTC TGAGCGGAAG TACTTCTGGG GGTACATACT CATCGGCTGG GGGGTACCCA 960
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 GGTGCTGGGA CACCTCAAC TCCTCACTGT GGTGGATCAT AAAGGGCCCC ATCTCACCT 1080
 CCATCTGGT AAATCTCATC CTGTTTATTT GCATCATCG AATCTGTCTT CAGAAACTGC 1140
 GGCCCCAGTA TATCAGGAAG AGTGACAGCA GTCCATATCT AAGGCTAGCC AGGTCCACAC 1200
 TCCTGCTGAT CCGCTGTGTT GGAGTACACT ACATCATGTT CGCCTTCTTT CCGACAAATT 1260
 TTAAGCCTGA AGTGAAGATG GTCTTTGAGC TCGTGTGGG GTCTTCCAG GGTTTTGTGG 1320
 TGGCTATCCT CTACTGCTTC CTCAATGGTG AGGTGCAGCG GGAGCTGAGG CGGAAGTGGC 1380
 GCGCTGGCA CCGTCAAGGC GTCTGGGCT GGAACCCCAA ATACCGGCAC CGGTGCGGAG 1440
 CGACCAACGG CGCCACGTGC AGCAGCGAGG TTTCCATGCT GACCCGCTC AGCCCAAGTG 1500
 CCGCCGCTC CTCCAGCTTC CAAGCCGAAG TCTCCCTGGT CTGACCACCA GGATCCAGC 1560
 CCAAGCGGCC CTTCGCCCTC CTTCCTCACT GCAGCAGAG CGGGGGACAG AGGCTTGCCC 1620
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 GGACTCCTT AGAGAAGCA GCGCTAGAGC CTGCTGGAG CGTTCTAGC AAGTGAGAGA 1740
 GATGGAGACT CCTCTCTGAG AGGATGCAAG TGAAGTCAAG TCATTAGACT CCTCTCCAA 1800
 AGGCCCGCTA CGCCAAATCA GGGCAAAAG TCTACATACT TTCACTCTGA CTCTGCCCC 1860
 TGCTGCTCT CTGCCCCAAT TGGAGGAAG CAACCGGTGG ATCTCAAAAC AACACTGGTG 1920
 TGACCTGAGG CGAGAAAGGT TCTGCCCGGG AAGGTACCA GCACCAACAC CACGTTAGTG 1980
 CCTGAAATTT ACCATTGCT GTCAAGTTCC TTTGGGTAA GCATTACCAC TCAGGCATTT 2040
 GACTGAAGAT CGAGTCACT ACCCTATTCT CTCTTTACGC TTAGTTATCA GCTTTTAAA 2100
 GTGGGTATT CTGGAGTTT TGTTTGGAGA GCACACCTAT CTTAGTGGTT CCCCACCGAA 2160
 GTGGACTGG CCTGGGTCA GTCTGGTGG AGGACGGTGC AACCAAGGA CTGAGGGAAT 2220
 CTGAAGCTC TGGAAATGA GAAGCAGCC ACCAGCGAAT GCTAGGTCTC GGAATAAGCC 2280
 TACCTGCTCT CCAAGTCTCA GTGGCTTCAT CTGTCAAGTG GGACTCTGTC ACACAGCCA 2340
 TTCTTATCTC TCTGTGCTGT GGAAGCAACA GGAATCAAGA GACTGCCCC CTGTCCACC 2400
 CACCTATGTG CCAACTGTG TAACTAGGCT CAGAGATGTG CACCCATGGG CTCTGACAGA 2460
 AAGCAGATCC TCACCTGCT ACACATACAG GATTGAACT CAGATCTGTC TGATAGGAAT 2520
 GTGAAAGCAC GGACTCTTAC TGCTAACTTT TGTGTATCGT AACCAGCCAG ATCCTCTTGG 2580
 TTATTTGTTT ACCACTGTGA TTATTAATGC CATTATCCCT GAATTCCTCT TGCCACCCCA 2640
 CCTCTCCTGG AGTGTGGCTG AGGAGGCCCT CATCTCATGT ATCATCTGGA TAGGAGCCTG 2700
 CTGGTCACAG CTCTCTCTGT CTGCCCTTCA CCCCAGTGGC CACTCAGCTT CCTACCCACA 2760
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 GGAATAAAAA AAAA

SEQ ID NO:177 PM72 Protein sequence

Protein Accession #: J02195

1 11 21 31 41 51
 MPPPPLLSLR RLGGWSAVT RLVVAAAGAR SRGGRGSGR AGGGGRGGVA RRRRLRLRAA 60
 RSLGSSSLQE ECDYVQMIIEV QHKQCLEEAQ LENETIGCSK MWDNLTCWPA TFRGQVVVLA 120

CPLIFKLPSS IQGRNVSRSC TDEGWHLEP GFYPIACGLD DKAAASLDEQQ TMFYGSVKTG 180
 YTGIVGLSLA TLIVATAILS LPRKLHCTRN YIEMHLFISF ILRAAAVPIK DLALFDSGES 240
 DQCSSEGSVGC KAAMVFFQVC VMANFFWLLV EGLYLYTLA VSFFSERKYP WGYILIGWV 300
 PSTFTMVWII ARIHFEDYGL LRCWDTINSS LWWIKGPIL TSILVNFILF ICTIRILLQK 360
 LRPPDIRKSD SSPYSRLARS TLLLIPLFGV HYIMFAFPD NFKPEVKMVF ELVVGSPQGF 420
 VVAIIYCFIN GEVQAE LRK WRRWHLQGV LGMNFKYRHS GGSNGATCST QVSHLTRVSP 480
 GARRSSSPQA EVSLV

10 Nucleic Acid Accession #: AL133619
 Coding sequence: 1-2070 (underlined sequences correspond to start and stop codons)

15 1 11 21 31 41 51
 ATGAGCGGTG CGGGGGTGGC GGCTGGGACG CGGCCCCCA GCTCGCCGAC CCCGGGCTCT 60
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 CTCAGGCAGA GCGACCCGCA GAAACGGAACT CTGGACCTGG AGAAAAGCCT GCAGTTCCTG 180
 CAGCAGCAGC ACTCGGAGAT GCTGGCCAG CTCCATGAG AGATCGAGCA TCTGAAGCGG 240
 GAAACAAGG GTGAGCCGGC CGCGGGCCCT AGGCCGCCCC TGCCCTCCCA GGCACACTCA 300
 20 ACACTGCCGC TCCCGCAGCA CAGAAACACA GCCATCAACT CCAGCACAGC CTTGGGCTCA 360
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 CCTGTATGCC AACCCAGTGG GTACAGGTTC TGGGGGACCT GGACAGATGC CGCTACCTCT 480
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 GGGCTGAGG TCATTGCAAG CGGCCAGGTG GCCACAGGCT GCTCCCCAGA CCTCCCTCCT 600
 25 CCAAGTAGAG CTGAATAGG AAGGAACCCC TGGGACAGCC CTGCCCCTGC TAGATCTTTG 660
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 40 TCTGTCAAGT CCATCTCTAA TTCAGCCAAC TCTCAAGGCA AGGCCAGGCC CCAGCCCGGC 1500
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 45 ACCACACTTA GGCAGTGGGA AGTGCTATC CGCGAGCTGT GGAATACCAA CCTCTGCAG 1800
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 AAACGGGGCC TGCATCGCTC AGTCTTTGA

SEQ ID NO:179 BFB Protein sequence:

Protein Accession #: T43457

55 1 11 21 31 41 51
 MSGAGVAGT RPPSSPTPGS RRRRQRPVSG VQSLRPQSPQ LRQSDPQKRN LDLEKSLQFL 60
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 60 GGTQDGEPLQ TVLAHLAALA FVCQPSGYRF WGIWTDAAIS SRGWTHLCSQ AQHVLLSGSP 180
 GPEVIAGRQV ATGCSFDLPP PSRAEMGRNP WDSPCPARSL PQIAAVARFR ISSPMALSPH 240
 MLGAQGIWTH SIQGSPLPAIW AATMGTKGGS RVLFPCHLSK ALFHPDSGPH PAQDPGLWSQ 300
 AHFPLSLGLG LTSQGHITGG WSQPGNIAAG AVERALPSQG DMEKGVGEGP FPSRCGNSSSE 360
 LFWAKCGPSR QPQPCSAQDA DRTREEMLS LGTCCSMCFK PSCFPDGPSP NHLSRASAPL 420
 65 GARWVCINGV WVEPGGSPFA RLKGGSSRTH RPOGKRGLA GGSADTVRSP ADSLSMSSPQ 480
 SVKSISSNSAN SQKARPQPG SPNKQDSKAD VSQKADLEEE PLENSKLDK VPGVQGQARK 540
 EKAEASNAGA ACMGNSQHQG RQMGAGAHPP MILPLPLRKP TTLRQCEVLI RELMVTNLLQ 600
 TQELRHLKSL LEGSQRPQAA FEEASFPRDQ EATHTFFKYST KSLSKKCLSP FVAERAILFA 660
 LRQTFKNNFA ERQKRLQAMQ KRRLHRSVL

70 Nucleic Acid Accession #: NM_012318.2
 Coding sequence: 138-2405 (underlined sequences correspond to start and stop codons)

75 1 11 21 31 41 51
 CTCGTGCCGA ATTCGGCAGC AGACCGCGTG TTCGCGCCTG GTAGAGATT TCTGAAGACA 60
 CCAAGTGGCC CGTGTGGAAC CAAACCTGCG CGCGTGGCCG GCGCGTGGGA CAACGAGGCC 120

5	CGGAGACGA AGGGGCAATG GCGAGGAAGT TATCTGTAAT CTGATCCCTG ACCTTTGCCCC 180
	TCTCTGTAC AAATCCCTT CATGAACATA AAGCAGCTGC TTTCCTCCAG ACCACTGAGA 240
	AAATTAGTCC GAATTGGGAA TCTGGCATTAT ATGTTGACTT GGCAATTTCC ACACGGCAAT 300
	ATCATCTACA ACAGCTTTTC TACCGCTATG GAGAAAATAA TTCTTTGTCA GTTGAAGGGT 360
	TCAGAAAATT ACTTCAAAAT ATAGGCATAG ATAGATTAA AAGAATCCAT ATACACCATG 420
	ACCACGACCA TCACTCAGAC CACGAGCATC ACTCAGACCA TGAGCCTCAC TCAGACCATG 480
	AGCATCACTC AGACCACGAG CATCACTCTG ACCATGATCA TCACTCTCAC CATATCATG 540
10	CTGCTTCTGG TAAATAAAG CGAAAAGCTC TTTGCCGAGA CCATGACTCA GATAGTTCCAG 600
	GTAAAGATCC TAGAAACAGC CAGGGGAAAG GAGCTCACC ACCAGAACAT GCCAGTGGTA 660
	GAAGGAATGT CAAGGACAGT GTTAGTGCTA GTGAAGTGAC CTCAACTGTG TACAACACTG 720
	TCTCTGAAGG AACTCACTTT CTAGAGACAA TAGAGACTCC AAGACCTGGA AAACCTCTCC 780
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	TGGCTGTAGT GAAACAAAT GAATCTGTGA GTGAGCCCG AAAAGGCTTT ATGTATTCCA 900
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	GCATGGGCAAT CAGGATTCGG CTGAATGCAA CAGAGTTCAA CTATCTCTGT CCAGCCATCA 1020
	TCAACCAAT TGATGCTAGA TCTTGCTCTG TTCATACAAG TGAAGAAG GCTGAAATCC 1080
	CTCCAAAGAC CTATTCATTA CAAATAGCCT GGGTTGGTGG TTTTATAGCC ATTTCCATCA 1140
	TCAGTTTCTT CTCTCTGCTG GGGTTATCT TAGTGCTCT CATGAATCGG GTGTTTTCA 1200
20	AAATTCTCTT GAGTTTCTCT GTGGCACTGG CCGTTGGGAC TTTGAGTGGT GATGCTTTT 1260
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	GTGCTATTT TGATTCACG TGGAAGGGTC TAACAGCTCT AGGAGCCCTG TATTTCACTG 1440
	TTCTGTAGT ACATGTCTCT ACATTTGATCA AACAATTTAA AGATAAGAAG AAAAAGAATC 1500
25	AGAAGAAACC TGAATATGAT GATGATGTGG AGATTAAAG GCACTGTGCC AAGTATGAAT 1560
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	GAGCAGCTC ACAAGAGCCC TCCCACTTTG ATTCTCAGCA GCTTCAGTC TTGGAAGAAG 1680
	AAGAGTCAAT GATAGCTCAT GCTCATCCAC AGGAAGTCTA CAATGAATAT GTACCCAGAG 1740
	GGTCAAGAA TAAATGCCAT TCACATTTCC ACGATACACT CGGCCAGTCA GACGATCTCA 1800
30	TTCAACACCA TCATGACTAC CATCATATTC TCCATCATCA CCACCACCAA AACCAACATC 1860
	CTCAGCTTCA CAGCAGCTGC TACTCTCGGG AGGAGCTGAA AGATGCCGGC GTGCCCACTT 1920
	TGGCTGGAT GGTGATAATG GGTGATGGCC TGCACAATT CAGGATGGC CTAGCAATTG 1980
	GTGCTGCTTT TACTGAAGGC TTATCAAGTG GTTTAAGTAC TTCTGTTGCT GTGTTCTGTC 2040
	ATGAGTTGCC TCATGAATTA GGTGACTTTG CTGTCTACT AAAGGCTGGC ATGACCGTTA 2100
35	AGCAGGCTGT CTTTATAAT GCATTGTGAG CCATGCTGGC GTATCTTGGG ATGGCAACAG 2160
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40	TCATGTAAG GTTTAAATGC TAGAGTAGCT TAAAGATTG TCATAGTTTC AGTAGGTCAT 2460
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	AGCAAGAGAA TAAAGGAGAA AAGAGAGGAA TCTGAGAAAT GGGGAGGCAT AGATTCTTAT 2880
	AAATATCACA AAATTGTGTT TAAATTAGAG GGGAGAAATT TAGAATTAAG TATAAAAAG 2940
	CAGAATTAGT ATAGAGTACA TTCAATTAAC ATTTTGTGTA GGATTTATTC CCGTAAAAAC 3000
50	GTAGTAGACA CTCTCATATA CTAATTAGTG TACATTTAAC TTTGTATAAT ACAGAAATCT 3060
	AAATATATTT AATTAATTTA AGCAATATAC ACTTGACCAA GAAATTGGAA TTTCAAATG 3120
	TTCTGCGGG TTATATACCA GATGAGTACA GTGAGTAGTT TATGTATCAC CAGACTGGGT 3180
	TATGCCAAG TTATATATCA CCAAAAGCTG TATGACTGGA TGTCTGTTT ACCTGGTTTA 3240
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	GAGCAATGT GTTTATATAC GGTACTGTAG CCATACTAGG CCTGCTCTG GCAATCTCTA 3420
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60 Protein Accession #: SEQ ID NO:181 BCR4 PROTEIN SEQUENCE
NP_036451

1	11	21	31	41	51	
65	MARKLSVILI	LTFLSVNTP	LHELKAAAPP	QTTEKISPWW	ESGINVDLAI	STRQVHLQOL 60
	FYRYGEANSL	SVGEFRKLLQ	NIGIDKIKRI	HIHHDHDS	DHEHSDHRE	HSDHEHSDH 120
	EHSDEHDS	HEHHAASGKN	KRKALCFDHD	SDSSGKDPNN	SQGEKAHRPE	HASGRNNVKD 180
	SVSASEVTST	VYNTVSEGTH	FLETIETPRP	GKLPFKDVSS	STPPSVTSKS	RVSRLAGRKT 240
70	NESVSEPRKG	FMYSRNTNEN	PQECFNASKL	LTSHGMSIQV	FLNATEPNYL	CPAINQIDA 300
	RSCLHTSEK	KAEIIPKTYT	LQIAWVGCFI	AISIISPLSL	LGVLVPLMN	RVFVKPLSF 360
	LVALAVGTLG	GDAFLHLLPH	SHASHSHSHS	HEEPAMEMKR	GPLPSHLSQ	NIEESAYFDS 420
	TKWGLTALG	LYFMFLVEHV	LTLIKQPKDK	KKNKKPKPEN	DDVLEIKKQL	SKYBSQLSTN 480
	EKKVDTDRT	EGYLRAQSQ	PSHFDSQQPA	VLEKEEVMIA	HAHPQEVYNE	YVPRGCKNKC 540
75	HSHFDTLGQ	SDDLHHRHD	YHILHHRHH	QNHPRSHSQ	RYSRLEKDA	GVATLAWMI 600
	MGDLGNFSD	GLAIGAAFT	GLSSGLSTSV	AVFCHLPHE	LGDFAVLLKA	GMTVKQAVLY 660
	NALSAMLAYL	GMAITGIFGH	YAENVSMWIF	ALTAGLFMYV	ALVDMVPEML	HNDASDEGCS 720
	RMGYFFLQNA	GMLLGFQIML	LISIPHKIV	PRINP		

SEQ ID NO:182 BCY2 DNA sequence

Nucleic Acid Accession #:

NM_001203

Coding sequence:

274-1782 (underlined sequences correspond to start and stop codons)

5 1 11 21 31 41 51

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 GTGAAAGGAA AGAAGATCA TTTCTGCCT TGTGATAAA GGTTCAGACT TCTGCTGATT 180
 10 CATAACCAAT TGGCTCTGAG CTATGACAAAG AGAGGAAACA AAAAGTTAAA CTTACAAGCC 240
 TGCCATAAGT GAGAAGCAAA CTCTCTGAT AACATGCTTT TGGGAAGTGC AGGAAAATTA 300
 AATGTGGGCA CCAAGAAAGA GGATGGTGAG AGTACAGCCC CCACCCCGCG TCCAAAGGTC 360
 TTGCGTTGTA AATGCCACCA CCATTGTCCA GAAGACTCAG TCAACAATAT TTGCAGCACA 420
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 15 GGTGCTCTG GACTAGAAGG CTCAGATTTT CAGTGTGCGG ACACCTCCAT TCCTCATCAA 540
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 CTGCTCCAT TGAAAAACAG AGATTTTGTG GATGGACCTA TACACCACAG GGCTTTACTT 660
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 20 ATTCTCTCTG GAGATACCTT GAGAGACTTA ATTGAGCAGT CTCAGAGCTC AGGAAGTGGA 840
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 25 GGTGCTGGA CCACTGTGTA CTAATCACA GACTATCATG AAAATGGTTC CCTTTATGAT 1140
 TATCTGAAGT CCACCACTCT AGACGCTAAA TCAATGCTGA AGTTAGCTA CTCTCTGTC 1200
 AGTGGCTTAT GTCAATTTACA CACAGAAATC TTAGTACTC AAGGCAACCC AGCAATTGCC 1260
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 30 ACTCGAGTTG GCACCAAAAG CTATATGCTC CCAGAAAGTGT TGGACGAGAG CTTGAACAGA 1440
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 35 ATGACAGAAT GCTGGCTCA CAATCCTGCA TCAAGGCTGA CAGCCTGCG GGTAAAGAAA 1740
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 40 CTTTCAGGGA GCGACTGGG CAAAGACAGA GAAGCTCCA GAAGGAGAGA TTGATCCGTG 1980
 TCTGTTTGTG GCGGGAGAAA CCGTTGGGTA ACTTGTTCAA GATATGATGC AT

SEQ ID NO:183 BCY2 Protein sequence

Protein Accession #:

NP_001184

45 1 11 21 31 41 51

MLRSAGKLN VGTKEDGES TAPTPRPKVL RCKCHHCPV DSVNNICSTD GYCFMIEED 60
 DSGLPVVTSG CLGLESGDFQ CRDTPHPQR RSIECCTERN ECNKDLHPTL PFLKNRDFVD 120
 50 GPIHHRALLI SVTVCSLLL V LILFCYFRY KRQETPRYS IGLEQDETYI PPGESLRDLI 180
 EQSQSSGSGS GLPLLVQRTI AKQIQMVQKI GKGRYGEVWM GKWRGEKVAV KVFFTTTEAS 240
 WFRTEIYQT VLMRHNILQ FAAADIKGTG SWTQLYLID YHENGSLYDY LKSTTLDAKS 300
 MLKLAYSVS GLCHLHTEIF STQKPAIAH RDLKSKNIV KINGTCCIAI LQLAVKFISD 360
 55 TNEVDIPPNT RVGTIKRYMP EVLDESINRN HFQSYIMADM YSFLILWEV ARRCVSGTIV 420
 EEYQLPYHDL VPSDPSYEDM REIVCIKKLR PSFPNRWSSD ECLRQMGKLM TECWAHNPAS 480
 RLTAIRVKKT LAKMSESQDI KL

SEQ ID NO:184 CBF9 DNA sequence

Nucleic Acid Accession #:

AC005383

Coding Sequence:

328-2751 (underlined sequences correspond to start and stop codons)

65 1 11 21 31 41 51

GACAGTGTTC GCGGCTGCAC CGCTCGGAGG CTGGGTGACC CGGTAGAAG TGAAGTACTT 60
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 70 CCTGGCGGTA GTTCTCTCGA CCTCAGCCGG GTCTGGGTCTG GCCGCCCTCT CCCAGGAGAG 180
 ACAAACAGGT GTCCACGCTG GCAGCGCGCG CCGGGGCGCC CCTCTGTGA TCCCGTAGCG 240
 CCGCTGCGCC CGAGCGCGCG CCGGCTCTGT GAGTAGAGCC GCCCGGGCAC CGAGCGCTGG 300
 TCGCCGCTCT CCTTCCGTTA TATCAACATG CCGCCTTTCC TGTGTCTGGA GCGCGTCTGT 360
 GTTTCTCTGT TTTCCAGAGT GCGCCCATCT CTCCCTCTCC AGGAAGTCCA TGTAAACAAA 420
 75 GAAACCATCG GGAAGATTTC AGCTGCCAGC AAAATGATGT GGTGCTCGGC TGCAGTGGAC 480
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 CACTTTGCCA TCACAGCTCG TGACGCTCTG GACATCAGCC CCGAGAGGGT CAGAGTGGGA 600
 GCATTCAGT TCAGTTCAC TCCTCATCTG GAATTCCTCT TGATTCATT TTCAACCCAA 660

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CAGGAAGTGA AGGCAAGAAT CAAGAGGATG GTTTTCAAAG GAGGGGCGCAC GGAGACGGAA 720
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CAGCTGAAG AAAGGGGTCT CACTGTGTTT GCTGTGGGG TCAGGTTTCC CAGGTGGGAG 900
GAGCTGCATG CACTGGCCAG CGAGCCTAGA GGGCAGCAG TGCTGTGGC TGAGCAGGTG 960
GAGGATGCCA CCAACGGCTT CTTCAGCACC CTGAGCAGCT CGGCCATCTG CTCCAGCGCC 1020
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GCACACTGTC CCTTCTACAG CTGGAAGAGA GTGTTCTTAA CCGACCTTGC CACTGCTTAC 1200
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TGGAGCTCTT GCTCTGTATG TGTGAGCCAG GGATGAGTTC TTGAGAGCGC CTTGAGGCAC 2640
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CTGCCACCTT TCCCTTGAGG ATAAACAAG GGTCTGAAG ACTTAAATT AGCGGCTGA 3000
CGTTCCTTTG CACACATCA ATGCTGCCA GAATGTTGTT GACACAGTAA TGCCAGCAG 3060
AGGCTTTTAC TAGAGCATCC TTTGGAGGCG GAAGCCACG GCCTTTCAAG ATGGAAGCA 3120
GCAGCTTTTC CACTTCCCA GAGACATTCT GGATGCATT GCATTGAGTC TGAAGGGGG 3180
CTTGAGGAC GTTGTGACT TCTTGGGAC TGCCTTTGT GTGTGGAAGA GACTTGGAAA 3240
GGTCTCAGC TGAATGTGAC CAATTAACCA GCTTGTGTA TGAATGGGGA GGGGCTGAGT 3300
TGTGCATGGG CCCAGGTCTG GAGGGCCACG TAAATCTGTT CTGAGTCTG AGCAGTGTCC 3360
ACCTTGAAG TCTTC

SEQ ID NO:185 C8F9 Protein sequence
Protein Accession #: none found

50
55
60
65
70
75

1 11 21 31 41 51
MPPFLLLEAV CVFLPSRVFP SLPLQEVHVS KETIGKISAA SKMMWCSAAV DIMFLDGSN 60
SVKGSPERS KHPAIVTCG LDISPERVRV GAQPSSTPH LEFLDSFST QOEVKARIKR 120
MVFKGGRTE ELALKYLLER GLPGGRNASV PQILIIVTDG KSQGDVALPS KQLKRGVTV 180
FAVGVRFPFM EELHALASEP RGQHVLLAEQ VEDATNGLFS TLSSSAICSS ATPDCRVEAH 240
PCEBRTLEMY REPAGNAPCW RGSRRTLAVL AAECPPYSWK RVFLTHPATC YRTTCGPGCD 300
SQPCQNGGTC VPBGDGYOC LCPLAPGGEA NCALKLSLEB RVDLLPLDS SAGTTLDDGFL 360
RAKVFPVRFP RAVLSSEDSRA RVGVATYSRE LLVAVPVGEY QDVFDLVWSL DGIFPRGGPT 420
LTSALRQAA ERGFGSATRT GQDRFRVVV LITESHSEDE VAGPARHARA RELLLGVGS 480
BAVRAELEET TGSPKHMVY SDPQDLFNQI PELQGLCSR QRPGRITQAL DLVFLDTS 540
SVGFENFAQM QSPVRSCALQ FEVNPDTQV GLVVYGSQVQ TAFGLDTKPT RAAMLRASQ 600
APYLLGVGSA GTALLHYDK VMTVQRGARP GVPRAVVLT GGRGAEDAV PAQKLRRNGI 660
SVLVVGVGFP LSEGLRLLAG PRDSLHVAA YADLRXHQDV LIBWLCGEAK QPVNLCKPSP 720
CMNEGSCVLQ NGSVRCRCD GWEGFHCENR EWSSCSVCVS QGMILETFLR RMAPVQEGSS 780
RTPPSNYREG LGTEMVPTFW NVCAFGP

SEQ ID NO:186 PAV1 DNA sequence

Nucleic Acid Accession #:

AF272890

Coding Sequence:

87-1520 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
TGCTACCCGC GCCCGGGCTT CTGGGGTGTG CCCCACACAC GCGCCAGCCC TGCCACACCC 60
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AGCCCGGTAA CCTGTGCTG GCCGCACCGC TCCCGGACGG CGCGGCCACC GCGGCGCGGC 180

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TGCTGGTGCC CGCGTCGCGG CCCGCCCTCGT TGCTGCCTCC CGCCAGCGAA AGCCCCGAGC 240
CGCTGCTCA GCACTGGACA GCGGGCATGG GTCTGCTGAT GGCGCTCACC GTGCTGCTCA 300
TCGTGGCGGG CAATGTGCTG GTGATCGTGG CCATCGCCAA GACGCCGCGG CTGCAGACGC 360
TCACCAACCT CTTCATCATG TCCCTGGCCA GCGCCGACCT GGTTCATGGG CTGCTGGTGG 420
TGCCGTTCCG GGCACCATC GTGGTGTGGG GCGGCTGGGA GTACGGCTCC TTCTTCTGCG 480
AGCTGTGGAC CTGAGTGGAC GTGCTGTGGG TGACGGCCAG CATCGAGACC CTGTGTGTCA 540
TTGCCCTGGA CCGCTACCTC GCCATCACCT CGCCCTTCGG CTACCAAGAG CTGCTGACGC 600
GGCGCGCGGC GCGGGGCTTC GTGTGCACCG TGTGGGCCAT CTCGGCCCTG GTGCTCTTCC 660
TGCCCATCTT CATGCACTGG TGGCGGGCGG AGAGCGACGA GCGCGCGCGG TGCTACCAAG 720
ACCCCAAGTG CTGCGACTTC GTACCAACCC GGGGCTACGC CATCGCTCGG TCCGTAGTCT 780
CCTTCTACGT GCCCTGTGTC ATCATGTGCT TCGTGTACCT GCGGGTGTTC CGCGAGGCC 840
AGAAGCAGTG GAAGAAGATC GACAGCTGCG AGCGCGGTTT CCTCGCGCGG CCAGCGCGGC 900
CGCCCTCGCC CTGCGCTCGG CCCGTCCCGG CGCCCGGCGC GCGCGCCGGA CCCCGCGGCC 960
CGCGCGCGCC CGCGCGCACG GCCCGGCTGG CCAACGGCGG TGCGGGTAAG CGCGCGGCTT 1020
CGCGCTGCTT GGCCTACGCT GACAGAGAGG CGCTCAAGAC GCTGGGCATC ATCATGGGCG 1080
TCTTCAAGCT CTGCTGGCTG CCCTTCTTCC TGGCCAAAGT GGTGAAGGCC TTCCACCGCG 1140
AGCTGTGGCC CGACCGCTC TTCTGCTTCT TCAACTGGCT GGGCTAGGCC AACTCGGCTT 1200
TCAACCCCAT CATCTACTGC CGCAGCCCGG ACTTCCGCAA GGCCTTCCAG GGACTGCTCT 1260
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CGCGCTGCTT GGCCTACGCT GACAGAGAGG CGCTCAAGAC GCTGGGCATC ATCATGGGCG 1380
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ACCGCGGGCC GCGCGCGGAC AGCGACTCGA GCCTGGACGA GCGCTGCGCG CCCGGCTTGG 1500
CCTCGGAATC CAAGGTGTAG GCGCGCGCGG GCGCGCGCGA CTCCGGGCAC GCGTTCACAG 1560
GGGAAGCAGG AGATCTGTGT TTAATTAAGA CCGATAGCAG GTGAATCGA AGCCCAACAT 1620
CCTCGTCTGA ATCATCCGAG GCAAGAGAGA AAGCCACGGA CCGTTCGACA AAAAGGAAG 1680
TTTGGGAAGG GATGGGAGAG TGGCTGCTG ATGTTCTCTG TTG
  
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30

Protein Accession #: SEQ ID NO:187 PAV1 Protein sequence
 AA011176

35
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1 11 21 31 41 51
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MGLLMALIVL LIVAGNVLVI VAIKTFRLQ TLTNLFMSL ASADLVMLL VVPFGATIVV 120
WGRKEVSGFF CELWTSVDVI CVTASIEFLC VIALDRYLAI TSPFRYQSLI TRARARGLVC 180
TVWAISALVS FLPILMHWWR AESDEARRCY NDPKCCDFVT NRAYAIASSV VSFYVPLCTM 240
APVYLRVFRE AQKQVKKIDS CERRFLGGPA RPPSPSPSPV PAPAAPPFPF RPAAAAATAP 300
LANGRAGKRR PSRLVALREQ KALKTLGIIM GVFTLCWLPF FLANVVKAFH RELVFDRLPV 360
FFNMLGYANS AFNPIIYCRS PDFKAPQGL LCCARRAARR RHATHGDRFR ASGCLARPGP 420
PPSPGAASDD DDDVVVGATP PARLLEFWAG CNGGAAASDD SSLDEPCRPG PASESKV
  
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SEQ ID NO:188 BCO2 DNA sequence

Nucleic Acid Accession #: AJ400877

Coding sequence:

81-3080 (underlined sequences correspond to start and stop codons)

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60

65

70

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80

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1 11 21 31 41 51
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CCGCAACCGC TGAGCCATCC ATGGGGGTCC CGGGCCGCAA CGTCCCAGG GCGGCCTGGG 120
CGGTGCTGCT GCTGCTGCTG CTGCTGCGCG CACTGCTGCT GCTGGCGGGG GCGGTCGCGC 180
CGGGTCGCGG CGGTGCGCGG GGGCCGCGAG AGGATGTAGA TGAGTGTGCC CAAGGGCTAG 240
ATGACTGCCA TGCGGACGCC CTGTGTGAGA ACACACCCAC CTCTACAAAG TGCTCTGTGA 300
AGCCTGGCTA CCAAGGGGAA GGCAGGCAGT GTGAGGACAT CGATGAATGT GGAAATGAGC 360
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GCAAGGAGGG GTTTTTCCTG AGTGACAATC AGCACACCTG CATTACCGC TCGGAAGAGG 600
GCCTGAGCTG CATGAATAAG GATCACGGCT GTAGTCACAT CTGCAAGGAG GCCCAAGGG 660
GCAGCGTGGC CTGTGAGTGC AGGCCCTGTT TTAGAGTGGC CAAGAACCAG AGAGACTGCA 720
TCTTGAACCT TAACCATGGG AACGGTGGGT GCCAGCACTC CTGTGACGAT ACAGCCGATG 780
GCCAGAGGTG CAGCTGCCAT CCACAGTACA AGATGCACAC AGATGGGAGG AGTGCCTTGG 840
AGCGAGAGA CACTGTGCTG GAGGTGACAG AGAGCAACAC CACATCAGT GTGGATGGGG 900
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TCCAGTTGGA TGGGAAGACA TGTAAGATA TTGATGAGTG CCAGACCCGC AATGGAGGTT 1080
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GTGACCAAG CTGCATCAAC CACCGTGGCA CATTGCTTG TGCTGCAAC CGAGGGTACA 1260
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CACCCCGTGT GTCCCTGCAC TGGGTAAGA GTGGTGGAGG AGACGGGTGC TTCTCAGAT 1500
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5 TGAGCTGCAT CGTAAAGCGA ACCGAGAAGC GGCTCCGTAA AGCCATCCGC ACGCTCAGAA 1860
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 20 TCAAGGCTCT GTTGTATGTC CTGGCCCATC CCGAGAATA TTTCAAGTAC ACAGCCAGG 3000
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 25 GAACCTGGTT TTCTTTCCC AGCATCGTGG ATGTAGACTG AGAATGGCTT TGAGTGGCAT 3300
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 TTGCTACGCC TAGGTGAGAC TCACCTGTCC TTCTGGGGTC TTAACCTCC TCAAGGAGTC 3420
 TGTAGTGAAA AGGAGGCCAC AGAATAAGCT GCTTATCTG AAACCTCAGC TTCTCTAGC 3480
 CCGGCCCTCT CTAAGGGAGC CCTCTGCACT CGTGTGCAGG CTCTGAOCAG GCAGAACAGG 3540
 30 CAAGAGGGGA GGGGAAGGAGA CCCTGCAAG CTCCCTCCAC CCACCTTGA ACCTGGGAGG 3600
 ACTCAGTTTC TCCACAGCCT TCTCCAGCCT GTGTGATACA AGTTGATCC CAGGAACTTG 3660
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 AGCACTCTG GAGACAT

35 SEQ ID NO:189 BC02 Protein sequence
 Protein Accession #: CAB92285

40 1 11 21 31 41 51
 MGVAAGNRNP AAWAVLLLL LLPPLLLAG AVPPGRGAA GPQEDVDECA QGLDDCHADA 60
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 HDGHNCLDVD ECLNNNGGQ HTCVNVMGSY ECCCKEGFLL SDNQHTCIHR SEEGLSCMNK 180
 45 DHGCSHICKE APRGSVACEC RPFELAKNQ RDCILTCNHG NGGQCHSCDD TADGPECSCH 240
 PQYKMHDTGR SCLEREDTVL EVTESNTTSV VDGDKRVKRR LLMETCAVNN GGCDDRTCKDT 300
 STGVHSCSPV GFTLLQDLGKT CKDIDECQTR NGGCDHFCKN IVGSFDCGCK KGFLLTDEK 360
 SCQDVDECSL DRTCDHSCIN HPGTFACACN RGYTLYGFIH CGDINECSIN NGGQQQVCVN 420
 TVGSYECQCH PGYKLHWNKK DCVEVKGLLP TSVSPRVSLL CGKSGGGDGC FLRCHSGIHL 480
 50 SSDVTTIRTS VTRKLNKGC SLKNAELFPE GLRPALEKH SSVKESFRVY NLTCSSGKQV 540
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 FHLQSGMNL DVAKKPPRTS ERQAESCGVG QGHAENQCVS CRAGYTDGA RERCILCPNG 660
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 55 PEAGRSTCFP CGGLATKHQ GATSFQDCET RVQCSPGHFY NITTHRCIRC PVGTYPQFEG 780
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 IQFKSNEGNS ARGFPVYVT YDEDYQELIE DIVRDGRLYA SENHQELKD KKLKALFDV 960
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60 SEQ ID NO:190 BFG1 DNA sequence
 Nucleic Acid Accession #: AF007170
 Coding sequence: 1-1725 (underlined sequences correspond to stop codon)

65 1 11 21 31 41 51
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 AGCTACCTCA AGCCCAAGAA CAAGGAAAGC ATGTACCACT CACTGACATA TGCCACCATC 180
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 70 ATGAAGGAGG CACAGATGCT GTTCAGAGG CACCGGAGGA AGTCTTCTGT AACAGATTCC 300
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 AACATGTGTA GCTTCATCAA AGCGGCATC AAAGTTCGAA ACAGCTACCA GACCTACAAG 480
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 75 GAAGGAGGAG TGAAGCTTGG TGTAGGGGCC TTCAACCTGA CACTGTTCAT GCTTCTACT 600
 AGGATCTCTA GGCTGTGGA GTTTGTGGGG TTTTCAGGAA ACAAGGACTA TGGGCTGCTG 660
 CAGCTGAGAG AGGGAGGCTC AGGGCACAGC TTCCGCTCTG TGCTCTGTGT CATGCTCTG 720
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 15 CGTGTCCAGG AGGCCGAGGA GAATTTTAGG AGCATCTCTG CCAATGAAAA GAAGATTAAA 1500
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 25 CCACTAGCTT ACTACTCACA CTTCATTCTA CTCTTTTGT AAATTTCCAA TTTAAAAATC 2340
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SEQ ID NO:191 BFG1 Protein sequence

Protein Accession #: AAC39582

35 1 11 21 31 41 51
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 40 QMLQQRHRRK SSVTDSFSSL VNRPTLGQFT EEEIHAFCY ABCLLQRAAL TFLQDENMVS 120
 FIKGGIKVRN SYQTYKELDS LVQSSQYCKG ENHPHFEGGV KLGVGAFNLT LSLMPLTRLR 180
 LLEFVGFSGN KDYGLLQLEE GASGHSFRSV LCVMLLLCYH TFLTFVLGTG NVNIEEAEKL 240
 LKPYLNRYPK GAIFLFFAGR IGVKGNIDA AIRFEBCCE AQQHWKQFHH MCYWELMWCF 300
 TYKGQWKMSY FYADLLSKEN CWSKATYIYM KAAVLSMFGK EDHKPFQDDE VELFRAVPL 360
 45 KLKLAGKSLP TEKFAIRKSR RYFSSNFISL PVPALMMYI WNGYAVIGKQ FKLTDGILEI 420
 ITKAEEMLEK GPENEYSVDD ECLVKLLKGL CLKYLGRVQE AEENFRSISA NEKKIKYDHY 480
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SEQ ID NO:192 BFO8 DNA sequence

Nucleic Acid Accession #:

NM_032583

Coding sequence:

1-4044 (underlined sequences correspond to start and stop codons)

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 60 TGGGGGAAGT ATGATGCTGC CTTGAGAACC ATGATTCCTT TCGTCCCAA GCGAGGTTT 240
 CCTGCCCCC AGCCCTGGA CAAATGCTGC CTGTTCTCT ACCTCACCGT GTCATGGCTC 300
 ACCCGCTCA TGATCCAAAG CTTACGGAGT CGCTTAGATG AGAACACCAT COCTCCACTG 360
 TCAGTCCATG ATGCTCAGA CAAAAATGTC CAAAGGCTTC ACCGCTTTG GGAAGAAGAA 420
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 65 ACAGGTGTA TTTTGGATG ACTTCGGGC ATCTGCTTCT GCATTGCCAG TGTACTCGGG 540
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 CATGGAGTGG GACTCTGCTT TGCCCTTTT CTCTCGAAT GTGTGAAGTC TCTGAGTTTC 660
 TCTCAGATT GGATCATCAA CCAACGCACA GGCATCAGT TCGAGCAGC TGTTCCTCC 720
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 70 ATCAGCTTCT TCACCGGTGA TGTAAACTAC CTGTTTGAAG GGGTGTGCTA TGGACCCCTA 840
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 75 TTGCAAAAA TCATTGAAG TATGGAAGT CTGACTTCT GCTCCAAACC TGGTGTGTC 1140
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5 CCAGAGGAAG AAGGGAACAG OCTGGGCCA GAGTTGCACA AGATCAACCT GGTGGTGTCC 1500
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 10 GGCGCATATG ACAAGGCCCG ATACCTCCAG GTGCTCCACT GCTGCTCCT GAATCGGGAC 1740
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 15 TTAGAATTTT GTGGCCAGAT CATTITGTTG GAAAAATGGGA AAATCTGTGA AAATGGAACT 2040
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 20 TACATCCAGG CAGCTGGAGG TTACATGGTC TCTTGCATAA TTTCTTCTT CGTGGTGTCTG 2340
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 25 CACAACAAGC TCTTCAACA GGTITTCGCG TGCCCATGA GTTCTTTGA CACCATCCCA 2640
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SEQ ID NO:193 BFO6 Protein sequence

Protein Accession #: NP_115972.1

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SEQ ID NO:194 BHEB DNA sequence

Nucleic Acid Accession #: AA83251

Coding sequence:

1-1749 (underlined sequences correspond to start and stop codons)

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SEQ ID NO:195 BHB8 Protein sequence

Protein Accession #: none found

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SEQ ID NO:196 CQA5 DNA SEQUENCE

Nucleic Acid Accession #:

AA088458

Coding sequence:

882-1995 (underlined sequences correspond to start and stop codons)

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SEQ ID NO:197 LBG2 DNA SEQUENCE

Nucleic Acid Accession #: X63629
Coding sequence:

54-2543 (start and stop codons are underlined)

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SEQ ID NO:198 LBG2 Protein sequence:

Protein Accession #:

CAA45177

65 1 11 21 31 41 51
 MGLPRGPLAS LLLQVCWLQ CAASEPCRAV FREAEVTLA GGAEQEPGQA LGKVFMGCPG 60
 QEPALFSDN DDFTVRNGET VQERRSLKER NPLKIFPSKR ILRRHKRDVW VAPISVPENG 120
 70 KGFPPORLNQ LKSNKDRDTK IFYSITPGA DSFFGVFAV EKSTGWLLN KPLDREELAK 180
 YELPFAVSE NGASVEDPMN ISIVTDQND HKPKFTQDTF RGSVLEGVLP GTSVMQVTA 240
 DEDDAIYTYN GVVAYSHSQ EPKDPHDLMF THIRSTGTIS VISSGLDREK VPEYTLTIQA 300
 TDMDDGSGTT TAVA VVELD ANDNAPMFDQ QKYEAHVPE AVGHVQRILT VIDLDAPNSP 360
 75 AWRATYLMG GDDGDHFTT THPESNQGL TIRKGLDFA KNQHTLYVEV TNEAPFVLKL 420
 FTSTATVTVH VEDVNEAPVF VPFSKVVEVQ EGIPTGEPVC VYTAEDPDKB NQKISYRILR 480
 DPAGWLAMD PDSGQVTA VGT LDREDEQFVR NNIEYVMVLA MDNGSPPTTG TGTLTLID 540
 VNDHGVPFEP RQITCNQSP VRHVLNITDK DLSFHTSPFQ AQLTDDSDIY WTAEVNEEGD 600
 TVVLSLKKFL KQDTYDVHLS LSDHGNKEQL TVIRATVCD C HGHVETCPG WKGGFIPVL 660
 GAVLALLFL LVLLLVRRK RKIKEPLLP EDDTRDNVVF YGEEGGGED QDYDITQLR 720

GLEARPEVVL RNDVAPITP TPMYRPRPAN PDEIGNFIE NLKAANTDPT APFYDTLLVF 780
DYEAGSGSDAA SLSSLTSSAS DQDQDYDYLN EWGSRFKKLA DMYGGGEDD

5 Nucleic Acid Accession #: NM_012152
Coding sequence: 43-1104 (underlined sequences correspond to start and stop codons)

SEQ ID NO:199 OB15 DNA SEQUENCE

10 1 11 21 31 41 51
CTTCTTAAAT TTTCTTTCTA GGATGTTTAC TTCTTCTCCA CAATGAATGA GTGTCACTAT 60
GACAAGCACA TGGACTTTTT TTATAATAGG AGCAACACTG ATACTGTCTGA TGACTGGACA 120
GGAAACAAAGC TTGTGATTGT TTTGTGTGTT GGGACGTTTT TCTGCTGTGT TATTTTTTTT 180
TCTAATCTCT TGGTCATCGC GGCAGTGATC AAAAACAGAA AATTTCATTT CCCCTTCTAC 240
15 TACCTGTGGC CTAATTTAGC TGCTGCGGAT TTCTTGGCTG GAATGCTTA TGTATTCTCTG 300
ATGTTTAAAC CAGGCCCCAGT TTCAAAAACT TTGACTGTCA ACCGCTGGTT TCTCGTCAG 360
GGGCTTCTGG ACAGTAGCTT GACTGCTTCC CTCACCAACT TGCTGGTTAT CGCCGTGGAG 420
AGGCACATGT CAATCATGAG GATGCGGGTC CATAGCAAAC TGACCAAAAA GAGGGTGACA 480
20 CTGCTCATTT TGCTTGTCTG GGCATCGGCC ATTTTATGTT GGGCGGTCCC CACTCTGGGC 540
TGGAAATGCT TCTGCAACAT CTCTGCGTGC TCTTCCCTGG CCCCCATTTA CAGCAGGAGT 600
TACCTGTGTT TCTGGACAGT GTCCAACTTC ATGGCCTTCC TCATCATGGT TGTGGTGTAC 660
CTGCGGATCT ACGTGTACGT CAAGAGGAAA ACCAAGCTCT TGTCTCCGCA TACAAGTGGG 720
TCCATCAGCC CCGGAGGAGC ACCCATGAAG CTAATGAAGA CGGTGATGAC TGTCTTAGGG 780
25 GCGTTGTGGS TATGCTGGAC CCGGGGCTG GTGGTCTGCT TCCTCGACGG CCTGAAGTGC 840
AGGCAGTGTG CGGTGCAACA TGTGAAAAGG TGGTTCCTGC TGCTGGCGCT GCTCAACTCC 900
GTCGTGAACC CCATCATCTA CTCTACAAG GACGAGGACA TGTATGGCAC CATGAAGAAG 960
ATGATCTGCT GCTTCTCTCA GGAGAACCCA GAGAGGGCTC CCTCTCGCAT CCCCTCCACA 1020
30 GTCTCAGCA GTGCTGACAC AGGCAGGCCA TACATAGAGG ATAGTATTAG CCAAGGTGCA 1080
GTCTGCAATA AAAGCATTTC CTAAACTCTG GATGCTCTC GGCACACCA GGTGATGACT 1140
GTCTTAGG

SEQ ID NO:200 OB15 Protein sequence:

35 Protein Accession #: NP_036284
1 11 21 31 41 51
MNECHYDKHM DFFYNRSNTD TVDDWTGTEK VIVLCVGTFF CLIFPFSNSL VIAAVIEKRR 60
40 FEPFFYYLLA NLAADFFPAG IAYVFLMFTN GPVSKTLTVN RWFLRQGLLD SSLTASLTNL 120
LVIAVEREMS IMRMVHSNLT TKKRVLLIL LVMAIAIFMG AVPTLGNCL CNISACSSLA 180
PIYSRSLVFP WTVSNLMAFL IMVVYLRITV VYVKKRTNVL SPHTSGSISR RRTFMKLMKT 240
VMTVLGAFVV CMTPLGLVLL LDGLNCRQCG VQHKRMFLL LALLNSVNP IYSYKDEDM 300
YGTMKMKMICC FSQENPERRP SRIPSTVLSR SDTGSQYIED SISQQAVCNK STS

SEQ ID NO:201 PAA6 DNA SEQUENCE

45 Nucleic Acid Accession #: AA589531
Coding sequence: 1-504 (underlined sequences correspond to start and stop codons)

50 1 11 21 31 41 51
ATGACCTACA GTTACTCATT TTTCAGGCCY GAGTTGATCG TTAATCATCT TAATTATGTT 60
CATTCTGAAG CCAACAGGAG AACCAAGACC AAAACTTTAT TGCTCTGCTT TCATTTCCTT 120
GATGAACCTT CTGGACTAAG CACACATCTT CCTTGTATTAT CTCTCTCAAA GGAGTGTGGA 180
55 GTGCTTCTAT TGGACATCCA CGGGAAGAAG GAAGACATGA GAATCAOCCA ACAGTCTTCC 240
CAGCTATACC TGTGGACAT GGTGGGTTTT ACAATATTTA AGAAGCTGTG GATGAGCCTC 300
ATACCCAGAG GGAACAAACG CTCCCAAAA AGAGTTACAG AAACCATCCT GAGAGATTTT 360
AAGCAGAAGC AAGATTCAAA GATCCAAGAG GAGAGACGAA GAGAGTCTGC AGGACCAAAC 420
60 CTCTCTTCAT TCTGTGTTGT GGGGAATGCT GGAAGAGGAG ACAGGCCCCA GATTTGGGCA 480
GGAAGTAAAC AGTATTTCAG CTGAGGCCAA TCTGAGCAGG AACATTCCAA TATTCTTCA 540
GCTACGTTGT CCCAGCACTT CACTGGTTAA CCTTTTATGT CCACCATTTG TGGATTTCAC 600
AGCTACTTGT CAATGGTGAA TATTGATCAT CATCATATC TACTGAGCTG CTACCATATC 660
CCAGCTACTC TTTGCAATGT GTTCATTATT TTCTCAACAC TCAGCATATT TGCAATATGT 720
70 TATGTAATAT CACAGACAAG GAAACTGAAC GCAGAAATGT TTTATTTCCT GCCAAACATC 780
ACATGAGGAT GAACAATGAA ACCGATTGGA AACCAGGATT GTCTGATTCC AACATCTCTG 840
65 GGTCTTTTTT CACTCTGATA TGCTGCAATT AAAAGCCAT TTCTAAGACT GT

SEQ ID NO:202 PAA6 Protein sequence:

70 Protein Accession #: none found
1 11 21 31 41 51
MTYSYGFRRP ELIVNHLNVV HSEANRRRTK KTLISLISPL DETSGLSLTH PCLSLSKECG 60
75 VLHLDLHGRK EDMRTTQSS QLYLWDMGGP TIFKNLQMSL IFRGNKRSR RVTETTLRDP 120
KQKQSSKIQB ERRRESAGPN LSSPWFVGNA GRGDRPQIWA GSKQFSQ

SEQ ID NO:203 PAR2 DNA SEQUENCE

Nucleic Acid Accession #: XM_050197
Coding sequence: 310-1971 (underlined sequences correspond to start and stop codons)

5 1 11 21 31 41 51
TCACACGTGC CAAGGGGCTG GTCACGGGA ACCAGCCTGC ACGCGCTGGC TCCGGGTGAC 60
AGCGCGCGCG CTGCGCCAGG ATCTGAGTGA TGAGACGTGT CCGCACTGAG GTGCCCCACA 120
GCAGCAGGTG TTGAGCATGG GCTGAGAAGC TGGACCGGCA CCAAGGGCT GGCAGAAATG 180
GGCGCTGGC TGATTCTAG GCACTTGGCG GCAGCAAGGA GGAGAGGCGG CAGCTTCTGG 240
AGCAGAGCGG AGACGAAGCA GTTCTGGAGT GCCTGAACGG CCGCTGAGC CCTACCCGCG 300
TGGCCCACTA TGGTCCAGAG GCTGTGGGTG AGCGCCTGC TCGGCACCG GAAAGCCGAG 360
CTCTTGTCTG TCAACTTGCT AACCTTTGGC CTGAGGTGT GTTGGCGCG AGGCATCAAC 420
TATGTGCCCG CTCTGCTGCT GGAAGTGGGG GTAGAGGAGA AGTTCATGAC CATGGTGTCTG 480
GGCATTGGTC CAGTGTGGG CTGGTCTGT GTCCGCTCC TAGGCTCAGC CAGTGACCAC 540
TGGGTGGAG GCTATGGCGG CGCGCGGCGG TTCATCTGGG CACTGTCTCT GGGCATCTCTG 600
CTGAGCCTCT TCTCATCTCC AAGGGCCGCG TGGCTAGCAG GGCTGCTGTG CCGGATCTCC 660
AGGCGCCTGG AGCTGGCACT GCTCATCTCT GGCCTGGGGG TGCTGGACTT CTGTGGCCAG 720
GATGTCTTCA CTCACTAGGA GGCCCTGCTC TCTGACTCT TCGGGGACCG GGACCACTGT 780
CGCCAGGCCT ACTCTGTCTA TGCCCTCATG ATCAGTCTTG GGGCTGCCT GGGCTACCTC 840
CTGCCCTGCA TTGACTGGGA CACCACTGCC CTGGCCCGCT ACCTGGGCAC CCAGAGGAG 900
TGCTCTCTTG GCTCTCTCAC CCTCATCTTC CTCACCTGCG TAGCAGCCAC ACTGCTGTGT 960
GCTGAGGAGG CAGCGCTGGG CCCCACCGAG CCAGCAGAA GGTGTCTGGC CCGCTCTCTG 1020
TGCGCCACT CTCTTCTTCA CCGGGCCGCG TTGGCTTTCC GGAACCTGGG CGCCCTGCTT 1080
CCCGGCTGCG ACCAGCTGTG CTGCGCATG CCGCGCACCC TCGCGCGGCT CTCTGTGGCT 1140
GAGCTGTGAC GCTGGATGGC ACTCATGACC TTCACGCTGT TTACACGGA TTCTGTGGG 1200
GAGGGGCTGT TCTCCAGGT GCCAGAGCT GAGCGGGGCA CCGAGGCGCG GAGACACTAT 1260
GATGAAGCGG TTGGATGGG CAGCCTGGGG CTGTCTCTGC AGTGGCCAT CTCCCTGGTC 1320
TTCTCTCTGG TCTTGGACCG GCTGGTGCAG CGATTGGCA CTGAGCAGT CTAATTGGCC 1380
AGTGTGGCAG CTCTCTCTGT GGCTGCGGT GCCCATGCCC TGTCCACAG TGTGGCGGTG 1440
GTGACAGCTT CAGCGCGCCT CACCGGCTTC ACCTCTCTAG CCGTGCAGAT CCTGCCCTAC 1500
ACACTGGCCT CCGCTTACCA CCGGAGAAAG CAGGTGTCTC TGCCCAATA CCGAGGGGAC 1560
ACTGAGGTG CTAGCAGTGA GGACAGCCTG ATGACCACTT TCGTCCAGG CCGTAAGCCT 1620
GGAGCTCCCT TCCCTAATGG ACACGTGGGT GCTGGAGGCA GTGGCTGCT CCGACCTCCA 1680
CCCGGCTCT GCGGGGCTCT TGCTGTGAT GTCTCCGTAC GTGTGGTGGT GGGTGAGCCC 1740
ACCGAGGCGA GGGTGTCTCC GGGCGGGGCG ATCTGCCTGG ACCTGCCCAT CCTGGATAGT 1800
GCCCTCTCTG TGTCCAGGT GGCCCATCTC CTGTCTATGG GCTCATATGT CCAGCTCAGC 1860
CAGTCTGTCA CTGCTATAT GGTGTCTGCC CGAGGCTCGG GTCTGGTCCG CATTTACTTT 1920
GCTACACAGG TAGTATTGGA CAAGAGCGAC TTGGCCAAAT ACTCAGCGTA GAAACTTCC 1980
AGCACATGGG GGTGAGGGG CTGCTCACT GGTCCACGC TCCCGCTCC TGTAGCCCC 2040
ATGGGGCTGC CCGGCTGGCC GCCAGTTCT GTTGTGCCA AAGTAATGTG GCTCTCTGCT 2100
GCCACCTGT GCTGCTAGG TGCGTAGCTG CACAGCTGGG GGCTGGGGCG TCCCTCTCTT 2160
CTCTCCCGAG TCTCTAGGG TGCTGACTG GAGGCTCTCC AAGGGGGTTT CAGTCTGGAC 2220
TTATACAGG AGGCGAGAAG GGCTCCATGC ACTGGAATGC GGGGACTCTG CAGGTGGATT 2280
ACCCAGGCTC AGGGTTAACA GCTAGCCTCC TAGTTGAGAC ACACCTAGAG AAGGGTTT 2340
GGGAGCTGAA TAACTCAGT CACCTGGTTT CCACTCTCTA AGCCCTTAA CCTGCAGCTT 2400
CGTTTAAATG AGCTCTTGA TGGGAGTTTC TAGGATGAAA CACTCTCCA TGGGATTTGA 2460
ACATATGAAA GTTATTGTGA GGGGAAGAGT CCTGAGGGGC AACACACAAG AACCAGGTCC 2520
CCTCAGCCCC ACAGGCACTG GTCTTTTTTG CTNGANTCCA CCCCCCCTT CTTTACCCCT 2580
TT

SEQ ID NO:204 PAR2 Protein sequence:

Protein Accession #: XP_050197

55 1 11 21 31 41 51
EVQRLWVSR LRRHKAQLLL VNLTFGLGV CLAAGITYVP PLLLEVGVVE KPMTHVLGIG 60
PVLGLVCPVL LGSASDWRG RYGRRRFFIW ALSLGILLSL FLIPRAGWLA GLLCPDPRPL 120
ELALLILGVG LDFPCGVCF TPLEALLSDL FRDPDHCRA YSVYAFMISL GGCLGYLLPA 180
IDWDTALAP YLGTQEBCLF GLLTLIFLTC VAATLLVAEE AALGPTPEAE GLSAPSLSPH 240
CCPCRARLAF RNLGALLPRL HQLCCMRPRT LRRLFVAELC SMMALMTFTL FYTDFVGEGL 300
YQGVRAEPG TEARRHYDEG VRMGSLGLFL QCAISLVFSL VMDRLVQRF TRAVYLASVA 360
AFPVAGATC LSHSVAVVTA SAALTGFTFS ALQILPYTSL SLVHREKQVF LFKYRGDTGG 420
ASSEDSLMTS FLPGFKPGAE FENGHVAGG SGLLEPPPAL CGASACTDVS RVVVGEPTGA 480
RVVPGRGICL DLAILDSAFI LSQVAPSLFM GSTVQLSQSV TAYMVSAAGL GLVATYFATQ 540
VVPKSLDLAK YSA

SEQ ID NO:205 PAJ3 DNA SEQUENCE

Nucleic Acid Accession #: AK002128
Coding sequence: 1-1593 (underlined sequences correspond to start and stop codons)

75 1 11 21 31 41 51
ATGTTTCCGC GGGGGCTGCT TGCGTGGATT TCCCGGGTGG TGGTTTGTCT GGTGCTCCTC 60
TGCTGTGCTA TCTCTGTCT GTACATGTTG GCTGCAACCC CAAAAGGTGA CGAGGAGCAG 120
CTGGCACTGC CAGGGGCCAA CAGCCCAACG GGAAGGAGG GGTACCAAGC GGTCTCTTCA 180
GAGTGGGAGG AGCAGCACCG CAACTACGTG AGCAGCCTGA AGCGGCAGAT CGCACAGCTC 240

5	AAGGAGGAGC	TGCAGGAGAG	GAGTGAGCAG	CTCAGGAATG	GGCAGTACCA	AGCCAGOGAT	300
	GCTGCTGGCC	TGGGTCTGGA	CAGGAGCCCC	CCAGAGAAAA	CCCAGGCCGA	CCTCCTGGCC	360
	TTCTCTGACT	CGCAGGTGGA	CAAGGCAGAG	GTGAATGCTG	GCGTCAAGCT	GGCCACAGAG	420
	TATGCAGCAG	TGCTTTTCGA	TAGCTTTACT	CTACAGAAGG	TGTACCAGCT	GGAGACTGGC	480
	CTTACCCGCC	ACCCCGAGGA	GAAGCCTGTG	AGGAAGGACA	AGCGGGATGA	GTGGTGGAA	540
	GCCATTGAAT	CAGCCTTGGA	GACCTGAAC	AATCTGACG	AGAACAGCCC	CAATCACCGT	600
	CCTTACACGG	CCTCTGATTT	CATAGAAGGG	ATCTACCGAA	CAGAAAGGGA	CAAAGGGACA	660
	TGTATGATGA	TACCTTTCAA	AGGGGACCAC	AAACACGAAT	TCAAACGGCT	CATCTTATTT	720
10	CGACCATTCG	GCOCCTCAT	GAAAGTGAAA	AATGAAAAGC	TCAACATGGC	CAACACGGTT	780
	ATCAATGTTA	TCGTGCTCT	AGCAAAAAGG	GTGGACAAGT	TCCGGCAGTT	CATGCAGAA	840
	TTCAGGGAGA	TGTGCATTGA	GCAGGATGGG	AGAGTCCATC	TCACTGTTGT	TACTTTTGGG	900
	AAAGAAGAAA	TAAATGAAT	CAAAGGAATA	CTTGAAAACA	CTTCCAAAGC	TGCCAACTTC	960
	AGGAACTTTA	CCTTCATCCA	GCTGAATGGA	GAATTTTCTC	GGGGAAAGGG	ACTTGATGTT	1020
	GGAGCCCGCT	TCTGGAAGGG	AAGCAACGTC	CTTCTCTTTT	TCTGTGATGT	GGACATCTAC	1080
15	TTACATCTCG	AATTCCTCAA	TACGTGTAGG	CTGAATACAC	AGCCAGGGAA	GAAGGTATTT	1140
	TATCCAGTTC	TTTTCAGTCA	GTACAATCCT	GGCATAATAT	ACGCCACCCA	TGATGCAGTC	1200
	CCTCCCTTGG	AACAGCAGCT	GCTCATAAAG	AAGGAAACTG	GATTTTGGAG	AGACTTTGGA	1260
	TTTGGGATGA	CGTGTCACTA	TCCGTACAGC	TTTCATCAATA	TAGGTGGGTT	TGATCTGGAC	1320
20	ATCAAAGGCT	GGGCGCGAGA	GGATGTGCAC	CTTTATCGCA	AGTATCTCCA	CAGCAACCTC	1380
	ATAGTGGTAC	GGAGCCCTGT	GCGAGGACTC	TTCCACCTCT	GGCATGAGAA	GCGCTGCATG	1440
	GACGAGCTGA	CCCCCGAGCA	GTACAAGATG	TGCATGCAGT	CCAAGGCCAT	GAACGAGGCA	1500
	TCCCACGGCC	AGCTGGGCTAT	GCTGGTGTTC	AGGCACGAGA	TAGAGGCTCA	CCTTCGCAAA	1560
	CAGAAACAGA	AGACAAGTAG	CAAAAAACA	TGA			

SEQ ID NO:206 PAJ3 Protein sequence:

Protein Accession #: NP_060841

30	1	11	21	31	41	51	
	MVRRLGLAMT	SRVVVLVLVL	CCAISVLYML	ACTPKGDEBQ	LALFRANSPT	GKEGYQAVLQ	60
	EWEQHRNV	SSLKRQIAQL	KEELQERSEQ	LRNGQYQASD	AAGLGLDRSP	PEKTQADLLA	120
	FLHSQVDKAE	VNAGVVKLATE	YAAVFPDSFT	LQKVYQLETO	LTRHPEEKPV	RDKRDELVE	180
35	AIESALETLN	NPAENSFNHR	PYTASDFIEG	TYRTERDKGT	LYELTFKGDH	KHEFKRLILF	240
	RPFGLIKVK	NEKLNMANFL	INVIVPLAKR	VDFRQFMQN	FREMCIEQDG	RVHLTVVYFG	300
	KEEINEVKGI	LENTSKAANF	RNFTFIQLNG	EFSRGLGLDV	GARPMKGSNV	LLFFCDVDIY	360
	PTSEFLMYCR	LNTQPGKKVF	YFVLFSQYNP	GIIVGHEDAV	PPLEQQLVIK	KETGFWRDFG	420
	FGMTCCQVRSD	FINTGGFDLD	LKGWGGEDVH	LYRKYLHSLN	IVVRTFVRGL	PHLWHEKRCM	480
40	DELTPQYKYM	CMQSKAMNEA	SHGQLGMLVF	RHEIAHLRK	QKQKTSKKKT		

SEQ ID NO:207 PAJ5 DNA SEQUENCE

Nucleic Acid Accession #: AF189723

Coding sequence: 1-2712 (underlined sequences correspond to start and stop codons)

45	1	11	21	31	41	51	
	ATGATTCCTG	TATTGACATC	AAAAAAAGCA	AGTGAATTAC	CAGTCAGTGA	AGTTGCAAGC	60
50	ATTCCTCCAG	CTGATCTTCA	GAATGGTCTA	AACAAATGTG	AAGTTAGTCA	TAGCGGAGCC	120
	TTTCATGGCT	GGAAATGAGT	TGATATTAGT	GAAGATGAGC	CAGTGTGGAA	GAAGTATATT	180
	TCTCAGTTTA	AAAATCCCTC	TATTATGCTG	CTTCTGGCTT	CTGCAGTCAT	CAGTGTTTTA	240
	ATGCATCAGT	TGATGATGCG	CGTCAGTATC	ACTGTGGCAA	TACTTTATCGT	TGTTACAGTT	300
55	GCCTTTGTTC	AGGAATATCG	TTTCAAAAAA	TCTCTTGAAG	AATTGAGTAA	ACTTGTGCCA	360
	CCAGAAATGCC	ATTGTGTGCG	TGAAGGAAAA	TTGGAGCATA	CAGTTGCCCG	AGACTTGGTT	420
	CCAGGTGATA	CAGTTTGCCT	TTCTGTGGGG	GATAGAGTTC	CTGCTGACTT	ACGCTTGTIT	480
	GAGGCTGTGG	ATCTTTCCAT	TGATGAGTCC	AGCTTGACAG	GTGAGACAAC	GCCTTGTTCCT	540
	AAGGTGACAG	CTCCTCAGCC	AGCTGCAACT	AATGGAGATC	TTGCATCGAG	AAGTAACATT	600
60	GCCTTTATGG	GAACACTGGT	CAGATGTGGC	AAAGCAAAAG	GTGTTGTCAAT	TGGAACAGGA	660
	GAAAATTCCTG	AATTTGGGGA	GGTTTATAAA	ATGATGCAAG	CAGAAGAGGC	ACCAAAAACC	720
	CCTCTGCAGA	AGAGCATGGA	CCTCTTAGGA	AAACAACCTT	CCTTTTACTC	CTTTGGTATA	780
	ATAGGAATCA	TCATGTTGGT	TGGCTGGTTA	CTGGGAAAAA	ATATCTCTGGA	AATGTTTACT	840
	ATTAGTGTAA	GTTTGGCTGT	AGCAGCAATT	CCTGAAGGTC	TCCCATTTGT	GTCACAGTGC	900
65	ACGCTAGCTC	TTGGTGTAT	GAGAATGGTG	AAGAAAAGGG	CCATTGTGAA	AAAGCTGCCT	960
	ATTGTTGAAA	CTCTGGGCTG	CTGTAATGTG	ATTGTTTCAG	ATAAAACTGG	AACACTGACG	1020
	AAGAAATGAAA	TGACTGTTAC	TCACATATTT	ACTTCAGATG	GTCTGCATGC	TGAGGTACT	1080
	GGAGTTGGCT	ATAATCAATT	TGGGGAAGTG	ATTGTTGATG	GTGATGTTGT	TCATGGATTC	1140
	TATAACCCAG	CTGTTAGCAG	AATTGTTGAG	GCGGGCTGTG	TGTGCAATGA	TGCTGTAAAT	1200
70	AGAAACAAAT	CTCTAATGCG	GAAGCCAACA	GAAGGGGCTT	TAATTGCTCT	TGCAATGAAG	1260
	ATGGGTCTTG	ATGGACTTGA	ACAAGACTAC	ATCAGAAAAG	CTGAATACCC	TTTGTAGCTCT	1320
	GAGCAAAAGT	GGATGGCTGT	TAAATGTGTA	CACCGAACAC	AGCAGGACAG	ACCAGAGATT	1380
	TGTTTTATGA	AAGGTGCTTA	CGAACAAGTA	ATTAAGTACT	GTACTACATA	CCAGAGCAAA	1440
	GGGACAGACT	TGACACTTAC	TCAGCAGCAG	AGAGATGTGT	ACCAACAAGA	GAAGGCACGC	1500
75	ATGGGCTCAG	CGGGACTCAG	AGTTCCTGCT	TTGGCTTCTG	GTCTCTGAAT	GGGACAGCTG	1560
	ACATTTCTTG	CCTCTGGTGG	AATCATTGAT	CCACCTAGAA	CTGGTGTGAA	AGAAGCTGTT	1620
	ACAACACTCA	TTCCCTCAGG	AGTATCAATA	AAAATGATTA	CTGGAGATTC	ACAGGAGACT	1680
	GCASTTGCAA	TCCGCACTCG	TCTGGGATTG	TATTTCCAAA	CTTCCCAAGC	AGTCTCAGGA	1740
	GAGAAATAG	ATGCAATGGA	TGTTTCAGCAG	CTTTTACAAA	TAGTACCAAA	GTTTGCAGTA	1800
80	TTTTACAGAG	CTAGCCCAAG	GCACAAGATG	AAAATTTATTA	AGTCGCTACA	GAAGAACGGT	1860
	TCAGTTGTAG	CCATGACAGG	AGATGGAGTA	AATGATGCAG	TTGCTCTGAA	GGCTGCAGAC	1920

5
10
15
ATTGGAATTG CGATGGGCCA GACTGGTACA GATGTTTGCA AAGAGGCAGC AGACATGATC 1980
CTAGTGGATG ATGATTTTCA AACCATAATG TCTGCAATCG AAGAGGGTAA AGGGATTAT 2040
AATAACATTA AAAATTTTCT TAGATTCCAG CTGAGCACGA GTATAGCAGC ATTAACCTTTA 2100
ATCTCATGG CTACATTAAT GAACCTTTCCT AATCCTCTCA ATGCCATGCA GATTTTGTGG 2160
ATCAATATTA TTATGATGG ACCCCAGCT CAGAGCCTTG GAGTAGAACC AGTGGATAAA 2220
GATGTCATTC GTAAACCTCC TCGCAACTGG AAGACAGCA TTTTGACTAA AAACCTTGATA 2280
CTTAAATAC TTGTTTCATC AATAATCATT GTTTGTGGGA CTTTGTITGT CTCTGGCGT 2340
GAGCTACGAG ACAATGTGAT TACACCTCGA GACACAACAA TGACCTTCAC ATGCTTTGTG 2400
TTTTTTGACA TGTTCRAATG ACTAAGTTC AGATCCAGA CCAAGTCTGT GTTTGAGATT 2460
GGACTCTGCA GTAATAGAAT GTTTTGCTAT GCAGTTCCTG GATCCATCAT GGGACAATTA 2520
CTAGTTATTT ACTTTCCTCC GCTTCAGAAG GTTTTCAGA CTGAGAGCCT AAGCATACTG 2580
GATCTGTGT TTCTTTTGGG TCTCACCTCA TCAGTGTGCA TAGTGGCAGA AATTATAAAG 2640
AAGTTGAAA GGAGCAGGGA AAAGATCCAG AAGCATGTTA GTTCGACATC ATCATCTTTT 2700
CTTGAAGTAT GA

SEQ ID NO:208 PAJ5 Protein sequence:

Protein Accession #: AAF27813

20
25
30
35
1
11
21
31
41
51
HIFVLTSSKA SELPVSEVAS ILQADLQNL NKCEVSHRA FHGMNEFDIS EDEPLWKKYI 60
SQPKNPLIML LLASAVISVL MEQPDDAVSI TVAILIVVTV AFVQEYRSEK SLEELSKLVP 120
PECHCVREBK LEHLARDLV PGDTVCLSVG DRVPADLRFP EAVDLSDIES SLTGETTPCS 180
KVTAPOPAAT NGDLASRSNI AFMGTIVRCG KAGGVVIGTG ENSEFGEVFK MMQAEAEFKT 240
PLQKSHDLLG KQLSFYSPGI IGIIILVGLW LGKDLLEHPT ISVSLAVAAI PEOLEIVVTV 300
TLALGVHRMV KRAIVKKLP IVETLGCENV ICSDKTGTLT KNEHTVTHIF TSDGLHAEVT 360
GVGYNQGEV IVDGDVHGF YNPAVERIVE AGCVNDAVI RNTLMGKPT EGALIALAMK 420
MGLDLQDDY IRKAEYFPSS BQKWEAVKCV HRTQODRPEI CFMKGAYEQV IKYCTTYQSK 480
GOTLVLTOOQ RDVVQOEKAR MGSAGLRVLA LASGPGLGOL TFLGLVGLID PRTGVKEAV 540
TTLIASGVSI KRIITGDSQET AVAIASRLGL YSKTSQSVSC ERIDAMDVQQ LSQIVPKVAV 600
FYRASPRHQM KIKSLQKNG SVVAMTGDGV NDAVALKAAD IGVAHQGTGT DVCKEADMI 660
LVDDDFQTIM SAIEBEGKIY NNKNFVRFO LSTSLAALT ISLATLAMPF NPLNAMQILW 720
INILMDGPPA QSLGVEPVDK DVIRKPPRNW KDSILTKNLI LKILVSSIII VCGTLFVFWR 780
ELRNRVITPR DTTMTFCFV PFDMEALSS RSQTKSVFEI GLCSNRMFCY AVLGSIMQOL 840
LVITYPPLOK VFQTESLSIL DLLFLGLTS SVCIVAEIK KVERSREKIQ KRVSSSTSSSP 900
LEV

SEQ ID NO:209 PAV4 VARIANT 1 DNA SEQUENCE

Nucleic Acid Accession #: N82098

Coding sequence: 1-1284 (underlined sequences correspond to start and stop codons)

45
50
55
60
65
1
11
21
31
41
51
ATGGGCTACC AGAGGCAGGA GCCTGTCATC CGGCCGCGAGA GAGGATTGCC TTATTCAATG 60
AAGCAAGCTG GGTTCCTTT GGAATATATG CTTTATATCT GGGTTTCATA TGTATACAGC 120
TTTCCCTTG TTTTATGAT AAAAGGAGGG GCCCTCTCTG GAACAGATAC CTACCACTCT 180
TTGGTCAATA AACTTTTCGG CTTTCCAGGG TATCTGCTCC TCTCTGTCTC TCAGTTTGTG 240
TATCTTTTFA TAGCAATGAT AAGTTACAAT ATAATAGCTG GAGATACTTT GAGCAAGTT 300
TTTCAAGAA TCCAGGAGT TGATCCTGAA AACGTGTTTA TTGGTCGCCA CTTTATTATT 360
GGACTTTCCA CAGTTACCTT TACTCTGCTT TTATCTTGT ACCGAAATAT AGCAAAAGCTT 420
GGAAAGGTCT CCTCATCTC TACAGGTTTA ACAACTCTGA TTCTTGAAT TGTAAATGCCA 480
AGGGCAATTT CACTGGGTCC ACACATACCA AAAACAGAA AGGCTTGGGT ATTGCAAAAG 540
CCCAATGCCA TTCAAGCGGT CGGGGTATG TCTTTTGCT TTATTGSCA CCATAACTCC 600
TTCTTAGTTT ACAGTTCTCT AGAAGAACC ACAGTAGCTA AGTGGTCCCG CTTTATCCAT 660
ATGTCCATCG TGATTTCTGT ATTATCTGT ATATTCTTG CTACATGTGG ATACTTGACA 720
TTTACTGGCT TCACCCAAGG GGACTTATTT GAAAATTACT GCAGAAATGA TGACCTGGTA 780
ACATTGGGAA GATTTTGTTA TGGTGTCACT GTCAATTTGA CATACCTAT GGAATGCTTT 840
GTGACAAGAG AGGTAAATGC CAATGTGTTT TTTGGTGGGA ATCTTTCATC GGTTTTCCAC 900
ATTGTTGTAA CAGTATGTT CATCACTGTA GCCACGCTTG TGTCATTGCT GATTGATTGC 960
CTCGGATAG TTCTAGAACT CAATGGTGTG CTCTGTGCAA CTCCCTCAT TTTTATCAT 1020
CCATCAGCCT GTTATCTGAA ACTGTCTGAA GAACCAAGGA CACACTCCGA TAAGATTATG 1080
TCTGTGTCA TGTCTCCAT TGGTGTCTGT GTGATGGTTT TTGGATTGCT CATGGCTATT 1140
ACAAATACTC AAGACTGCAC CCATGGGCAG GAAATGTCT ACTGCTTTC TGACAATTTT 1200
TCTCTACAA ATACCTCAGA GTCTCATGTT CAGCAGACAA CACAACCTTC TACTTTAAAT 1260
ATTAGTATCT TTCAACTCGA GTA

SEQ ID NO:210 PAV4 Variant 1 Protein sequence:

Protein Accession #: none found

75
80
1
11
21
31
41
51
MGYQROEPIV PPOGRFLPYM KOAGFPLGIL LLFWVSVYTD PSLVLLIKGG ALSGTDYQOS 60
LVNKTGPPFG YLLSVLQPL YPFIAMISYN ILAGDTLSKV PQRIPGVDP NVPICRHPII 120
GLSTVTFELP LSLVKNLAKL GKVSLSITGL TTLILGIVMA RAISLGPHIP KTEDAWVFAK 180
PNAIQAVGVN SFAPICRHNS PLVYSSLEEP TVAKWSRLIH MSIVLSVFC IFFATCGVLT 240
FTGFTQGDLP ENYCRNDLV TFGRCYGVV VILTYMEXF VTREVIANVF FGGNLSVVFH 300
IVTVVMYDIL LGIVLELNGV LCATFLIFII PSACYLKLSE EPRTHSDKIM 360
SCVRLPIGAV VHVPGFVMAI THTQDCTHQG EMFYCFDINF SLTHTSBSHV QTTQLSTLIN 420

ISIPQLE

5 Nucleic Acid Accession #: N62096
Coding sequence: 1-1203 (underlined sequences correspond to start and stop codons)

SEQ ID NO:211 PAV4 VARIANT 2 DNA SEQUENCE

10 1 11 21 31 41 51
ATGGGCTACC AGAGGCAGGA GCCTGTCTATC CCGCCGCGAGT TTTCCCTTGT TTTATTGATA 60
AAAGGAGGGG CCCTCTCTGG AACAGATACC TACCAGTCTT TGGTCAATAA AACTTTCCGC 120
TTTCCAGGGT ATCTGCTCCT CTCTGTCTCT CAGTTTCTGT ATCCTTTTAT AGCAATGATA 180
AGTTACAATA TAATAGCTGG AGATACTTTG AGCAAAAGTTT TTCAAAGAT CCCAGGAGTT 240
15 GATCCTGAAA ACCTGTATTAT TGGTCGCCAC TTCAATTATTG GACTTTCCAC AGTTACCTTT 300
ACTCTGCCTT TATCCTTGTA CCGAAATATA GCAAAGCTTG GAAAGTCTCT CCTCATCTCT 360
ACAGGTTTAA CAACCTCTGAT TCTTGGAAAT GTAATGGCAA GGGCAATTTC ACTGGGTCCA 420
CACATACCAA AAACAGAAGA CGCTTGGGTA TTTGCAAAAG CCAATGCCAT TCAAGCGGTC 480
GGGGTTATGT CTTTTGCAAT TATTTGCCAC CATAACTCCT TCTTAGTTTA CAGTTCTCTA 540
20 GAAGAACCCA CAGTAGCTAA GTGGTCCGCG CTATATCCATA TGTCCATGCT GATTCTCTGA 600
TTTATCTGTA TATTTCTTGC TACATGTGGA TACTTGCAT TTAAGTGGCT CACCCAGGGG 660
GACTTATTAG AAAATTACTG CAGAAATGAT GACCTGGTAA CATTTGGAAG ATTTGTTTAT 720
GGTGTCACTG TCAATTTGAC ATACCCATG GAATGCTTTG TGACAAGAGA GGTAAATTGCC 780
25 AATGTGTTTT TTGGTGGGAA TCITTTCTATG GTTTTCCACA TTGTTGTAAC AGTGATGGTC 840
ATCAGTGTAG CCACGCTTGT GTCAATGCTG ATTGATTGCC TCGGGATAGT TCTAGAAGTC 900
AATGTGTGTC TCTGTGCAAC TCCCTCTATT TTTATCAATC CATCAGCCTG TTATCTGAAA 960
CTGTCTGAAG AACCAAGGAC ACACCTCCGAT AAGATTATGT CTGTGTCTAT GCTTCCCAT 1020
GGTGTGTGTC TGTATGTTT TGGATTCGTC ATGGCTATTA CAAATACTCA AGACTGCACC 1080
30 CATGGGCAGG AAATGTCTTA CTGCTTTCCT GACAATTTCT CTCTCACAAA TACCTCAGAG 1140
TCTCATGTTT AGCAGACAC ACAACTTTCT ACTTTAAATA TTAGTATCTT TCAACTCGAG 1200
TAA

SEQ ID NO:212 PAV4 Variant 2 Protein sequence:

35 Protein Accession #: none found

1 11 21 31 41 51
40 MGYRQEPVI PPQFSLVLLI KGGALSGETDT YQSLVNKTFG FPGYLLLSVL QFLYPFIAMI 60
SYNLIAGDTL SKVFRIPGV DPNVFIGRH FIIGLSVTVF TLPLSLYRNI AKLRVSLIS 120
TGLATLILGI VMARALSLG HIFKTEDAWV FAKPNALQAV GVMSFAPICH HNSFLVYSSL 180
EETVAKWNR LIEMISIVSV FICIFPATCG YLTFTGFTQG DLFENYCRND DLVTFGRFCY 240
45 GVTVILTYFM ECVTVREIVL NVFFGGNLSS VFHIVTVMV ITVATLVSLI IDCIGIVLEL 300
NGVLCAETPL FIIPSACYLK LSEEPRTSD KIMSCVMLPI GAVVMVFGPV MAITNTQDCT 360
HGQEMFYCFP DNFLSLTISE SHVQQTQLS TLNISIFQLE

SEQ ID NO:213 PAV4 VARIANT 3 DNA SEQUENCE

50 Nucleic Acid Accession #: N62096
Coding sequence: 1-1140 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
55 ATGGGCTACC AGAGGCAGGA GCCTGTCTATC CCGCCGCGAG TCAATAAAAC TTTCCGCTTT 60
CCAGGGTATC TGCTCCTCTC TGTCTCTCAG TTTTGTATC CTTTTATAGC AATGATAAGT 120
TACAAATATA TAGCTGGAGA TACTTTGAGC AAAGTTTTC AAAGAATCCC AGGAGTTGAT 180
CCTGAAACAG TGTTTATGCG TGCCCACTTC ATTATTGGAC TTTCCACAGT TACCTTTACT 240
CTGCCTTTAT CCTGTGACCG AAATATAGCA AAGCTTGGAA AGGTCTCCCT CATCTCTACA 300
60 GGTTTAACAA CTCTGATTTCT TGGAAATTGTA ATGGCAAGGG CAATTTCACT GGTGCCACAC 360
ATACCAAAAA CAGAAGACGC TTGGGTATTT GCAAAGCCCA ATGCCATCA AGCGGTCCGG 420
GTTATGCTCT TTGCAATTTAT TTGCCACCAT AACTCCTTCT TAGTTTACAG TTCTCTAGAA 480
GAACCCACAG TAGCTAAGTG GTCCCGCCTT ATCCATATGT CCATCGTAT TCTGTATTT 540
ATCTGTATAT TCTTTGCTAC ATGTGGATAC TTGACATTTA CTGGCTTCAC CCAAGGGGAC 600
65 TTATTTGAAA ATTACTGCAG AAATGATGAC CTGGTAACAT TTGGAAGATT TTGTTATGGT 660
GTCACGTGCA TTTTGACATA CCTATGGAA TGCTTTGTGA CAAGAGAGGT AATTGCCAAT 720
GTGTTTTTTG GTGGGAATCT TTCAATCGGT TTCCACATTC TTGTAACAGT GATGGTCACT 780
ACTGTAGCCA CGCTTGTGTC ATTTGCTGATT GATTGCCCTG GGATAGTCT AGAACTCAAT 840
GGTGTGCTCT GTGCAACTCC CTCAATTTT ATCAATCCAT CAGCCTGTTA TCTGAAACCTG 900
70 TCTGAAGAAC CAAGGACACA CTCCGATAAG ATTATGTCTT GTGTCTATCT TCCCATTTGG 960
GCTGTGGTGA TGGTTTTTGG ATTCGTCATG GCTATTACAA ATACTCAAGA CTGACCCCAT 1020
GGGCAGGAAA TGTCTCTACT CTTTCTCTGAC AATTTCTCTC TCACAAATAC CTGAGAGTCT 1080
CATGTTCTAG AGACACACA ACTTCTACT TTAATATTA GTATCTTTCA ACTCGAGTAA

SEQ ID NO:214 PAV4 Variant 3 Protein sequence:

75 Protein Accession #: none found

80 1 11 21 31 41 51

MGYQRQEFVI PPQVNRTPGP PGYLLLSVLQ FLYPFIAMIS YNIIAGDTLS KVFQRIPOVD 60
 PENVFIGRHF IIGLSTVTFT LPLSLYRNIA KLKVSLSIST GLTTLILGIV MARAISLGPH 120
 IPKTBDAWVF AKENAIQAVG VMSFAFICHH NSPLVYSLSLE EPTVAKWSRL IHMSIVISVF 180
 ICIFPATCGY LTPTGTQGD LPENYCRNDD LVTPGRPCYO VTIVLTYPME CFVIREVIAN 240
 VFFGGNLSV FRIVVTMVI TVATLVSLLI DCLGIVLELN GVLCAITLIP IIPSACTYKL 300
 SEEPRTSDK IMSCVMLPIG AVVMVFGFVM AITNTQDCTH GQEMFYCFPD NPSLINTSES 360
 HVQQTTLQST LNISIFQLE

10

SEQ ID NO:215 PAV4 VARIANT 4 DNA SEQUENCE:

Nucleic Acid Accession #: N62098
 Coding sequence: 1-1389 (underlined sequences correspond to start and stop codons)

15

1 11 21 31 41 51
 ATGGGCTACC AGAGGCAGGA GCGTGTATC CCGCCGCGA GAGATTAGA TGACAGAGAA 60
 ACCCTGTGTT CTGAACATGA GTATAAAGAG AAAACCTGTC AGTCTGCTGC TCTTTTAAAT 120
 GTGTCAACT CGATTATAG ATCTGGTATA ATAGGATTGC CTATTCAAT GAAGCAAGCT 180
 GGTTTCCTT TGGGAATATT GCTTTTATTC TGGGTTTCAT ATGTTACAGA CTTTCCCTT 240
 GTTTTATGCA TAAAGAGAG GGCCTCTCTCT GGAACAGATA CCTACCAGTC TTTGGTCAAT 300
 AAAACTTTG GCTTTCAGG GTATCTGCTC CTCTCTGTC TFCAGTTTMT GTATCCTTTT 360
 ATAGCAATGA TAAGTTACAA TATAATAGCT GGAGATACTT TGACAAAGT TTTTCAAAGA 420
 ATCCAGGAG TTGATCCTGA AAACGTGTTT ATTTGGTCGCC ACTTCATTAT TGGACTTTCC 480
 ACAGTTACCT TTACTCTGCC TTTATCCTTG TACCGAAATA TAGCAAAGCT TGGAAAGGTC 540
 TCCCTCATCT CTACAGGTTT AACAACTCTG ATTCTTGGAA TTGTAATGCC AAGGGCAAT 600
 TCACCTGGTC CACACATACC AAAAACAGAA GACGCTTGGG TATTGTCAAA GCCCAATGCC 660
 ATTCAAGGG TCGGGGTAT GTCTTTTGCA TTTATTTGCC ACCATAACTC CTTCCTAGTT 720
 TACAGTTCTC TAGAAGAAC CACAGTAGCT AAGTGGTCCC GCCTTATCCA TATGTCCATC 780
 GTGATTCTG TATTATCTG TATATCTTT GCTACATGTG GATACCTGAC ATTTACTGGC 840
 TTCAACCAAG GGGACTTAT TGAATAATAC TGCAGAAATG ATGACCTGGT AACATTGGA 900
 AGAATTTGTT ATGGTGTAC TGTCAATTTG ACATACCCTA TGGAAATGCT TGTGACAAGA 960
 GAGGTAATG CCAATGTGTT TTTTGGTGGG AATCTTTCAT CGGTTTTCCT CATTTGTTGA 1020
 ACAGTGATGG TCATCACTGT AGCCACGCTT GTGTCTATGC TGATTGATTG CCTCGGGATA 1080
 GTCTAGAAC TCAATGGTGT GCTCTGTGCA ACTCCCTCA TTTTATCAT TCCATCAGCC 1140
 TGTATCTGA AACTGTCTGA AGAACCAAGG ACACACTCCG ATAAGATTAT GTCTTGTGTC 1200
 ATGCTTCCA TTGGTGTCTG GGTGATGGTT TTTGGATTGG TCATGGCTAT TACAATACT 1260
 CAAGACTGCA CCCATGGGCA GGAATGTTT TACTGCTTTC CTGACAAATT CTCTCTCACA 1320
 AATACCTCAG AGTCTCATGT TCAGCAGACA ACACAACCTT CTACTTTAAA TATTAGTATC 1380
 TTTCAATGA

45

SEQ ID NO:216 PAV4 Variant 4 Protein sequence:
 Protein Accession #: none found

50

1 11 21 31 41 51
 MGYQRQEFVI PPQRDLDDRE TLVSEHEYKE KTCQSAALFN VVNSIIGSGI IGLFYSMKQA 60
 GFPLGILLLF WSVYTFDFSL VLLIRGGALS GTDTYQSLVN KTFGFPGYLL LSVLQFLYFF 120
 IAMSINILIA GDTLSKVFQR IPGVDPENVF IGRHFIIIGLS TVTFLPLSL YRNIAKLGKV 180
 SLISTGTTTL ILGIVMARAI SLGPHLPKTE DAKVFAKFA IQAVGVMSFA FICHENSFLV 240
 YSSLREPTVA KMSRLIHMSI VISVFICLFF ATCGYLTFTG FTQGDLFENY CRNDDLVTFG 300
 RFCYGVTVIL TYPMECFVTR EVIANVFFGG NLSSVFHIV TVMVTATL VSLIDCLGI 360
 VLELNGVLC TPLIFTIPSA CYLKLSEPR THSKIMSCV MLPIGAVVMV PGFVMAITNT 420
 QDCTHQGEMF YCFPDMFSLT NTSSEHVQQT TQLSTIANISI FQ

60

SEQ ID NO:217 PAV9 DNA SEQUENCE

Nucleic Acid Accession #: NM_017638
 Coding sequence: 1-3501 (underlined sequences correspond to start and stop codons)

65

1 11 21 31 41 51
 ATGGAGGATG CCTTCGGGGC AGCCGTGGTG ACCGTGTGGG ACAGCGATGC ACACACCAAG 60
 GAGAAGCCCA CCGATGCCTA CGGAGAGCTG GACTTCACGG GGGCCGGCCG CAAGCACAGC 120
 AATTTCCTCC GGCTCTCTGA CCGAACGGAT CCAGCTGCAG TTTATAGTCT GGTTCACAGC 180
 ACATGGGGCT TCCGTGCCCC GAACCTGGTG GTGTCACTGC TGGGGGGATC GGGGGGCCCC 240
 GTCTTCCAGA CTTGCTGACA GGACCTGCTG CGTCTGTGGC TGGTGGGGGC TGCCAGAGC 300
 ACAGAGCTGC GGAATGTAC TGGGGGTCTG CACACGGGCA TGGCCGGGCA TGTGTGTGTG 360
 GCTGTACGGG ACCATCAGAT GGCCAGCACT GGGGGACCCA AGGTGGTGGC CATGGGTGTG 420
 GCGCCCTGGG GTGTGGTCCG GAATAGAGAC ACCCTCATCA ACCCAAGGG CTGCTTCCCT 480
 GCGAGGTACC GGTGGCCGGG TGACCCGGAG GACGGGGTCC AGTTTCCCTT GGACTACAA 540
 TACTCGGCTC TCTTCTGCTT GGACGACGGC ACACAAGGCT GCTTGGGGGG CGAGAACCCG 600
 TTCCGCTTGC GCTCTGAGTC CTACATCTCA CAGCAGAAAG CGGGCTGGG AGGACTGGA 660
 ATTGACATCC CTGTCTGCTT CCTCTGATT GATGCTGATG AGAAGATGTT GACCGGAATA 720
 GAGAACGCCA CCCAGGCTCA GCTCCATGT CTCTCTGTGG CTGGCTCAGG GGGAGCTGG 780
 GACTGCTTGG CCGAGACCTT GGAAGACACT CTGGCCCCAG GAGTGGGGGG AGCCAGGCAA 840
 GGCGAAGCCC GAGATCGAAT CAGGCGTTTC TTTCCCAAG GGGACCTTGA GGTCTTCGAG 900
 GCCCAGGTGG AGAGGATTAT GACCCGGAAG GAGCTCTTGA CAGTCTATT TCTGAGGAT 960

5	GGGTCTGAGG AATTCGAGAC CATAGTTTTC AAGGCCCTTG TGAAGGCTTG TGGGAGCTCG 1020
	GAGGCTTCAG CCTACCTGGA TGAGCTGCGT FTGGCTGTGG CTGGAACCG COTGGACATT 1080
	GCCGAGAGTG AACTCTTTTCG GGGGGACATC CAATGGCGGT OCTTCCATCT CGAAGCTTCC 1140
	CTCATGGAGC CCTGCTGAA TGACCGGCTT GAGTTCTGTC GCTTGTCTAT TCCACAGGCG 1200
	CTCAGCTGG GCCACTTCTT GACCCCGATG CGCCTGGCCC AACTCTACAG CGGGGGCGCC 1260
	TCCACTTCGC TCATCCGCAA CCTTTTGGAC CAGGCGTCCC ACAGCGCAGS CACCAAAGCC 1320
	CCAGCCCTAA AAGGGGGAGC TGCAGGAGCT CGGCCCTCTG ACGTGGGGCA TGTGCTGAGG 1380
	ATGCTGCTGG GGAAGATGTG CGCGCCGAGG TACCCCTCCG GGGCGGCTG GGACCTTCAC 1440
10	CCAGGCCAGG GCTTCGGGGA GAGCATGTAT CTGCTCTCGG ACAAGGCCAC CTCGCCGCTC 1500
	TCGCTGGATG CTGGCTCGG GCAGGCCGCC TGGAGCGAOC TGCTTCTTTG GGCAGTGTG 1560
	CTGAACAGG CACAGATGGC CATGTACTTC TGGGAGATGG GTTCCATGTC AGTTTCTCTCA 1620
	GCTCTTGGGG CCTGTTTGTCT GCTCCGGGTG ATGGCAAGCC TGGAGCTTGA CGCTGAGGAG 1680
	GCAGCCAGGA GGAAGAACCT GGCCTTCAAG TTTGAGGGGA TGGCGGTGA CCTCTTTGCG 1740
15	GAGTGTATC GCAGCAGTGA GGTGAGGGCT GCCCGCTCC TCTTCCGCTG CTCGCCGCTC 1800
	TGGGGCTGAC TGAGCTGCTT CCAGCTGGCC ATGCAAGCTG ACGCCGCTGC CTCTCTTTGCG 1860
	CAGGATGGGG TACAGTCTCT GCTGACACAG AAGTGGTGGG GAGATATGGC CAGCACTACA 1920
	CCCATCTGGG CCTCTGTTCT CGCCTTCTTT TGCCTTCCAC TCATCTACAC CGGCTTCATC 1980
	ACCTTCAGGA AATACAGAAG GAGGCCACCA CGGGAGGAGC TAGAGTTTGA CATGGATAGT 2040
20	GTCAATTAATG GGAAGGGGCG TGTCCGGGAG CGGAGCCAGS CCGAGAAGAC GCGCTGGGG 2100
	GTCCCGCGCG AGTCCGGGCG TCCGGGTTGC TCGGGGGGCG CTTGCGGGGG GCGCCGCTGC 2160
	CTACGCGCGT GGTTCACCTT CTGGGGCGCG CCGGTGACCA TCTTCATGGG CAACGTGCTC 2220
	AGCTACCTGC TGTCTCTGCT GCTTTTCTCG CGGGTGTCTG TCGTGGATTG CCAGCCGGCG 2280
	CGCCCGGCT CCTCTGAGCT GCTGCTCTAT TTCTGGGCTT TCACGCTGCT GTGCGAGGAA 2340
25	CTCCGCGAGG GCTTGAAGCG AGCGGGGGCG AGCCTCGCCA GCGGGGGGCG CGGCGCTGGC 2400
	CATGCGCTAC TGAGCCAGCG CTGCGGCTC TACCTGCGCG ACAGCTGGAA CCACTGCGAC 2460
	CTAGTGGCTC TCACCTGCTT CCTCTGSGCG GTGGGCTGCC GGTGACCCC GGGTTTGTAC 2520
	CACCTGGGCG GCACGTGCTT CTGCTGCGAC TTCATGCTTT TCACGCTGCG GCTGCTTCAC 2580
	ATCTTCAGG GCAACAAACA GCTGGGGGCG AAGATCGTCA TCGTGAAGCA GATGATGAAG 2640
30	GACGTGTCTT TCTTCTCTTT CTCTCTCGCG GTGTGGCTGG TAGCCTATGG CGTGGCCACG 2700
	GAGGCGCTCC TGAGCCAGCG GACAGTGAAC TTCCCAAGTA TCCGTGCGCG CGTCTTCTAC 2760
	CGTCCCTACC TGCAGATCTT CGGCGAGATT CCCAGGAGS ACATGACGCT GGCCTTCATG 2820
	GAGCAGACGA ACTGCTCTGC GGAGCCCGCG TTCGGGCAC ACCCTCCTGG GGCACAGGCG 2880
	GGCACTCAGG TCTCCAGTGA TGCCAACGCG CTGCTGCTGC TGCTCTCTGT CATCTTCTGT 2940
35	CTCGTGGGCA ACATCTCTGT GGTCAACTTG CTCATTGCCA TGTTCAGTTA CACATTGGCG 3000
	AAAGTACAGG GCACACAGCG TCTCTACTGG AAGGCGCAGC GTTACCGGCT CATCCGGGAA 3060
	TTCCACTCTC GGCCTCGGCT GGCCTCGGCG TTTATCGTCA TCTCCACTT GCGCCTCTCT 3120
	CTCAGGCAAT TGTGCGAGCG ACCCCGAGCG CCCAGCGCT CCTCCCGGCG CCTCGAGCAT 3180
	TTCCGGGTTT ACCCTTCTTA GGAAGCGAG CGGAAGCTGC TACGTGGGA ATCGGTGCTAT 3240
40	AAGGAGAAGT TCTGCTGGCG ACGCGCTAGG GACAAGCGGG AGAGCGACTC CGAGCGCTCT 3300
	AAGCGCAGCT CCCAGAAAGT GGAATTGGCA CTGAACAGC TGGACACAT CCGCGAGTAC 3360
	GAACACGCCG TGAAGTGTCT GGAGCGGGAG GTCCAGCAGT GTAGCCCGCT CTTGGGGTGG 3420
	GTGGCGAGG CCTGAGCCG CTCTGCTTTC CTGCCCCGCG GTGGGCGGCG ACCCCCTGAC 3480
	CTGCTGGGT CCAAAGACTG A

45

SEQ ID NO:218 PAV8 Protein sequence:

Protein Accession #: none found

50	1 11 21 31 41 51	HEAPGAHV VVWDSDAHTT EKPTDAYGEL DFTGAGRKHS HPLRLSDRTD PAAVYSIVTR 60
		TWGFAPNLV VSVLGGSGGP VLQTLWQDLL RRLGLVRAAGS TGAMIVTGGI HTGIGRHVGV 120
		AVRDEQMAST GGTKVVAHGV APWGVVRNRD TLINPKGSFP ARYRWGDFE DGVQFPLDYN 180
55		YSAPFLVDGD THGCLGGENR FRLRLSEYIS QKRTGVGGTG IDIFVLLLLI DGDKRLTRI 240
		ENATQAQLFC LLVAGSGGAA DCLAETLEDT LAPSGSGARQ GEARDRIIRF FPRGDLVLQ 300
		AQVERIDTRK ELTVYSSED GSEEPETIVL KALVKACGSS EASAYLDEL R LAVANRVDI 360
		AQSELFRGDI QWRSPHLEAS LMDALLNDRF EFRVLLISHG LSLGHFLTFM RLAQLYSAAP 420
		SNSLIRNLID QASHSAGTKA PALKGGAAEL RPPDVGVHLR MLLGKMCAPR YPSGGAWDPH 480
60		PQGFGESMY LLSDKATSEF SLDAGLGQAF WSDLLWALL LNRAQMAHYF WEMGSNAVSS 540
		ALGACLLLV MARLEPDAEE AARRKDLAFK PEGMGVDLFG ECVRSSEVRA ARLLLRRCPL 600
		WGDATCLQLA MQADARAPFA QDGVQSLITQ KWWGDMASTT PIWALVLAF CPPLIYTRLI 660
		TFRKSEETPT REELEFDMDS VINGEGPVGT ADPAKRTPLG VPRQSGRPGC CGRCGGRRC 720
		LRRWFEPWGA FVTIPMGNVV SYLLFLLIFS RVLLVDFQPA PPGSLELLLY FWAPTLCEE 780
65		LRQLSGGGG SLASGSPGFG HASLSQRLRL YLADSWNQCD LVALTCLFLG VGCRLTPGLY 840
		HLGRITVLCID FMVFTVRLH IFTVKNQLGP KIVIVSRMK DVFFFLFPLG VWLVAYGVAT 900
		EGLLRFRDSD FPSILRRVEY RPYLQIFGQI PQEDMDVALM EHSNCSSEPG FWAHPFGAQA 960
		GTCSVQYANW LVVLLVLIPL LVANILLVNL LIAMPSYTFG KVGNSDLYW KAQRVRLIRE 1020
		FTSRPALAPP FTVISHLRL LRQLCRRPRS PQPSPALEH FRVYLSKEAE RKLLTWESVH 1080
70		KENFLARAR DKRESDBRL KRTSQKVDLA LKQLGHIREY BQRLKVLERE VQCCSRVLGW 1140
		VAALERSAL LPPGGPPFPD LPSKSD

SEQ ID NO:219 PBF1 DNA SEQUENCE

Nucleic Acid Accession #: AA054237

Coding sequence: 1-894 (underlined sequences correspond to start and stop codons)

75

80	1 11 21 31 41 51	ATGGAGCCGC GGGCGCTCGT CACGGCGCTC AGCCTCGGCC TCAGGCTGTG CTCCTTGGGG 60
		CTGCTCGTCA CGGCATCTT CACCGACAC TGGTACGAGA CCGACCCCGC GCGCCACAAG 120
		GAGAGCTGCG AGCGCAGCGG CGCGGGCGCC GACCCCCCGC ACCAGAAGAA CCGCCTGATG 180

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CCGCTGTGCG ACCTGCGCGT GCGGGACTCG CCCCCGCTGG GCGCGCGGCT GCTCCCGGGC 240
GGCCCGGGGG GCGCCGAGCC CGAGTCTGCG CGCTGCTGCC TGGGGCTCGG CGGCTGGAC 300
GCGGAGTGGG GCGCGGCCCT CTTCGCCACC TACTCGGGCC TCTGGAGGAA GTGCTACTTC 360
CTGGGCATCG ACCGGGACAT CGACACCCCT ATCTGAAAG GTATTGCGCA GCGATGCAAG 420
GCCATCAAGT ACCACTTTTC TCAGCCCATC CGCTTGGGAA ACATTCTCTT TAATTTAACC 480
AAGACCATAC AGCAAGATGA GTGGCACCTG CTTCAATTAA GAAGAATCAC TGCTGGCTTC 540
CTCGGCATGG CCGTAGCCGT CCTCTCTGCG GGCTGCAITG TGGCCACAGT CAGTTTCTTC 600
TGGGAGGAGA GCTTGAACCA GCACGTGGCT GGACTCCNGT TCCTCATGAC AGGGATATTT 660
TGCAACATTT CCTCTGTAT TTATGCCGCC AGTATCTCGT ATGATTGAA CCGGCTCCCA 720
AAGCTAATTT ATAGCCTGCC TGCTGATGTG GAACATGGIT ACAGCTGGTC CATCTTTTGC 780
GCCTGCTGCA GTTTAGGCTT TATTGTGGCA GCTGGAGGTC TCTGCATCGC TTATCCGTTT 840
ATTAGCCGGA CCAAGATTGC ACAGCTAAG TCTGGCAGAG ACTCCACGGT ATGA

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SEQ ID NO:220 PBF1 Protein sequence:

Protein Accession #: none found

1 11 21 31 41 51

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MEPRALVTAL SLGLSLCSLG LLVTAIFTDH WYETDPRRHK ESCERSRAGA DPPDQKNRLM 60
PLSHLPLRDS PPLGRRLFLG GPGRADPESW RSLGLGLGLD AECGRFLPAT YSGLWRKCYF 120
LGIDRDIIDL ILKRIAQRCT AIKYHFSQPI RLRLNIFNLIT KTIQDDEHL LHLRLITAGF 180
LGMVAVLLC GCTVATVSFF WEESLTQKVA GLLFLMTGTF CTISLCTYAA SISYDLNRLP 240
KLIYSLPADV EHGYSWSIFC AWCSLGFIVA AGGLCIAYFF ISRTKIAQLK SGRDSTV

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SEQ ID NO:221 PC4 DNA SEQUENCE

Nucleic Acid Accession #: NM_016570
Coding sequence: 1-1134 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51

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ATGAGGCGAC TGAATCGGAA AAAAACTTTA AGTTTGGTAA AAGAGTTGGA TGCCTTTCOG 60
AAGGTTCCCTG AGAGCTATGT AGAGACTTCA GCCAGTGGAG GTACAGTTTC TCTAATAGCA 120
TTTACAACTA TGCGTTTATT AACCAATATG GAATCTCTAG TATATCAAGA TACATGGATG 180
AAGTATGAAT ACGAAGTAGA CAAGGATTTT TCTAGCAAAAT TAAGAATTAA TATAGATATT 240
ACTGTTGCCA TGRAGTGTC AATATGTTGGA GCGGATGTAT TGGATTAGC AGAAACAATG 300
GTTGCATCTG CAGATGGTTT AGTTTATGAA CCAACAGTAT TTGATCTTTC ACCACAGCAG 360
AAAGAGTGGC AGAGGATGCT GCAGCTGAAT CAGAGTAGGC TACAAGAAGA GCATTCACTT 420
CAAGATGTGA TATTTAAAG TGCTTTTAAA AGTACATCAA CAGCTCTTCC ACCAAGAGAA 480
GATGATTCAT CACAGCTTCC AAATGCATGC AGAATTCATG GCCATCTATA TGTCATATAA 540
GTAGCAGGGA ATTTTACAT AACAAGTGGC AAGGCAATTC CACATCTCTG TGCTCATGCA 600
CATTTGGCAG CACTTGTCAA CCATGAATCT TACAATTTT CTATAGAAAT AGATCATTTG 660
TCTTTTGGAG AGCTTGTTC AGCAATTAAT AATCCTTTAG ATGGAAGTGA AAAAATTGCT 720
ATAGATCACA ACCAGATGTT CCATATTTT ATTACAGTTG TGCCAACAAA ACTACATACA 780
TATAAATAT CAGCAGACAC CCATCAGTTT TCTGTGACAG AAAGGGAACG TATCATTAA 840
CATGCTGCAG CAGAGCATGG AGTCTCTGGG ATATTATGAA AATATGATCT CAGTCTCTTT 900
ATGGTGACAG TCACTGAGGA GCACATGCCA TTCTGGCAGT TTTTGTGAAG ACTCTGTGGT 960
ATTGTTGGAG GATCTTTTTC AACAACAGGC ATGTTACATG GAATTGGAAA ATTATAGTT 1020
GAAATTAATT GCTGTGTTT CAGACTTGA TCCTATAAAC CTGTCAATTC TGTTCCTTTT 1080
GAGGATGGCC ACACAGACAA CCACCTACCT CTTTTAGAAA ATAATACACA TTGA

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SEQ ID NO:222 PC4 Protein sequence:

Protein Accession #: NP_057654

1 11 21 31 41 51

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MRLNRKRTL SLVKELDAFP KVPESTVETS ASGGTVSLIA PTIMALLTIM EFSVYQDTNM 60
KYEYEVKDFK SSKLRINIDI TVAMKQYVG ADVLDLAETM VASADGLVYE PTVFDLSPQQ 120
KEWQRMQLLI QSLRQEHSL QDVIPKSAFK STSTALPPRE DDSSQSFNAC RIHGHLYVNR 180
VAGNFHITVG KAIIPHPRGHA HLAALVNIES YNFSHRIDHL SPGELVPAII NPLDGTAKIA 240
IDENQMFQVF ITVVPKLET YKISADTHQF SVTERERIIN HAAGSHQVSG IPMKYDLSSL 300
MVTVTREHMF FWQFFVRLCG IVGGIFSTTG MLEGIGKPIV EIIICRFRLG SYKPVNSVFP 360
EDGHTDMHLP LLENNTN

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SEQ ID NO:223 PEZ3 DNA SEQUENCE

Nucleic Acid Accession #: NM_001935.1
Coding sequence: 76-2301 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51

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CGCGCGCTCT CCGCGCCCGG GTGACTTCTG CCTGCGCTCC TTCTCTGAAC GCTCACTTCC 60
GAGGAGACGC CGACGATGAA GACACCGCTG AAGATTCTTC TGGGACTGCT GGGTGTGCT 120
CGCTTGTGCA CCACTATCAC CGTGCCCGTG GTTCTGCTGA ACAAGGCAC AGATGATGCT 180
ACAGCTGACA GTCGCAAAAC TTCACTCTA ACTGATTACT TAAAAATAC TTATAGACTG 240
AAGTTATACT CCTTAAGATG GATTTCAGAT CATGAATATC TCTACAAACA AGAAAAATAT 300

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ATCTTGGTAT TCAATGCTGA ATATGGAAAC AGCTCAGTTT TCTTGGAGAA CAGTACATTT 360
GATGAGTTTG GACATTCTAT CAATGATTAT TCAATATCTC CTGATGGGCA GTTTATTCTC 420
TTAGAATACA ACTACCTGAA CCAATGGAGG CATTCCTACA CAGCTTCATA TGACATTTAT 480
GATTTAATAA AAGGCGAGCT GATTACAGAA GAGAGGATTC CAAACAACAC ACAGTGGGTC 540
ACATGGTCAC CAGTGGGTCA TAAATTTGCA TATGTTTGGT ACAATGACAT TTATGTTAAA 600
ATTGAACCAA ATTTACCAAG TTACAGAATC ACATGGACGG GGAAGAAGA TATAATATAT 660
AATGGAATAA CTGACTGGGT TTATGAAGAG GAAGTCTTCA GTGCTACTC TGCTCTGTGG 720
TGGTCTCCAA ACGGCACCTT TTTAGCATAT GCCCAATTTA ACGACACAGA AGTCCCACTT 780
ATTGAATPACT CCTTCTACTC TGATGAGTCA CTGCAGTACC CAAAGACTGT ACGGGTTCCT 840
TATCCAAAGG CAGGAGCTGT GAATCCAAC GTAAAGTTCT TTGTTGTAAA TACAGACTCT 900
CTCAGCTCAG TCACCAATGC AACTTCCATA CAAATCACTG CTCCTGCTTC TATGTTGATA 960
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CTCAGGAGGA TTCAGAACTA TTCGGTCATG GATATTTGTG ACTATGATGA ATCCAGTGA 1080
AGATGGAACCT GCTTAGTGGC ACGGCAACAC ATTGAAATGA GTACTACTGG CTGGGTGGA 1140
AGATTTAGGC CTTCAGAAAC TCAATTTTACC CTGTAGTGA ATAGCTTCTA CAAGATCATC 1200
AGCAATGAAG AAGGTACAG ACACATTTGC TATTTCCAAA TAGATAAAAA AGACTGCACA 1260
TTTATTACAA AAGGCACCTG GGAAGTCATC GGGATAGAAG CTCTAACCA TGATATCTA 1320
TACTACATTA GTAATGAATA TAAAGGAATC CCAGGAGGAA GGAATCTTTA TAAAAATCAA 1380
CTTATTGACT ATACAAAAGT GACATGCCCT AGTTGTGAGC TGAATCCGGA AAGGTGTGAG 1440
TATCATCTCT TGTCAATCAG TAAAGAGGCG AAGTATTATC AGCTGAGATG TTCCGGTCTC 1500
GGTCTGCCCC TCTATACTCT ACACAGCAGC GTGAATGATA AAGGGCTGAG AGTCTGGGAA 1560
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GACACTGTCT TCAGACTGAA CTGGGCCACT TACCTTGCAA GCACAGAAAA CATATAGTA 1800
GCTAGCTTTG ATGGCAGAGG AAGTGGTTAC CAGGAGGATA AGATCATGCA TGCAATCAAC 1860
AGAAGACTGG GAACATTTGA AGTTGAAGAT CAAATTTGAAG CAGCCAGACA ATTTTCAAAA 1920
ATGGGATTTG TGGACAACAA ACQAATTGCA ATTTGGGCTC GGTCAATATG AGGGTACGTA 1980
ACCTCAATGG TCGTGGGATC GGGAAAGTGGC GTGTTCAGAT GTGGAATAGC CGTGGCGCCT 2040
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CCAGAGACAA ACGTTCACCA TTACAGAAAT TCAACAGTCA TGAGCAGAGC TGAATAATTT 2160
AAACAAGTTG AGTACTCTCT TATTCATGGA ACAGCAGATG ATAACGTTCA CTTTCAGCAG 2220
TCAGTCTAGA TCTCCAAAGC CCGTGGTCGAT GTTGGAGTGG ATTTCCAGGC AATGTGGTAT 2280
ACTGATGAAG ACCATGGAAT AGCTAGCAGC ACAGCACACC AACATATATA TACCCACATG 2340
AGCCACTTCT TAAACAATG TTTCTCTTTA CCTTAGCACC TCAAAATACC ATGCCAATTA 2400
AAGCTTATTA AAATCAATTT TTGTTTTCAT TATCTCAAAA CTGCACTGTC AAGATGATGA 2460
TGATCTTTAA AATACAGCA CAAATCAAGA AACTTAAGGT TACCTTTGTT CCAAAATTTT 2520
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TTGAATATAT CGGTGGGTTT TTATTTGTTA AAATCATTTT TGCATCAGCT GCTGAAACAA 2640
CAAAATAGGA TTGTTTATAT GGAGGCTTTG CATAGATTCC CTGAGCAGGA TTTTAACTCT 2700
TTTCTAAGCT GACTGGTTCA AATGTTGTTT TCTTCTTTAA AGGGATGGCA AGATGTGGGC 2760
AGTGATGTCA CTAGGGCAGG GACAGGATAA GAGGGATTAG GGAGAGAAGA TAGCAGGGCA 2820
TGGCTGGGAA CCCAAGTCCA AGCATACCAA CACGAGCAGG CTACTGTGAG CTCGCCCTCG 2880
AGAAGAGCTG TTCACCCAGA GACTGGCACA GTTTTCTGAG AAAGACTATT CAAACAGTCT 2940
CAGGAATCTA AATATCGAAA GCACTGACTT CTAAGTAAAC CACAGCAGTT GAAAGACTCC 3000
AAAGAAATGT AAGGGAAACT CGCAGCAACG CAGCCCCAG GTGCCAGTTA TGGCTATAGG 3060
TGCTACAAAA ACACAGCAAG GGTGATGGGA AAGCATTTGA AATGTGCTTT TAAAAAATA 3120
TACTGATGTT OCTAGTGAAA GAGGCAAGCTT GAACTGAGA TGTGAACACA TCAGCTTGCC 3180
CTGTTAAAG ATGAAAAATAT TTGATACACA AATCTTAAC TGAAGAGTC CTTGCATCAA 3240
TTTTTCTTAT TTCAATTTCT TGAGTGTCTT AATTAAGAAG ATATTTTAAC TTCTTTGGAC 3300
TCATTTTAAA AAATGGAACA TAAATACAA TGTATGTAT TATTATTCOC ATTCACATA 3360
CTATGGAAAT TCTCCAGCTC ATTAATAAAA TGTGCTTCA TTTTTTC

SEQ ID NO:224 PEZ3 Protein sequence:

Protein Accession #: NP_001926.1

1 11 21 31 41 51
| | | | |
MRTFVKILLG LLGAAALVTI ITVPVLLANK GTDDATADSR KTYTLTDYLK NTRYRLKLYSL 60
RWISDHEYLY KQENNILVFN AEYGNSSVFL ENSTFDEPGH SINDYSISPD GQFILLEVNY 120
VKQMRHSYTA SYDIYDLNKR QLITEERIPN NTQWVWSPV GHKLAYVWNN DIYVKLEPNL 180
PSYRITWIGK EDIIYNGITD WYVEEVFSA YSALWNSPNG TFLAYAOFND TEVPLIEYSF 240
YSDSLQYFK TVRVFPYKAG AVNPTVKPFV VNIDSLSSVT NATSIQITAP ASMLIGDHYL 300
CDVWATQER ISLQNLRIQ NYSVMDICDY DESSGRWNCL VARQHEMST TGVVGRFRPS 360
EPHFTLDGNS FYKIIISNEEG YRHICYFQID KKDCTFITKG TWEVIGIEAL TSDYLYYISN 420
EYKHPGGRN LYKIQILIDYT KVTCLSCSLN PERCQYYSVS FSKKAYYQL RCGSGPLPLY 480
TLESSVNDKG LRVLEDNSAL DRMLQNVMP SKLDFIILN ETKFWMQML PPHFDKSKY 540
PLLLDVYAGP CSQKADTVFR LNWATYLAST ENIVASFQD RGSQVQDKI MHAINRRLGT 600
FEVEDQIEAA RQFSKMGFVD NKRIAIWGS YGGYVTSMLV GSGSGVFKCG IAVAPVSRWE 660
YDVSYYTERY MGLPTPEDNL DRYRNSTVMS RAENFKQVEY LLHGTADDN VHFQQAQIS 720
KALVDVGVDV QAMWYTDDEH GIASSTAHQH IYTHMSHPK QCFSLP

SEQ ID NO:225 PB2 DNA SEQUENCE

Nucleic Acid Accession #: none found
Coding sequence: 1-261 (underlined sequences correspond to start and stop codons)

80 1 11 21 31 41 51
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ATGGCTCTGG CGAAGGTGAG GGAGSCCAAAC GCAAAATGACA ATGOCATCAG AGTTGACAAC 60
 AGAAGTGTGA TTAAGTGGCG TGCTAACCAG TGTTCCCTGC ATGAGGCAGA AAGTGAATCC 120
 AGAAACCTCT AGGAGCTCTG GATGGGCTCG CTCCTCTTGA TGGGGGTCTT AGAAGCATGT 180
 GTGGAAATGA GGCTCTGTCT AGTCTGGTCC CTGAGAGATG ACAAGGAGCA GAGCCCCCAC 240
 CAGCCACAC TGGATGTCTA A

SEQ ID NO:226 PB2 Protein sequence:

Protein Accession #: none found

1 11 21 31 41 51
 MALAKVREPN ANDNAIRVDN RSVIKVRANQ CSLHEAESES RNPQELWMGL LLLMGVLEAC 60
 VEMRFLSVWS LRDDKEQSPH QPTLDV

SEQ ID NO:227 PB2 DNA SEQUENCE

Nucleic Acid Accession #: none found
 Coding sequence: 1-482 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 ATGCCAAATG CTGAGTTAGA AGCAAAGAGC CTTGGAAGCA GTAAATGTTT AAAAAGTGGT 60
 CTCATCTCTG CTGTATGTTG TGGATCAGCA AATATAGTCA GCCCTCTACT TGAGCAAAAT 120
 ATTGATGTAT CTCTCAAGA TCTGGACAGA CGGCCAGAGA GTATGCTGTT TCTAGTCATC 180
 ATCATGTGGA CCAGTTTGTG GGAAGACAAT CTTTCCATGG GCTGGGGGAA GCTAGAAGAT 240
 TTTATGCTTA TTGAAGAAGA AATGAAGAAG CACGGAAGTA CTCATGTGGG ATTCCCGAAG 300
 AACCTGACTA ATGGTGGCGG TGCTGGCAAT GGTGATGATG GATTAATTC TCACAGGAAG 360
 AGCAGAACAC CTGAAGGCCA GCAATTTCTT GACACTGAGA ATGAAGAGTA TCACAGGTTT 420
 GTCAAGATC AGATAGTTGT AGATATGCGG CGTTATTTCT GA

SEQ ID NO:228 PB2 Protein sequence:

Protein Accession #: none found

1 11 21 31 41 51
 MPNAELEAKS LGSSKCLKTA LILAVCCGSA NIVSPLLEQN IDVSSQDLDR RPESMLFLVI 60
 DMWTSFVEIN LSHGWKLEED FMALEKEEMK HGSTHVGFPE NLINGAAAGN GDDGLIPFRK 120
 SRTFESQQFP DTENEYHHRF VKDQIVVDMR RYF

SEQ ID NO:229 PE22 DNA SEQUENCE

Nucleic Acid Accession #: NM_014253
 Coding sequence: 65-8242 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 GACTGCTTGC ATTAAAGGAC TTCTCTCATCC TTTTTCATCAT GAAACTGAGC TTGCTTAATC 60
 AGAGATGGAG CAAACTGACT GCAAACCTTA CCAGCCTCTA CCAAAAGTCA AGCATGAAAT 120
 GGATCTAGCT TACACCAATT CTCTGTATGA GAGTGAAGAT GGAAGAAAC CAAGACACTC 180
 ATCAACTCTC AGGAGAGCCG TGACAGAGTA TAACCAAGGAG CTGAGGATGA ATTACAATAG 240
 CCAGAGTAGA AAGAGGAAG AAGTAGAATA ATCTACTCTA GAGATGGAAT TCTGTGAAC 300
 CTCTCACTCT CTGTGCTCTG GCTACCAAAAC AGACATGCAC AGCGTTTCTC GGCAATGGCTA 360
 CCAGCTAGAG ATGGGATCTG ATGTGGACAC AGAGACAGAA GGTGCTGGCT CACCTGACCA 420
 TGCACTAAGA ATGTGGATAA GGGGAATGAA ATCAGAGCAT AGTTCTCTGT TGTCCAGCCG 480
 GGCCAACTCT GCATTATCCT TGACTGACAC TGACCATGAA AGGAAGTCTG ATGGGGAAAA 540
 TGGTTTCAAA TTCTCTCTCT TTTGTTGTGA CATGGAGGCT CAAGCTGGGT CTACTCAAGA 600
 TGTGACAGAC AGCCCAACCA ACCAGTTTAC CTTCAGACCC CTCCCAACCG CACCTCCGCC 660
 TCTCATGACC TGCACTGTG CCAGGAAGCC ACCCCCTGCA GCGGACTCTC TTCAGAGGAG 720
 ATCAATGACT ACCCGCAGCC AGCCAGGCC AGCTGCTCCA GCTCCCCCAA CCAGCACGCA 780
 GGATTCAGTC CATCTGCATA ACAGCTGGGT CCTGAACAGC AACATACCAT TGGAGACCA 840
 GCATTCCCTG TTCAAAACATG GATCTGGTTC CTCTGCGATC TTCAGTGCAG CCAGTCAGAA 900
 CTACCCCTCT ACATCAATA CCGTGTACTC GCGCCCTCCC AGGCTCTCTC CTGGAAGCAC 960
 CTCTTCCCGA CTTGCTTTTA CCTTTAACA ACCTTACAGG TGCTGCAACT GGAAGTGCAC 1020
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 AGTGCAATTT TTGGGCTGCA CTTGGCAGTT GCAACCAATT GAAGGAGAGC TGTATGCAAA 1140
 TGGAGTATGC AAGGGAACCA GGGGGACCGA GTCCATGGAC ACTACTTACT CTCAATTTG 1200
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 TTTCCAGATT ACTATCCACC ATCCAAATATA TCTGAAGTTC AATATTCTTT TAGCCAAGGA 1380
 CTCTCTGCTG GGAATTTATG GCAGAAGAAA CATTCACACT ACACATACTC AGTTTGATT 1440
 TGTAAACTCA ATGATGGCA AACAGCTGGT CAAGCAGGAC TCCAGGGGCT CTGATGATAC 1500
 ACAGCACTCC CCTCGGAACC TGATCTTAC TTTGCTTCAG GAGACAGGTT TCATAGAGTA 1560
 TATGGATCAA GGCCTTGGT ATCTGGCGTT TTACAATGAT GGAAGAAAGA TGGAGCAAGT 1620
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 TGGAGAGTGT ATCTCTGGCC ATTGTCTATT TTTCCAGGA TTCTTGGAC CTGACTGTGC 1740
 TAGAGATTCC TGCCCTGTGC TGTGTGGTGG GAATGGAGAA TACGAGAAAG GACACTGTGT 1800
 CTGCCCCGCT GGTGGAAGG GGCCAGAGTG TGACGTTCCG GAAGACAAT GCATTGATCC 1860
 AACATGCTTT GGCCACGCA CCTGCATCAT GGGAGTCTGC ATCTGTGTGC CAGGATACAA 1920

	AGGAGAAATA	TGCGAGGAAG	AGGACTGCCT	AGACCCAAATG	TGTTCCAAAC	ATGGCATCTG	1980
	TGTAAAGGA	GAATGTCACT	GTCTACTGG	CTGGGGAGGA	GTAACTGTG	AAACACCACT	2040
	TCTGTATGT	CAAGAGCAGT	GCTCAGGACA	CGGAACCTTT	CTTCTGGACG	CTGGAGTATG	2100
5	CAGCTGTGAT	CCCAAGTGA	CAGGATCTGA	CTGCTCAACA	GAGCTGTGTA	CCATGGAGTG	2160
	TGCTAGCCAT	GGAGTCTGCT	CAAGAGGAAT	TTGCCAGTGT	GAAGAAGGCT	GGGTAGGACC	2220
	AACATGTGAG	GAAGCTCTCT	GTCTATCTCA	TTGTACTGAG	CATGGCCAAT	GCAAAGATGG	2280
	AAAATGTGAG	TGTAGCCCTG	GATGGGAGGG	CGACCACTGC	ACAAATGCTC	ACTACTTAGA	2340
	TGCTGTCCGA	GATGGCTGCC	CAGGGCTCTG	CTTTGGAAAT	GGACGATGTA	CCCTGGATCA	2400
10	AAATGGTTGG	CAGCTGTGAT	GTCAAGTGGG	TTGGAGTGGG	ACAGGCTGCA	ATGTTGTCTAT	2460
	GGAAATGCTT	TGTGGAGATA	ACTTGGACAA	TGATGGAGAT	GGTTTAAACG	ACTGTCTGGA	2520
	TCTGTACTGT	TGTCAACAAA	GCAACTGTTA	TATAAGTCTT	CTCTGCCAGG	GCTCACCAGA	2580
	TCTCTTGAC	CTCATTCAGC	AAAGCCAAAC	TCTCTTCTCT	CAGCACACTT	CAAGACTTTT	2640
	TTATGATCGA	ATCAAAATCC	TCATTGGCAA	GGACAGTACT	CATGTCTATC	CTCCTGAGGT	2700
15	GTCAATTGAC	AGCAGGCGTG	CCTGTGTGAT	TGGAGGCCAA	GTGGTGGCCA	TAGATGGAAC	2760
	TCTCTAGTG	GGAGTGAATG	TCAGTTTCTT	GCACCACTAG	GATATGGGT	TTACCATCAG	2820
	CCGCCAAGAT	GGAAAGCTTG	ACCTCGTGGC	CATCGGTGGC	ATCTCTGTCA	TCTTAATCTT	2880
	CGACCGATCC	CTTTCTCTGC	CTGAGAAGAG	AACACTCTGG	TTGCCTTGGA	ATCAGTTTAT	2940
	TGTGTAGAG	AAAGTCACCA	TGCAGAGAGT	TGTATCAGAC	CGGCCATCCT	GCGATATCTC	3000
20	CAACTTTTAT	AGCCCAATCC	CTATTGTGCT	TCCTTCAACG	CTCACATCAT	TTGGAGGGTC	3060
	CTGTCCAGAG	AGGGGAACCTA	TTGTTCTCTA	GCTGCAGGTT	GTACAGGAGG	AAATTCOCAT	3120
	TCCCTCCAGC	TTTGTGAGCG	TGAGTTACCT	GAGCAGCCGC	ACCCCTGGGT	ATAAAAACCT	3180
	GCTACGGATC	CTTCTGACAC	ATTCAACGAT	TCCCGTAGGC	ATGATAAAG	TACACCTCAC	3240
	AGTAGCTGTG	GAAGGGCCAG	TCACACAGAA	GTGGTTTCCC	GCCGCAATTA	ATCTTGTCTA	3300
25	CACATTTTCT	TGGAACAAGA	CCGATATCTA	TGGACAGAG	GTTTGGGGCC	TGGCAGAGGC	3360
	TTTGGTATCT	GTGGGATATG	AATATGAAC	GTCCCTCTAC	TTTATCTCT	GGGAGCAAAG	3420
	GACAGTCGTT	TTACAAAGTT	TTGAGATGGA	TGCTTCTAAC	CTAGGAGACT	GGTCTTTGAA	3480
	TAAGCATCAC	ATTTTGAATC	CTCAAGTGG	AATCATACAT	AAAGGGAATG	GAGAAAAAT	3540
	GTTCATTTCC	CAGCAGCCCC	CAGTCATATC	AACCAATAAG	GGTAATGGAC	ACCAAGAGGAG	3600
30	TGTAGCTTTC	AGCCAATGCA	ATGGCCAGC	CCACACACAC	AAACTCTTTG	CTCCTGTCCG	3660
	CTTAGCTTCT	GGCCTGATG	GCACTGTGTA	TGTTGGCCAG	TTCAATTTTG	TAAGGAGAAT	3720
	ATTTCCCTCG	GGAACTCCG	TTAGTATTTT	GGAAATTAAG	ACAGTCCCTG	CTCACAAATA	3780
	CTATCTGGCT	ATGGACCTTG	TGCTGGAATC	ACTCTATCTA	TCAGACACCA	ATACTCGCAA	3840
	AGTCTACAG	TTGAAATCTC	TTGTGGAGAC	GAAAGATCTG	TCCAAGAAAT	TTGAAGTGGT	3900
35	GGCAGGAAT	GTGATCTAGT	GCCTTCCCTT	TGACAGAGT	CATTGTGGAG	ATGGTGGGAG	3960
	AGCATCGGAA	GCTTCACTGA	ATAGCCCTCG	AGGCATCACA	GTTGATAGGC	ATGGATTTAT	4020
	TTACTTTTGT	GATGGGATCA	TGATTCGCAA	AATTGATGAG	AATGCTGTGA	TCACAACTGT	4080
	AATCGGCTCA	AATGGTCTGA	CTTCCACACA	ACCCTGAGC	TGTGACTCAG	GAATGGACAT	4140
	CACCTCAGTG	CGATTAGAGT	GGCCAACAGA	CCTTGCAGTA	AATCTATGAG	ACAATTCATT	4200
40	GTATGCTTTC	GATTAACAAT	TTGTGCTGCA	AAATTTCTGAG	AACAGGCGTG	TTCCGATCAT	4260
	CGCAGGAGCG	CCCATCTACT	GCCAGGTGCC	AGGCATCGAT	CATTTCCTGG	TCAGCAAGGT	4320
	AGCAATTCAC	TCCACTCTAG	AGTCAGCGAG	GGCCATCAGT	GTCTOCCACA	CGGGGCTGCT	4380
	CTTCATAGCT	GAACAGAGCG	AGAGGAAAGT	AAACCGCAT	CAGCAAGTAA	CCACCAATGG	4440
	GGAGATCTAC	ATCATCGCTG	GTGCCCCCAC	TGACTGTGAC	TGCAAAATTTG	ATCCAAACTG	4500
45	TGACTGTGTT	TCAGGTGATG	GTGGCTATGC	CAAAGATGCA	AAGATGAAG	CCCTTCTCTC	4560
	CTTAGCAGTG	TGCGCTGATG	GAACCTCTTA	TGTGGCAGAC	CTGGGAAATG	TTGGAATTCG	4620
	TACCATCAGC	AGGAACCAAG	CCCACCTGAA	TGACATGAAC	ATTTATGAGA	TTGCTTCACC	4680
	CGCTGATCAG	GAACTCTACC	AGTTCACTGT	AAATGGAACC	CACCTACACA	CCCTGAACCT	4740
	GATTAACAAG	GACTATGTTT	ATAACTTCAC	CTACAATTTCT	GAAGGTGACT	TGGGGCGGAT	4800
50	TACCAAGCAG	GAATGCAATT	CAGTGCACAT	TGCGCGTGAT	GCAGGCGGAA	TGCGGTATG	4860
	GCTTGTGATG	CCTGCGGAG	AGGTATACCT	GCTGACTATA	AGCAGCAATG	GAGTCTTGAA	4920
	AAGAGTGTCA	GCCCAAGGCT	ATAATCCGCG	CTTAATGACC	TATCCAGGAA	ACACAGGGCT	4980
	TCGTGCTACC	AAAAGTAAAG	AAAATGGATG	GACAACCGTT	TATGAGTATG	ACCCCGAGGG	5040
	ACACCTGACC	AATGCAACGT	TTCCCACTGG	AGAGGTGACG	AGCTTCCACA	GTGAOCTGGA	5100
55	GAAGCTGACA	AAAGTGGAGC	TAGATACTTC	CAACCGTGAA	AATGTCTCTA	TGTCAACCAA	5160
	CTTGACGGCA	ACTAGTACCA	TATATATTTT	AAAACAAGAA	AATACTCAAA	GTACCTATCG	5220
	GCTGAATCCA	GATGTTTCCC	TGCGTGTCC	TTTTGCCAGC	GGGATGGAGA	TCGGGCTCAG	5280
	CTCAGAGCCC	CACATCTTGG	CAGGGGCAGT	CAACCTTACC	CTGGGCAAAAT	GCAACATCTC	5340
	ATTGCCCCGA	GAGCACAATG	CAAACTCAT	CGAGTGGCGG	CAGAGGAAGG	AGCAAAACAA	5400
60	AGGCAATGTT	TCGGCTTTTG	AAAGGAGGCT	GAGGGCCAC	AACAGAAACC	TACTCTCCAT	5460
	AGATTGTTAG	CATATTAACC	GCACAGGAAA	GATCTATGAT	GACCATCGAA	AATTCACCTT	5520
	TCGAATCTTT	TATGACCAGA	CTGGGCGACC	CATTCTGTGG	TCTCTGTGAA	CGAGATATAA	5580
	TGAAGTGAAC	ATCACATATT	CACCTTCGGG	ATTGGTGACG	TTTATTCAAA	GAGGAACGTG	5640
	GAATGAAAAA	ATGGAATATG	ACCAGAGTGG	GAAATTTATT	TCAAGAACTT	GGGCTGATGG	5700
65	GAAAAATTGG	AGCTATACCT	ACTTAGAAAA	ATCTGTGATG	CTTCTOCTAC	ACAGCCAGCG	5760
	GCGTTACATC	TTTGTAGTATG	ACCAATCAGA	TTGCCCTGCT	TCAGTTACCA	TGCTAGCAT	5820
	GCTGGGCCAC	AGCTTACAAA	OCATGCTTTC	AGTGGGCTAC	TACCGTAATA	TCTACACCCC	5880
	ACCGGACAGT	AGCACTTCTT	TTATCCAAGA	CTATAGTCGA	GATGGCCGAT	TGCTACAGAC	5940
	CCTGCATCTG	GGGACAGGGC	GCAGAGTCTT	ATACAAGTAC	ACCAAGCAAG	CAAGGCTTTC	6000
70	TGAGGTTCTC	TATGTATCCA	CTCAGGTCAC	ATTAAACAT	GAAGAGTCTT	CTGGAGTGAT	6060
	TAAGCAATA	CACCTGATGC	ATGACGGATT	CATCTGCACA	ATCAGATACA	GGCAACACGG	6120
	ACCTCTTATT	GGACGCCAGA	TTTTAGATT	CAGTGAAGAA	GGCCTGTGTA	ATGCACGGTT	6180
	CGACTACAGC	TACAACAAAT	TCCGAGTCAC	AAGCATGCAA	GCTGTAAATCA	ATGAACCCCC	6240
	TTTGCTTATA	GATCTTTTAC	GATATGTGTA	TGTTCTTGGC	AGAACAGAGC	AGTTTGGAAA	6300
75	ATTCAAGTAT	ATTCAATTACG	ATTAAATCA	GTCATAACT	ACTACAGTGA	TGAACACAC	6360
	CAAAATCTTC	AGTGCAATTC	GACAAGTCAT	TGAAGTCCAA	TATGAAATCC	TAAAGGCAAT	6420
	TGCCACTTGG	ATGACCAATC	AATATGATAA	TGTGGGCCGA	CATGGTAATA	TGTGCATAG	6480
	GOTAGGAGTA	GATGCCAATA	TAAACAAGTA	CTTCTATGAA	TACGATGCTG	ATGGGCAACT	6540
	TCAGACTGTT	TCTGTAAATG	ACAAAACCCA	GTGGCGTTAT	AGTTACGATC	TGAATGGAGA	6600
80	CATCAACCTG	TTAAGCCATG	GGAAGAGTGC	TGCTCTTACT	CCTCTCCGAT	ATGACCTCCG	6660
	AGACCGCATC	ACCAGATTAG	GAGAAATCA	GTATAAAATG	GATGAAGATG	GCTTCTGAG	6720

	GCAGAGGGGA	AATGATATTT	TTGAATATAA	TTCTAATGGC	CTGCTGCAGA	AAGCCTACAA	6780
	TAAGGCTTCT	GGCTGGACTG	TGCAGTATTA	CTATGATGGG	CTTGGGCGAC	GTGTCCGGAG	6840
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SEQ ID NO:230 PEZ2 Protein sequence

Protein Accession #: NP_055068

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SEQ ID NO:231 PFD4 DNA SEQUENCE

Nucleic Acid Accession #: NM_000441

Coding sequence:

225-2567 (underlined sequences correspond to start and stop codons)

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	TTTTTCTTAA	GTGCCAACAA	TTTTCTAGAT	ATTATATACA	ACACAGGCTT	TGATCTTGGG	3780
	GACTTTTCCC	ATATATTCTA	CACCTGGAGT	AATGAAGTTG	TACTTCAATT	CTAGAGAAAA	3840
70	GTATACCCCA	GGTCCCAAT	TGAGAAATGC	TTGCTTGATT	GAAAACGACA	TCATCCCTTG	3900
	GTATAGTCCA	GGGATGTGGT	TCAGGACCCC	TGCATTACCC	AAAAATTGTT	CACACTCAAG	3960
	TCCTGCAATC	ATCCCTGCTC	AAAGATAGAA	TGGCTTCTCT	GTTTTCTTCT	TGAAATACAA	4020
	CCAGAAACAA	TGTGTCTATT	TCTGAAAGAA	TAGGATTAAT	GATCATACAA	ATGGGTTAAT	4080
	CCTGAATTCT	CGTGTGTAAT	CTGGTTACAG	CATAACTAGG	ATTATAATGC	TGCTCAATT	4140
75	TCACAGCACT	ACTTGCTTAT	ATTGACAACA	AATCATCTCG	CTAAAGAGTG	AATGTAGGCC	4200
	AGGCGCGGTG	GCTCATGCTT	GTAATCCAG	CACCTTGGGA	GGCGAGGCG	GGTGATCAC	4260
	GAGGTCAGGA	GATCGAGACC	ATCCTGGCTA	ACATGGTAAA	ACCCCGTCTC	TACTAAAAAT	4320
	AGAAAAAAG	AAATTAGCCT	AGCGTGGTGG	CTGGCGGCGC	CCTGTAGTCC	CAGCTATTTG	4380
	GGAGGCTAAG	GCAGGAGAA	GGCGTGAACC	CGGGAGGCGG	AGCTTGCAGT	GAGCCGAGGT	4440
80	CGTGCCACTG	CACCTCCAGC	TGGGGGACAG	AGCAAGACTC	CGTCTCAAAA	AAAAAATAAA	4500

5
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15
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AAAAAAAAA AGAGTGAATG TAATAGTCTT GCAGAAAAATG AATGAATACC TTTGTTCAAT 4560
AAAGGAAATA TGCACTGCTC ACITTTTTTGA AGGAAATGOC AAAGTTACGT TTTACACAA 4620
GGCTAGAGTT TGTAAATTCT GGGTTCATTT GTGATGACAT AAGTCAGCAA ACTGCGGGAA 4680
TACTGTCTCT TCTATGTATT TTGTGAATAG TAAGCATAAT TTTAGTTTTG TATTATCAAT 4740
GAAAATTTCA CTGGAATTA AAGCTGCCTT TTGTTATATT TTTAACCTAT AGGATAAGAT 4800
TCCAGTATTG TATATGAGTT TTAACAAATT AAAAAATCAA ATCATGTACA TTTGAAAATA 4860
TTTGACACACA TTTAAAAATA AATGTAAAGT TGTCTTTTAA ACTACTCGGA TGTGTCTCTT 4920
CTGAACAAAA

SEQ ID NO:232 PF04 Protein sequence:

Protein Accession #: O43511

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1 11 21 31 41 51
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FPPLITYFIF GTSRHLSVGP PPVVSVMVGS VVLSMAPDEH FLVSSSNGTV LNTMTIDTAA 180
RDTARVLIAS ALTLVGLIQ LIFGLQIGF IVRYLADPLV GGFTTAAAPQ VLVSQLEKIVL 240
NVSTKNYNGV LSIITYLVEI FQNIQDNLIA DFTAGLLTIV VCMVVKELND RFRHKIPVPI 300
PIEVITITIA TALSYGANLE KQYNAGIVKS IPRGFLPEEL PPVSLPSEML AASPSIAPVA 360
YAIASVSGKV YATKYDYTID GNQFIAPGI SNIFSGFFSC PVATFALSRT AVQESTGGKT 420
QVAGIISAAI VMATIALALCK LLEPLQKSVL AAVVIANLKG MPMQLCDIPR LWRQNKIDAV 480
IWVFTCIVSI ILGLDLGLIA GLIFGLLTIV LRVQFPWSNG LGSIPSTDIY KSTKNYKNIE 540
BPQGVKLEF SSPIFYGNVD GPKKCIKSTV GFDAIRVYNK RLKALRKIQK LIKSGQLRAT 600
KNGIISDAVS TNAPEFDED IEDLEELDIP TKKLEIQVDW NSELPVKVNV PKVPIHSLVL 660
DCGASIFLDV VGVRSKRVIV KEFQRIDVNV YFASLQDYVI EKLEQCGFPD DNIRKDTFFL 720
TVHDAILYLQ NQVKSQEGQG SILETTITLIQ DCKDTLELIE TELTEELDV QDEAMRTLAS 780
QDEAMRTLAS

SEQ ID NO:233 PFH2 DNA SEQUENCE:

35
40

Nucleic Acid Accession #: NM_016029
Coding sequence: 228-1097 (underlined sequences correspond to start and stop codons)

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45
50
55
60
65

1 11 21 31 41 51
CTGCGATCCC GCAGGGCAGC GACGCGACTC TGGTGCGGGC CGTCTCTTTC CCCCAGAGCT 60
GGGCGTGGCG GGGCGCAATG AACTGGGAGC TGCTGCTGTG GCTGCTGGTG CTGTGCGGCG 120
TGCTCCTGCT CTGTGGTGCAG CTGCTGCGCT TCCTGAGGGC TGACGGCGAC CTGACGCTAC 180
TATGGGCCGA GTGGCAGGGA CGACGCCCAG AATGGGAGCT GACTGATATG GTGGTGTGGG 240
TGACTGGAGC CTGAGTGGGA ATTGGTGAGG AGCTGGCTTA CCAGTTGTCT AAACAGAGAG 300
TTTCTCTTGT GCTGTGAGCG AGAAGAGTGC ATGAGCTGGA AAGGGTGAAA AGAAGATGCC 360
TAGAGAAATG CAATTTAAAA GAAAAAGATA TACTTGTTTT GCGCTCTGAC CTGACCGACA 420
CTGGTTCCTA TGAAGCGGCT ACCAAAGCTG TTCTCCAGGA GTTTGGTAGA ATGCACATTC 480
TGGTCAACAA TGTGGAATG TCCACAGGTT CTCTGTGCAT GGATACCAGC TTGGATGTCT 540
ACAGAAAGCT AATGAGGCTT AACTACTTAG GGACGGTGTG CTTGACAAAA TGTGTTCTGC 600
CTCACATGAT CGAGAGGAAG CAAGGAAAGA TTGTACTGTT GAATAGCATC CTGGGTATCA 660
TATCTGTACC TCTTTCCATT GGATCTGTG CTAGCAAGCA TGCTCTCCGG GGTTTTITTA 720
ATGCCCTTCG AACAGAACTT GCCACATACC CAGGTATAAT AGTTTCTAAC ATTTGCCAG 780
GACCTGTGCA ATCAATATT GTGGAGAATT CCTAGCTGG AGAAGTCACA AAGACTATAG 840
GCAATAATGG AGACCACTCC CACAAGATGA CAACCACTCG TTGTGTGCGG CTGATGTTAA 900
TCAGCATGGC CAATGATTGG AAGAAGATT GGATCTCAGA ACAACCTTTC TTGTTAGTAA 960
CATATTGTG GCAATACATG CCAACCTGGG CCTGGTGGAT AACCAACAG ATGGGGAAGA 1020
AAAGGATTGA GAACCTTAAG AGTGGTGTGG ATGCAGACTC TTCTTATTTT AAAATCTTTA 1080
AGACAAACA TGACTGAAA GAGCACTGT ACTTTTCAAG CCACTGGAGG GAGAAATGGA 1140
AAACATGAAA ACAGCAATCT TCTTATGCTT CTGAATAATC AAAGACTAAT TTGTGATTTT 1200
ACTTTTAAAT AGATATGACT TTGCTTCCAA CATGGAATGA AATAAAAAAT AAATAATAAA 1260
AGATTGCCAT GAATCTTGCA AA

SEQ ID NO:234 PFH2 Protein sequence:

Protein Accession #: NP_057113

70
75

1 11 21 31 41 51
MNWELLMLL VICALLLLLV QLLRFLRADG DLTLMAEWQ GRRPEMELTD MVVWVTGASS 60
GIGELAYQL SKLGVSLVS ARRVELEERV KRRCLENGNI KEDILVLP LDTDTGSHEA 120
ATKAVIQEPG RIDILVNNGG MSQRSLCHMD SLDVYRKLIE LNYLQTVSLT KCVLPMMIER 180
KQKIVTVMS ILGIIIVPLS IGYCASHAL RGPFNGLRTE LATPYGIIVS NICPGVPQSN 240
IVENSAGEV TKYIGANGDQ SEKHITSRCV RLMLISMND LKEVMISEQP PLLVTTYLMQY 300
MPTWAMWITN KMKKKRIENF KSGVDADSSY FKIFKTEHD

SEQ ID NO:235 ACCS DNA SEQUENCE

80
Nucleic Acid Accession #: NM_000450

Coding sequence: 1-1833 (underlined sequences correspond to start and stop codons)

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   GCCTGGTCTT ACAACACCTC CACGGAAGCT ATGACTTATG ATGAGGCCAG TGCTTATTGT 120
   CAGCAAAGGT ACACACACCT GGTTCGAATT CAAAACAAAG AAGAGATTGA GTACCTAAAC 180
   TCCATATTGA GCTATTTCAC AAGTTATTAC TGGATTGGAA TCAGAAAAGT CAACAATGTG 240
   TGGGTCTGGG TAGGAACCCA GAAACCTCTG ACAGAAGAAG CCAAGAACTG GGCTCCAGGT 300
10  GAACCCAAAC ATAGGCAAAA AGATGAGGAC TGCOTGGAGA TCTACATCAA GAGAGAAAAA 360
   GATGTGGCCA TGTGGAAATG TGAGAGGTGC AGCAAGAAGA AGCTTGCCCT ATGCTACACA 420
   GCTGCTGTGA CCAATACATC CTGCAGTGGC CACGGTGAAT GTGTAGAGAC CATCAATAAT 480
   TACACTTGCA AGTGTGACCC TGGCTTCAGT GGACTCAAGT GTGAGCAAT TGTGAAGTGT 540
   ACAGCCCTGG AATCCCTTGA GCATGGAAGC CTGGTTTGCA GTCACCCACT GGGAAACTTC 600
   AGCTACAAAT CTTCCTGCTC TATCAGCTGT GATAGGGGTT ACCTGCCAAG CAGCATGGAG 660
   ACCATGCAAT GTATGTCTCT TGGAGAATGG AGTGCTCCTA TTCCAGCCTG CAATGTGGTT 720
   GAGTGTGATG CTGTGACAAA TCCAGCCAAT GGGTTGTGG AATGTTTCCA AAACCTCGA 780
   AGCTTCCCAT GGAACACAAC CTGTACATTT GACTGTGAAG AAGGATTGTA ACTAATGGGA 840
   GCCCAGAGCC TTCAGTGTAC CTCATCTGGG AATTGGGACA ACAGAGAAGC AACGTGTAAA 900
20  GCTGTGACAT GACAGGCCGT CGGCCAGCCT CAGAATGGCT CTGTGAGTGT CAGCCATCC 960
   CCTGCTGGAG AGTTCACCTT CAAATCATCC TGCAACTTCA CCTGTGAGGA AGGCTTCATG 1020
   TTGCAGGGAG CAGCCAGGTG TGAATGCACC ACTCAAGGGC AGTGGACACA GCAAAATCCCA 1080
   GTTTGTGAAG CTTTCCAGTG CACAGCCTTG TCCAAACCCG AGCGAGGCTA CATGAATTGT 1140
   CTTCCTAGTG CTTCCTGGAG TTTCGGTTAT GGGTCCAGCT GTGAGTCTC CTGTGAGCAG 1200
25  GGTTTTGTGT TGAAGGGATC CAAAAGGCTC CAATGTGGCC CCACAGGGGA GTGGGACAAC 1260
   GAGAGAGCCA CATGTGAAGC TGTGAGATGC GATGCTGTCC ACCAGCCCCC GAAGGGTTGT 1320
   GTGAGGTGTG CTCATTCCCC TATTGGAGAA TTCACTTACA AGTCTCTCTG TGCTTTCAGC 1380
   TGTGAGGAGG GATTGTGAAT ATATGGATCA ACTCAACTTG AGTGCACATC TCAGGGACAA 1440
   TGGACAGAAG AGSTTCCTTC CTGCCAAGTG GTAAATGTTT CAAGCCTGGC AGTTCGGGGA 1500
30  AAGATCAACA TGAGCTGCAG TGGGGAGCCC GTGTTTGCCA CTGTGTGCAA GTTCGCCTGT 1560
   CCTGAAGGAT GGAGCCTCAA TGGCTCTGCA GCTCGGACAT GTGAGGCCAC AGGACACTGG 1620
   TCTGGCCTGC TACCTACCTG TGAAGCTCCC ACTGAGTCCA ACATTCCTCT GTAGCTGGA 1680
   CTTTCTGCTG CTGGAATCTC CCTCTGACA TTAGCACCAT TTCTCCTCTG GCTTCGGAAA 1740
   TGCTTACGGA AAGCAAAAGA ATTTGTTCCT GCCAGCAGCT GCCAAAGCCT TGAATCAGAC 1800
35  GGAAGCTACC AAAAGCCTTC TTACATCCTT TAA

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SEQ ID NO:238 ACC5 Protein sequence:

Protein Accession #: NP_000441

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   DVGMNDERC SKKLALCYT AACTINTSCSG HGECEVTINN YTCKCDPGFS GLKCEQIVNC 180
   TALESPHESG LVCSEPLGNP SYNSSCSISC DRGYLPSSMB TMQCHSSGEW SAPIPACNVV 240
   ECDAVIMPAN GFVECPNPNG SFPNNTCTF DCEBGFELMG AQSLQCTSSG NWNDEKPTCK 300
50  AVTCRAVRQP QNGSVRCSEH PAGEFTFKSS CNFTCEBGFH LQGPQAVECT TQGWTTQQLP 360
   VCEAFQCTAL SNPERGYMNC LPSASGSFRI GSSCEFSCEQ GFVLKGSKRL QCGPTGEMDN 420
   EKPTCEAVRC DAVEQPPKGL VRCAHSPIGE FTYKSSCAFS CEEGFELYGS TQLECTSQGQ 480
   WTEEVPSQVQ VKCSSLAVPG KIMMSCSGEP VFGTVCKPAC FEGWTLNGSA ARTCGATGEW 540
   SGLLPTCEAP TESNIFLVAG LSAAGLSLLT LAFPLLNLRK CLRKARKFVP ASSQSLES 600
55  GSYQKPSYLL

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SEQ ID NO:237 PM28 DNA SEQUENCE

Nucleic Acid Accession #: N51002

Coding sequence: 1-3793 (underlined sequences correspond to start and stop codons)

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   GAAAGGGATC GTCTTCTAGA CACCTTTCGG GAGACCCAGG AAAGCCTCTC ACTTGCCAG 180
   CAAAGACTTC AGGATGTCTAT CTATGACCGA GACTCACTCC AGAGACAGCT CAATTCAGCC 240
   CTGCCACAGG ATATCGAATC CCTAACAGGA GGGCTGGCTG GTTCTAAGGG GCGTGATCCA 300
   CCGGAATTTG CTGCACTGAC AAAAGAATTA AATGCTGCA GGGAAACAAC TCTAGAAAAG 360
70  GAAGAAGAAA TCTCTGAAGT TAAAGCTGAA AGAACAACA CAAGACTATT ACTGGAGCAT 420
   TTGGAGTGGC TTGTGTACAG ACATGAAAGA TCACTAAGAA TGACGGTGGT AAAACGGCAA 480
   GCCCAGTCTC CCTCAGAGT ATCAGTGAA GTTGAAGTTC TCAAGGCACT GAAATCTTTG 540
   TTTGAGCACC ACAAGGCCTT GGAATGAAAG GTAAGGGAGC GACTGAGGCT TTCTTTAGAA 600
   AGAGTCTCTG CACTGGAAGA AGAAGTAGCT GCTGCTAATC AGGAGATTGT TGCTTTGCGT 660
   GAACAAATG TTTATATACA AAGAAAAATG GCATCAAGCG AGGGATCCAC AGAGTCAGAA 720
75  CATCTTGAAG GGATGGAACC TGGACAGAAA GTCCATGAGA AGCGTTTGTG CAATGGTTCT 780
   ATAGACTCAA CCGATGAAAC TAGTCAAATA GTTGAAGTAC AAGAATTGCT TGAAGAAGCA 840
   AACTATGAAA TGGCCACAGT GAAAGAACGT TTAGCAGCCC TTCTTTCCCG AGTGGGAGAG 900
   GTGGACAGG AAGCAGAGAC AGCAAGAAAG GATCTCATTA AAACAGAAGA AATGAACACC 960
   AAGTATCAA GGCACATTAG GGAGGCCATG GCACAAAAGG AAGATATGGA AGAAGAAGTT 1020
80  ACAACCTTG AAAAGCGTTA CCTCAGTGCT CAGAGAGAAAT CTACCTCCAT ACATGACATG 1080

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	AATGATAAAC	TAGAAAAATGA	GTTAGCAAAT	AAAGAAGCTA	TCCTACGGCA	GATGGAAGAG	1140
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	AGAAAGGCTG	AAACCTTGCC	TGAAGTAGAG	GCTGAACCTG	CTCAGAGAAT	TGCAGCCCTA	1260
5	ACCAAGGCTG	AGAGAGAGCA	TGGAATATTT	GAAGAACGTA	TGAGACATTT	AGAGGGTCAA	1320
	CTTGAAGAGA	AGAATCAAGA	ACTTCAAAGA	GCTAGGCAAA	GAGAGAAAAT	GAATGAGGAG	1380
	CATAACAGA	GATTATCGGA	TACGGTTGAT	AGACTTCTGA	CTGAATCCAA	TGAACGCCCTA	1440
	CAACTACACT	TAAAGGAAAG	AATGGCTGCT	CTAGAAGAAA	AGAATGTTTT	AATTCAAGAA	1500
	TCAGAAACTT	TCAGAAAGAA	TCTTTAAGAA	TCTTTACATG	ATAAGGAAAG	ATTAGCAGAA	1560
10	GAATTTGAAA	AGCTGAGATC	TGAACCTGAC	CAATTGAAAA	TGAGAACTGG	CTCTTTAATT	1620
	GAACCCACAA	TACCAAGAAC	TCATCTAGAC	ACCTCAGCTG	AGTTGCGGTA	CTCAGTGGGA	1680
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	GGCCGCAATG	GTGTGCGAAG	AGATGAGCCA	AAGGTGAAAT	CTCTTGGGGA	TCACGAGTGG	1800
	AATAGAACTC	AACAGATTGG	AGTACTAAGC	AGCCACCCCT	TTGAAAGTGA	CACCTGAAATG	1860
	TCTGATATTG	ATGATGATGA	CAGAGAAACA	ATTTTATAGT	CAATGGATCT	TCTCTCTCCA	1920
15	AGTGGTCATT	CCGATGCCCC	GACGCTAGCC	ATGATGCTTC	AGGAACAAAT	GGATGCCATC	1980
	ATCAAGAAAA	TCAGGCTAAT	TCAGGAAGAA	AAAGAACTTA	CAGAGTTGCG	TGCTGAAGAA	2040
	ATTGAAATA	GAGTGGCTAG	TGTGAGCCTC	GAAGGCCCTG	ATTTGGCAAG	GGTCCACCCA	2100
	GGTACTCTCA	TTACTGCCTC	TGTTACAGCT	TCATCGCTGG	CCAGTTTCATC	TCCCCCAAGT	2160
20	GGACACTCAA	CTCCAAGACT	CACCCCTCGA	AGCCCTGCCA	GGGAAATGGA	TCGGATGGGA	2220
	GTCAATGACG	TCTGAGGAAA	CACTGGGAAA	AGATTGCAAT	TGTGGAAGAA	2280	
	GATGGTCGAG	AGGACAAGC	AACAATTAAT	TGTGAAACTT	CTCTCTCTCC	TACCCCTAGA	2340
	GCCTCAGAA	TGACTCACAC	TCTCCCTTCT	TCCTACCA	ATGATGCTCG	AAGTAGTTTA	2400
	TCTGTCTCTC	TTAGGCCAGA	AAGCCTCGGG	CTTGGTAGTG	CCAACAGCAG	CCAAGACTCT	2460
25	CTTCACAAAG	CCCCCAAGAA	GAAAGGAATC	AAGTCTTCAA	TAGGACGTTT	GTTTGGTAAA	2520
	AAAGAAAAAG	CTCGACTTGG	GCAGCTCCGA	GGCTTTATGG	AGACTGAAAG	TGCAGCTCAG	2580
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	AAGCATGAAC	TTCTTGAAG	AGCTCGGAGA	AAGGATTAC	CTTTTGGCCA	GTGGGATGGG	2700
	CCAAGTGGG	TCGATGGCT	AGAGCTTTGG	TTGGGAATGC	CTGCGTGGTA	CGTGGCAGCC	2760
30	AGCCGAGCCA	ACGTGAAGAG	TGGTGCCATC	ATGCTCTGCT	TATCTGACAC	TGAGATCCAG	2820
	TGAGAAATG	GAATCAGCAA	TCCACTGCAT	CGCTTAAATC	TTGATTTAGC	AATCCAGGAG	2880
	ATGTTTCCCT	TACCAAGTCC	TTCACTCTCT	CCAACATCTC	GAACTCTCTC	AGGCAACGTT	2940
	TGGGTGACTC	ATGAAGAAAT	GGAAATCTTT	GCAGCTCCAG	CAAAAACGAA	AGAACTCTAG	3000
	GAAGGAAGCT	GGGCCCAGTG	TCCGGTTTTT	CTACAGACCC	TGGCTTATGG	AGATATGAAT	3060
35	CATGATGGGA	TTGGAATGTA	ATGGCTTCCC	AGCTTGGGGT	TACCTCAGTA	CAGAAGTTAC	3120
	TTTATGGAAT	GCTTGGTAGA	TGCAAGAAATG	TTAGATCACC	TAACAAAAAA	AGATCTCCGT	3180
	GTCCATTAA	AAATGGTGGG	TAGTTTCCAT	CGAACAAAGT	TACATATGG	AATTATGTGC	3240
	TTAAAGAGGT	TGAATTATGA	CAGAAAGAA	CTAGAAAGAA	GACGGGAAGC	AAGCCACAT	3300
	GAATATAAG	ACGTGTTGGT	GTGGAGCAAT	GACCGAATTA	TTGCTGGAT	ACAAGCAATT	3360
40	GGACTTCGAG	AATATGCAAA	TAAATATACT	GAGAGCGGTG	TGCATGGCTC	ACTTATAGCC	3420
	CTGGATGAAA	GCTTTGACTA	CAGCAGCTTA	ACTTTATAT	TACAGATTCC	AACACAGAAC	3480
	ACCCAGGCAA	GGCAGATTCT	TGAAGAGAG	TACAAATACC	TCTTGGCCCT	GGGAAGTGA	3540
	AGGCGACTAG	ATGAAGTGA	TGACAAGAAC	TTACAGACGT	GATCAACCTG	GAGAAGGCAG	3600
	TTTCTCTCTC	GTGAAGTACA	TGGAATCAGC	ATGATGCTCG	GGTCTCTAGA	AACATTACCA	3660
45	GCTGGATTTA	GGTTAACAC	AACCTCTGGG	CAATCAAGAA	AAATGACAAC	AGATGTGCTG	3720
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50 SEQ ID NO:238 PM28 Protein sequence:
Protein Accession #: none found

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	EEKISELKAE	RNMRLLEH	LECLVSRER	SLRMVVKRG	AQSPSGVSSE	VEVLKALKSL	180
	FEHKKALDEK	VRELRVSL	RVSALRELA	AANQIVALE	EQNVHQRKM	ASSEGSTESE	240
60	HLEGMEPGQK	VHEKRLSNGS	IDSTDETSQI	VELQELLEKQ	NYEMAQMKER	LAALSRRVGE	300
	VEQEASTARK	DLIKTEEMNT	KYQDIREAM	AQKEDMEERI	TTLEKRYLSA	QRETSIHDM	360
	NDKLENELAN	KEATLRQMBE	KNRQLQERLE	LAEQKLQOTM	RKAETLPEVE	ABLAQRIAAE	420
	TKAERHGN	KEERMHLEGO	LEEKNOELQR	ARQREKMEEE	HNKRLSDIVD	RLLTESNERL	480
	QLHLKERRMA	LEEKNVLIQE	SETFRKNLEE	SLHDKERLAE	ETEKLRSELD	QLKMRGTSLI	540
	KPTIPRTHLD	TSAELRYSVG	SLVDSQSDYR	TTKVRIRFR	GRMGVRRDEP	KVKSIGDREW	600
65	NRTQQIGVLS	SHPPESDTEM	SDIDDDRET	IFSSMDLLSP	SGHSDAQTLA	MLQEQDLDAI	660
	NKEIRLIQEE	KESTELRAEE	IENRVASVSL	EGLNLARVHP	GTSTASVTA	SSLASSPFP	720
	GESTPKLTPR	SPAREMDRMG	VMTLPSDLRK	HRRKIAVVEE	DGREDKATIK	CETSPPTPR	780
	ALRMTHLTPS	SYHNDARSSL	SVSLEPESLG	LGSANSSQDS	LHKAPKKKGI	KSSIGRLFGK	840
70	KEKARLQDLR	GFNSTEAAAQ	ESLGLGLGT	QAEKDRRLK	KHELLEARR	KGLPFAQWDG	900
	PTVVAMLEW	LGMFAWVAA	CRANVKSgai	MSALSDTEIQ	REIGISNPLH	RLKLRLAIQE	960
	MVSLTSPSAP	PTSTPTSGNV	WVTHEEMENL	AAPAKTKESE	EGSWAQCFVF	LQTLAYGDMN	1020
	HEWIGNEWLP	SLGLPOVRSY	FMECLVDARM	LDHLTKKDLR	VHLKMDVSFH	RTSLQYGLMC	1080
	LKRLNYDRKE	LERRREASQ	EIKDVLVSN	DRIIRWQAI	GLREYANNIL	ESGVHGSLLA	1140
75	LDENPYSSSL	TLLQLIPTQN	TQARQILERE	YNNLLALGTE	RRLDESDDKN	FRRGSTMRQ	1200
	PPPREVEGTS	MPFGSSETLP	AGPRLTTTSG	QSRKMTTIVA	SSRLQRLDMS	TVRTYSCLB	

SEQ ID NO:239 PC14 DNA SEQUENCE

80 Nucleic Acid Accession #: NM_016570
Coding sequence: 1-1134 (underlined sequences correspond to start and stop codons)

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 AAGTATGATG ACGAAGTAGA CAAGGATTTT TCTAGCAAAT TAAGAATTA TATAGATATT 240
 ACTGTTGCCA TGAAGTGTCA ATATGTTGGA GCGGATGTAT TGGATTTAGC AGAACAATG 300
 10 GTTGCACTCG CAGATGGTTT AGTTTATGAA CCAACAGTAT TTGATCTTTC ACCACAGCAG 360
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25 SEQ ID NO:240 PC14 Protein sequence:
 Protein Accession #: NP_057854

1 11 21 31 41 51
 30 MRLNRKRL SLVKELDAFF KVPESYVETS ASGGTVSLIA FTTMALLTIM EFSVYQDTVM 60
 KYEYEVDRDF SSKLRINIDI TVAMKCOYVG ADVLDLAETH VASADGLVYE PTVFDLSPQQ 120
 KEMQRMLQLI QSLRQEELH QDVIFKSAFK STSTALPPRE DDSSQSNAC RIEGHLYVNK 180
 VAGNPHITVG RAIPHPRGHA HLAALVNHEH YNPSHRIDHL SPGLVFAII NPLDGTKEIA 240
 IDHNQMFQYF ITVVPFKLET YKISADTHQF SVTERERILN HAAGSHGVSG IFMKYDLSSL 300
 35 MVTVTTEHMP FWOQFVRLCG IVGGIFSTTG MLEGIGKFIY EIIICRFRLG SYKPVNSVFF 360
 EDGHTDNHLP LLENNTHE

SEQ ID NO:241 PBA7 DNA SEQUENCE

40 Nucleic Acid Accession#: AA219134

Coding sequence: 24-1815 (underlined sequences correspond to start and stop codons)

45 AATTOGCGCT TGCTTAATTA AGCATGTTTA CCTTCTGTG ATCTGTCACT GCTGCTGTCA 60
 GTGGCTCTCT GGTGGGTTAT GAACCTGGGA TCATCTCTGG GGCTCTTCT CAGATCAAAA 120
 CCTATTAGC CTTGAGCTGC CATGAGCAGG AAATGGTGTG GAGCTCCCTC GTCATTGGAG 180
 CCTCTCTGCT CTCACCTACC GGAGGGGTCC TGATAGACAG ATATGGAAGA AGGACAGCAA 240
 TCATCTGTG ATCTGCTCG CTGGACTCG GAAGCTTAGT CTGATCTCT AGTTTATCCT 300
 ACACGGTCT TATAGTGGGA CGCATTGCCA TAGGGGTTTC CATCTCCCTC TCTTCCATTG 360
 50 CCACCTGTGT TTACATGCCA GAGATTGCTC CTCAACACAG AAGAGGCCCT CTGTGTGTCAC 420
 TGAATGAGCT GATGATTGTC ATCGGCATTC TTCTGCTTA TATTCAAAAT TACGCATTTG 480
 CCAATGTTTT CCATGGCTGG AAGTACATGT TTGGCTTGT GATTCCCTTG GGAGTTTTCG 540
 AAGCAATGCA AATGATTTTT CTTCCTCCAA GCCCTCGGT TCTGGTGATG AAAGGACAAG 600
 AGGGAGCTGC TAGCAAGGTT CTGGAAAGGT TAAGAGCACT CTCAGATACA ACTGAGGAAC 660
 55 TCACCTGTAT CAATCTCTCC CTGAAAGATG AATATCAGTA CAGTTTGTGG GATCTGTTTC 720
 GTTCAAAAAG CAACATGGCG ACCCGAATAA TGATAGGACT AACACTAGTA TTTTGTGATC 780
 AAATCACTGG CCAACCAAAC ATATTGTCT ATGCATCAAC TGTTTTGAAG TCAGTTGGAT 840
 TTCAAGCAA TGAGGCAGCT AGCCTCGCT CCACCTGGGT TGGAGTCTG AAGGTCAATTA 900
 GCACCATCC TGCCACTCTT CTTGTAGACC ATGTGGGCAG CAAAACATTC CTCTGCATTG 960
 60 GCTCTCTGT GATGGCAGCT TCGTTGTGTA CCATGGGCAT CGTAAATCTC AACATCCACA 1020
 TGAACCTCAC CCATATCTGC AGAAGCCACA ATTCTATCAA CCAGTCTCTG GATGAGTCTG 1080
 TGATTTATGG ACCAGGAAAC CTGTCAOCCA ACAACAATAC TCTCAGAGAC CACTTCAAAAG 1140
 GGATTTCTC CCATAGCAGA AGCTCACTCA TGCCCTGAG AAATGATGTG GATAAGAGAG 1200
 GGGAGACGAC CTCAGCATCC TTGCTAAATG CTGGATTAAG CCACACTGAA TAACAGATAG 1260
 65 TCACAGACCC TGGGGACGTC CCAGCTTTTT TGAATGGCT GTCCTAGCC AGCTTGCTTG 1320
 TTTATGTTG TGTCTTTTCA ATTGTTCTAG GAACCAATGCC CTGGCTGGTG CTCAGCGAGA 1380
 TCTTCTCTGG TGGGATCAGA GGAAGAGCCA TGGCTTTAAC TTCTAGCATG AACTGGGGCA 1440
 TCAATCTCT CATCTCGCTG ACATTTTGA CTGTAACCTA TCTTATTGGC CTGOCATGGG 1500
 TGTGCTTTT ATGATAAATC ATGAGTCTAG ATCTTATTGG CCTGOCATGG GTGTGCTTTA 1560
 70 TATATACAT CATGAGTCTA GCATCCCTGC TTTTGTGTG TATGTTTATA CTTGAGACAA 1620
 AGGGATGCTC TTGGGAACAA ATATCAATGG AGTAGCAAA AGTGAATAT GTGAAAAACA 1680
 ACATTTGTTT TATGAGTCAT CACCAAGAAG AATTAGTGCC AAAACAGCCT CAAAAAGAA 1740
 AACCCAGGA GCAGCTCTTG GAGTGTAAAC AGCTGTGTGG TAGGGGCCAA TCCAGGCAGC 1800
 75 TTCTCCAGCA GACCTAATGG CCTCAACACC TTCTGAACGT GGATAGTGCC AGAACACTTA 1860
 GGAGGGGTGCT TTGGACCAA TGCAATGTTG CGACTCTGT GCTCTCTTT CAGTGTCAATG 1920
 GAACCTGTTT TGAAGAGACA CTCTGAAATG ATAAGACAG CCTTTAATCC CCTCTCTCMC 1980
 CAGAAAGAAC CTCAAAAGGT AGATGAGGTA CAAGGTCTTA AGTATCTCT TTTCTGAGC 2040
 AGGATATCAG GTTAAAAAAA AAAAGTFACT GGCTGGTTTA ATACTTTCTA CCTTCTTCA 2100
 AGAGCAGCCT TTGAATAGAC TATGTCCTAG TGAAGACATC AACCTCCGCC TTAAGCTATG 2160
 80 TATGTATGGA GGCAAGTCC AGCTTTATTA TGCAGACACA CAAGTGGTCT GGACATGAGG 2220
 GTACAGTTTC TGCTACCAA GACACTACTT GCACGTGATC TTACGCAAAA AAGAACCAGA 2280

ACACACAGTG TGGACAACCTG CCCATATATT CTATCTAGAT TAGGAGAGGG TCCTGGCTAG 2340
 GATTTTAGTG GTAATTCCTA GTTACATTCA ACAAGTATAA AGATTATAGA GCTTATTTTA 2400
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 AAATGCGATAG AAAAGACAAT TTAAAAATOC TGGGACCATA TTTATTTAGA AGTAGCTGTT 2580
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 CTGTTAAGA GGTCTTACTA ATAAAAATTG GGTATGATAG AAAAWCCACA ATCAAAWCTT 3000
 GAACCAATA ACATATTAAA TTACTAATAT TTAAGTGATG GAAGACACAC AAAAAACTTA 3060
 AAAGCACGAA CAACCTAACT TGAAAAAGAA TTTTAAATA TGATTAACCT GAAGAAAAAGA 3120
 GAACTCTAAG AGCCAAAGCT CTTTATTAT TAGCTTGGAA TTTTCTATT GGTCTCTAAC 3180
 AAATGTGCC AATGTCATAT AAGGAAACAT GATCTATTAC ATTCCTTTAT AACAATGTGG 3240
 AGAGACTATA AACCTATGTA AGTAGTAAAA CTATATYAGA GACTCAGGAG ACTGACTAAA 3300
 AGGCTGGAT CTGCACTGTA TTATCTGTAT AAAAAATGGC AGGGGGAAGC TAAAAAGGAA 3360
 GGAGATTGGA GATCTCAAT CTATCATGGT GTATTTCATA CGCAAATCAG AGCATGCATT 3420
 GTTTTGTGTT TTGGAAAGA GAAGGGAAGT GTGTCTGCTC CATGTTTCTC TCCGTGTTT 3480
 ATAGTICAAA CTTATATAT ACTTCAGGTA TTTTGTGTT AGCCTTCAT TATAAATGGG 3540
 CAGGAAATG TTATCAACC TAGCCAGTTT ATTACTAGTG ACCTTGACTT CAGTATCTTG 3600
 AGCATCTTT TATATTTTC TTTATTATC CTGAGTCTGT AACTAAACAA TTTGTCTTC 3660
 AAAATTTTAT CCAATATCCA TTGCAACACA CCAATCAAG CTCTTGATT TCAAAAAATA 3720
 AAAAGGGGGA AATACITACA ACTGTACAT ATATATTAC AGTTTTTATT TATAAAAAAA 3780
 ATTTACAGTA CTTATGAGGA GCCAGCAGAA GACATCAGAG CACTCAGTTC TCCCATCTT 3840
 TGTAAAGGTT AGCGAATTAC CCATGGACAC TGTTAGGTGA GGCTCATTCG GCAGCCCTGA 3900
 AAACAAACCT GGTACACATG TCTTACCTC CTOCTTCAG ATAAAGCACT TCGATTATCT 3960
 ATTGATCTGC CCAGTTTCCA AGTCATGCGA ATACTAAAAA GGTTACATCA TCTGGATCTG 4020
 TACCTGGCT ATATAAGCAT GTTTCCTCC TATCTATGT TCTTTTTTT GTGAACATT 4080
 GAAAAACAGG AGGTGACTTA TTACTGTTAA TTAACACTAA ATGAAAAATG TCAAGTCTT 4140
 AAAACAGTGA GCTGTAACT CTTTCATGTA ATTTTATCT CTATGAAATT GGCTATCTTA 4200
 CTGAATCTTA AATAAAGGA AATAAACACT TTTTITWAA AAAAAAGGAA AATAAAMARW 4260
 MWAAAAATCT CAATGAAATA TTTCACAAGA AGGAAAAA

Protein Accession #: AAF91431

SEQ ID NO:242 PBA7 Protein sequence:

MFTFLSSVTA AVSGLLVGYE LGHSGALLQ IKTLALSCH EQEMVSSVL IGALLASLTG 60
 GVLDTRYGRR TAILSSCLL GLGSLVLIS LSYTVLIVGR IAGVSISSLS SIATCVYIAE 120
 IAPQERRGLL VSNELMIVI GILSAYISNY AFANVFHGWK YMFGLVPLG VLQAIAMYFL 180
 PPSRFLVMK GQEGAASKVL GRLRLSDIT EELTVIKSSL KDEYQYSFWD LFRSKDNMRT 240
 RIMIGLILVF FVQITGQPNL LFYASTVLKS VGFQSNBAAS LASTGVGVVK VISTIPATLL 300
 VDHVGSKTF CIGSSVMAAS LVTMGIVNLN IEMNFTICR SHNSINQSLD ESIVYGPGLN 360
 STNNITLRDH PKGSSHSRS SLMPLRNDVD KRGETTSASL LNAGLSHTEY QIVDPGDVP 420
 AFLKWLSLAS LLVYVAFST GLGPMFWLVL SEIFFGGIRG RAMALTSSMN WGINLLISLT 480
 FLTVIDLGL PWYCHITIM SLDLGLPWV CFYITMSLA SLFFVVMFIP ETKGCSLEQI 540
 SMELAKVNYV KNNICFMSHH QEELVPKQPQ KRKPQEQLE CNKLCGRGQS RQLSPET

SEQ ID NO:243 PBA4 DNA sequence:

Nucleic Acid Accession#: AA172056

Coding sequence: 121-339 (underlined sequences correspond to start and stop codons)

TTTAGCCACC AGAGGANTTC TCTTGAAATA CCAAAAATCC ATCAGTATCT TGAATCATGC 60
 TGGATTTTGA AGAATTCCTA AGAAGCCATG TAAAGGGGGC TCTCTGGCCT TGAAATAGTG 120
 ATGTTTTTTA TACAGAAAGG AGAATGCAGA ATGGTCAGAC TATCATGCAC TGTTAAATTT 180
 GATTTCAGA AATTACAGGA AAACCTTCCA AAGTCCATC TCACAGAANN TTATTITNCC 240
 AAGAATTCCA AGATAAGTTT AGTTTATGG AAGACTTTTA TGTGGTTTTT ACTCACTCTT 300
 CATCTCAGAC ATCGACAGAT GATTACATCA CTTATAGTTC TAGTAAATTT ATTAATATAA 360
 AACTCAGAGA CATTCCAATA TCCACATTGC TTACACCATT AGGCATAGAT TCAGTGTGAC 420
 CTATGACAA TGAATAATGAG CTGTTTGTG ATTTAAAGGT TTAATTTCT CTAACCAAAAC 480
 TGCTTGATCC AGATGACGGA CTGCAAAATG TAATATTGT TCTGGAAGAA CAATCAAAATA 540
 AGACTTAAGA GGAAGGGGAA TGGCCACAAT CCACTGAAA TTTTCTTAA AAAAGTGTGC 600
 AGCTACTAA ATCAGAATGA AATAGAAAGT ACAAGATTAT AAACAAAATG CAATCAAACT 660
 TTTCTTAAGC TTACTAAAG TATTTCATC TGAATAATTC AAGCAACTTT GTTCAACATT 720
 AAATTGACAA TCTAAACTAA CAAGTCTTT GAATTATGC ATGGTAGTAA ACATTCCTC 780
 TATTAACTTT ATTACCTAAG GCTAAACCTA AAATTTTAA GCAAAATAG AAAAATAGTC 840
 TTCACATC AAAAAATAAA GTTGTGTTA TTAGTATTT TCCCAATAAA ATTGTCGTT 900
 CTTGTTTTT TATTGGAGA GTCTGTGCAA AATGTCATA AAAATAAATT AGCACTAGAA 960
 ATTATTTCTA AATACAAA

SEQ ID NO:244 PBQ8 DNA SEQUENCE

Nucleic Acid Accession#: X51405

Coding sequence: 3-1721 (underlined sequence corresponds to start and stop codon)

1 11 21 31 41 51

5
 10
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AAATGGCGTG CCCGTCCTC CGCGGCCCC CTGCCTCGCA GTGGTTTCTC CTGCAGCTCC 60
CCTGGGCTCC GCGGCGAGTA GTGCAGGCGG TGGAGCGCGG GCTTTGCCCG TCCTCTCTGG 120
GTGGGCCAG TGCGCGGGCT GACACTCATI CAGCCGGGGA AGGTAGAGCG AGTAGAGGCT 180
GGTGCGGAAC TTGCGGCCCC CAGCAGCGCC GCGCGGCTAA GCCCAGGGCC GGGCAGACAA 240
AAGAGGCGCG CCGCGTAGGA AGGCACGGCC GCGCGCGCGG GAGCGCAGCG ATGGCGGGCG 300
GAGGGGCGAG CGCGCTGCTG CTCTGTGCG GGGCACTGCG TGCGTGGGG TGCGTCTCTG 360
GCGCGGAAGC CCAGGAGGCC GGGGCGCGCG CCGCGGGCAT GAGCGCGCGC CGCGCGCTGC 420
AGCAGAGGGA CGGCATCTCC TTGAGTAGCC ACCGCTACCC CGAGCTGCGC GAGGCGCTCG 480
TGTCCGTGTG GCTGCACTGC ACCGCCATCA GCAGGATTFA CACGCTGGGG CGCAGCTTCG 540
AGGGCGCGGA GCTCCTGGTC ATCGAGCTGT CCGACAACCC TGGCGTCCAT GAGCCTGGTG 600
AGGCTGAATT TAAATACATT GGGAAATATG ATGGGAATGA GGCTGTGGGA CGAGAACTGC 660
TCATTCTCTT GGGCCAGTAC CTATGCAACG AATACCAAGA GGGGAACGAG ACAATGTGCA 720
ACCTGATCCA CAGTACCCGC ATTACATCA TGCTTCCCT GAACCCAGAT GGCTTTGAGA 780
AGGCAGCGTC TCAGCCTGGT GAACCAAGG ACTGTTTGT GGGTGAAGC AATGCCCAGG 840
GAATAGATCT GAACCGGAAC TTTCAGAGC TGGTAGGAT AGTGTACGT AATGAGAAAG 900
AAGGTGGTCC AATATATCAT CTGTGAAAA ATATGAAGAA AATGTGGAT CAAAACACAA 960
AGCTTGCTCC TGAGAACAGG GCTGTCAATC ATTGGATTAT GGATATTCTT TTTGTGCTTT 1020
CTGCCAATT CTGAGGAGG GACCTTGTGG CCAATTATCC ATATGATGAG ACGCGGAGTG 1080
GTAGTGCTCA GGAATACAGC TCCCTCCCGA ATGAGGCCAT TTTCCAAGC TTGGCGCGGG 1140
CATACTCTTC TTTCACCCCG GCCATGTCTG ACCCCAATCG GCCACCATGT CGCAAGATG 1200
ATGATGACAG CAGCTTTGTA GATGGAACCA CCAACGGTGG TGCTTGGTAC AGCGTACCTG 1260
GAGGGATGCA AGACTTCAAT TAOCCTAGCA GCAACTGTTT TGAGATCACC GTGGAGCTTA 1320
GCTGTAGAGA GTTCCACCT GAAGAGACTC TGAGAGCTTA CTGGAGGAT AACAAAAACT 1380
CCCTCATTAG CTACCTTAG CAGATACACC GAGGAGTTAA AGGATTGTG CGAGACCTTC 1440
AAGTAAACC AATTCGGAAT GCCACCATCT CCGTGAAGG AATAGACCAC GATGTTACAT 1500
CCGCAAGAGA TGGTATTAT TGGAGATTGC TTATACCTGG AAATATATAA CTTACAGCCT 1560
CAGCTCCAGC CTATCTGGCA ATAACAAAGA AAGTGGCAGT TCCTTACAGC CCTGCTGCTG 1620
GGGTGATTT TGAATGGAG TCATTTTCTG AAGGAAAGA AGAGGAGAAG GAAGAAATGA 1680
TGGAAATGTT GAAATGATG TCAGAAACTT TAAATTTTAA AAAAGGCTTC TAGTTAGCTG 1740
CTTTAAATCT ATCTATATAA TGTAGTATGA TGTAAATGCG TCTTTTTTTT AGATTTTGTG 1800
CAGTTAATAT TTAACATTGA TTTATTTTAT AATCATTTAA ATATTATACA ACTTTCTCTA 1860
AAATAAATAG CCTCTTAGGT AAAAATATAA GAACCTGATA TATTTCATTC TCTTATATAG 1920
TATTCTATTT CTTACCTATA TTACACAAAA AAGTATAGAA AAGATTAAQ TAATTTTGCC 1980
ATCTAGGCT TAAATGAAT ATTCTGTGTA TTATTACAA TGCAGAAATT TTTGAGTAAT 2040
TCTAGCTTTC AAAAATTAGT GAAGTCTTTC TACTGTAAAT GGTGACAAAG TCACATAATG 2100
AATGCTATTG AAAAGGTTAA CAGATACAGC TCGGAGTTGT GAGCACTCTA CTGCAAGACT 2160
TAAATGATTC AGTATAAATT GTCTGTTTTT TCTGTGCTG ACTAATCTATA AGCATGATCT 2220
TGTAAAGAAC TAGAAGAAA AGCGCAGAAA TTAGATCGTC GGGAAACGAGA AATGCAAAAC 2280
AATAAAATTT GACTCTCTGC TTGTACATAT AGGAGCAATA CTATTATAT ATGTAGTCCG 2340
TTAACTACTC TTAAGATTAT AGGTTTCTCT CTGTGTTGTA GAGTGGCCCA GAATGCAATT 2400
CTGAATGAAT AAAGGTTAAA AAAAAATCCC CAGTGAAGAAA AAA
  
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45
 Protein Accession#: SEQ ID NO:245 PBQ8 Protein sequence
 P16870

50
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MAGRGGSAALL ALGALAACG WLLGAEAEQEP GAPAAGMRRR RRLQVEDGIS FEYHRYPELR 60
EALVSVWLQK TAISRIYTVG RSFEGRELLV IELSDNPGVH EPGEPEFKYI GNMHNGNEAVG 120
RELLIFLAQY LCNEYQKENE TIVNLIHSTR IHIMPSLNFDF GFEKAASQPG ELKDWVFGRS 180
NAQGIDLNRN FFDLDRIVYV NEKEGGPNNH LLKNMKKIVD QNTKLAPETK AVIHWIMDIP 240
FVLSANLHGG DLVANYPYDE TRSGSAHEYS SSFDDAIRQS LABAYSSFP AMSDFNRPFC 300
RKNDSSSFV DGTINGGAWY SVPGGMQDFN YLSSNCFEIT VELSCKEPPP EBLTKTYWED 360
NKNLSISYLE QHGRGVKGFV RDLQGNPIAN ATISVEGDH DVTSAKDGDY WRLLPFGNYK 420
LTASAPGYLA ITKKVAVPYS PAAGVDFFLE SFSEKKEEEK EELMEVWKMM SBTLNF
  
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60
 Nucleic Acid Accession#: SEQ ID NO:246 PBV4 DNA sequence
 AF038968
 Coding sequence: 91-1107 (underlined sequence corresponds to start and stop codon)

65
 70
 75
 80

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GGGGGACGCT GAGCGCGCAG GGCGGCGCGG GCCTCGCCTC GTCTCTCTCT CTGCGCCTGG 60
GTCCGGTGGG TGAGCGCGAG AGCCAGAGAG ATGTCCGGAAT TCACAGATAA CCCGTTTGCC 120
GACCCGGATC TCAACAATCC CTTCAGGAT CCATCAGTTA CACAAGTAC AAGAAATGTT 180
CCACCAGGAC TTGATGAATA TAATCCATTC TCGGATTCTA GAACACCTCC ACCAGCGCGT 240
GTGAAGATGC CTAATGTACC CAATACACAA CCAGCAATAA TGAAACCAAC AGAGGAACAT 300
CCAGCTTATA CACAGATTGC AAAGGAACAT GCATTGGCCC AAGCTGAATC TCTTAAGCGC 360
CAAGAGAAGC TAGAAGAAA AGCGCAGAAA TTAGATCGTC GGGAAACGAGA AATGCAAAAC 420
CTCAGTCAAC ATGTAGAGAA AATATTTTGG CCACCTCTTC CTAGCAATT TCTGTGCGGA 480
CCTGTGTTCT ATCAGGAATT TTCTGTAGAC ATTCTGTAG AATTCACAAA GACAGTAAAG 540
CTTATGTACT ACTTGTGGAT GTTCCATGCA GTAACTCTGT TCTAATATAT CTTCGGATGC 600
TTGGCTTGGT TTTGTGTTGA TTCTGCAAGA GCGGTGTGAT TTGGATTGAG TATCCTGTGG 660
TTCTTGCTTT TACTCTCTTC TTCAATTGTC TGTGTTGACA GAACACTTTA TGGAGCTTTC 720
AGGAGTGACA GTTCATTTAG ATTCTTTGTA TTCTTCTTGG TCTATATTGG TCAGTTTGGT 780
GTCACTGTAT TCAGACTGCG AGGATTTCAT AACTGGGGCA ATTGTGGTTG GATTTCATCC 840
CTTACTGGTC TCAACCAAAA TATTCCTGTT GGAATCATGA TGATAATCAT AGCAGCACTT 900
TTCAAGCAT CAGCAGTCAAT CTCACTAGTT ATGTTCAAAA AAGTACATGG ACTATATCGC 960
ACAACAGGCT CTAGTTTGA GAAGGCCCAA CAGGAGTTTG CAACAGTGT GATGTCCAC 1020
AAAACCTGTC AGACCGCAGC TGCAAAATGCA GCTTCAACTG CAGCATCTAG TGCAGCTCAG 1080
  
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5 AATGCTTTCA AGGTAACCA GATTTAAGAA TCCTCAAACA ATACACTGTT ACCTTTTGAC 1140
 TGTACCTTTT TCCTCAGTTA CTGTATCTCA CAATATTTTT TATGTTCAAA ACACACAGTA 1200
 CAGACAGCAT GGATATTTCG GTTTCACITG TGCATGGGCT AAAACCAGGA AAACCTCCTT 1260
 GTCTTATTAC TTACCTAAT AGTTCTCTAA TATTTCACTG CCCCTTCAG AAAAATATTT 1320
 10 ACATGCTAAA TAATATCTCT CCATATTTTT GGGGGATGAC ATTCAGTGAA TTATTTCACT 1380
 GGTGACCCAC TGAAATTTAA TAATGGTACT TATGATTAAA AACGATTTTA ATACTAAGT 1440
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 TTCAATTCCTT TTTCCTTATT TATATTGAAA GAAATAGGCC AGCAGAGACT TAGGGATTTT 1560
 15 AAATGGCTT GCTTTTTCAG TGTTCAGTC ACCAGTGAAG AGCCTATGTG CATTTTGTAG 1620
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 ATAACAATCT CTAATTGCA TGGGCACCAC ATTTCTTTATA TTAAACAAT TAGTGTTTTG 1740
 GCTTCTGTAC TGCTTATGTT TGTAGGATTC AGGGGTTAAT GGAATCACAG AAATGATATT 1800
 CTGCAAGAA TTTCTTTTAA TAAAAAGTT GGGGGTGCAA TATAAGAA GTATATATA 1860
 20 TGCAATACAT TATCCAAAAG AGAAGGTAGT TAATGCAGTA GAAAGTAGT GTAATAATT 1920
 CTTTTC

SEQ ID NO: 247 PBV4 Protein sequence:

20 Protein Accession #: MSDFDSNFFA DFDLNNPFKD PSVTQVTRNV PFGLDEYNPF SDSRTPPGG VKMPNVFNTQ 60
 PAIMKPTIEH PAYTQIAKEH ALAQALLKR QEELERKAAH LDRREMQN LSQHGRKNW 120
 25 PPLPSNFPVG PCFYQFVVD IPVEFQKTVK LMYLWLMFHA VTLEFNIFGC LAWFCVDSAR 180
 AVDFGLSILW FLTLTCSFV CWYRFLYGAF RSDSSFRFFV FFFVYICQFA VHVLAAGFH 240
 NWNCGWISS LTGLNQNPV GIMMIMIAL FTASAVISLV MFKKVHGLYR TTGASFEKAQ 300
 QEFATGVMSN KTVQTAAANA ASTAASSAAQ NAFKGNQI

SEQ ID NO: 248 PBH2 DNA sequence

30 Nucleic Acid Accession#: none found
 Coding sequence: 1-613 (underlined sequence corresponds to start and stop codon)

35 ATGAGAGACA ATAAATCGTG TGCTTTTTC ATGGGAAAGT TAAATGTTTG TTTGAAGGC 60
 ACAGTAATAG CAGGCTATTC AGTGTTCGCC ACTACCTGCA TCATTCATCT GGCTGTAGCT 120
 AGTGCACTAC AATTTCCTAA AAAGTCTTCT CACCTCACA GGACTGCTCT ACATCTGGCC 180
 TCTGCCAATG GAAATTCAGA AGTAGTAAAA CTCTGCTGG ACAGACGATG TCAACTTAAT 240
 ATCCTTGACA AAAAAAGAG GACAGCTCTG ACAAAGGCCG TACAATGCCA GGAAGATGAA 300
 40 TGTGGGTAA TTTTCTGGA ACATGGCACT GATCCGAATA TTCCAGATGA GTATGGAAAT 360
 ACCGCTCTAC ACTATGCTAT CTACAATGAA GATAAATTA TGGCCAAAGC ACTGCTCTTA 420
 TACGGTCTG ATATCGAATC AAAAAACAAG CATGGCTCA CACCACTGTT ACTTGGTGA 480
 CATGAGCAAA AACAGCAAGT GGTGAAATTT TTAATCAAGA AAAAAGCAAA TTAAATGCA 540
 45 CTGGATAGAT ATGGAAGGTG TGTGACCTTG GGAACGTTAT TTACCACCAA ATATGTTGTC 600
 ATATATGAAA AGTAG

SEQ ID NO: 249 PBH2 Protein sequence:

Protein Accession #: none found
 50 MRDNKScaff MGKLNVCfEG TVIAGYSVFA TTCIHLAVA SALQFPKSS HPHRTALHLA 60
 SANGNSEVVK LLLDRROQLN ILDNKERTAL TKAVQCQEDC CALMLLEHGT DPNIPDEYGN 120
 TALHYATNE DKLMARALL YGADIESKNK HGLTPLLGV HEQKQVVKF LIKKKANLNA 180
 LDRYGRCVL GTLFTTKYVV IYK

SEQ ID NO: 250 PBH1 DNA sequence

Nucleic Acid Accession#: XM_005829
 Coding sequence: 1-3043 (underlined sequence corresponds to start and stop codon)

60 ATGGTGATCA TCTATCTTC TTTCTGCAAT TATTACATGG AGTCTACAG AGAAGAGCTT 60
 CCCACATTC ACTATTGAT TGACATTCAG TTGCAACAG GAAAGGTTAC TCAGCCGGGA 120
 GAGGACACTT CCTACCATCA ATGCGCTCAG CTTGAAGCCA GAGACGAAG CACCGACAGT 180
 TTATTATTAA ACAATGGCAG CAGCGCCACG CTGAAGACAC GAACGCGCTG TTATGGAACC 240
 65 CCCAGAGGTC TCCCCATCG TAGCCTGCTC CAGCCGACTC CGCCACATG TAAAACGAAG 300
 ATCAGGAGCA GATTTGAAGA ATTACAAAGT GAATTGGTGC CAGTCAGCAT GTCAGAGACA 360
 GACCACATAG CCTCTACTTC CTCTGATAAA AATGTTGGGA AAACACCTGA ATTAAGGAA 420
 GACTCATGCA ACTTGTTTTC TGGCAATGAA AGCAGCAAAAT TAGAAAATGA GTCCAAACTA 480
 TTGTCATTAA ACACGTATAA AACTTTATGT CAACCTAATG AGCATAATAA TCGAATTGAA 540
 70 GCCAGGAAA ATTATATTCC AGATCATGGT GGAGGTGAGG ATCTTGTGC CAAAACAGAC 600
 ACAGGCTCAG AAAATCTGA ACAAATAGCT AATTTTCCTA GTGGAAATTT TGCTAAACAT 660
 ATTTCAAAAA CAATGAAAC AGAACAGAAA GTAACACAAA TATTTGGTGA ATTAAGGTCA 720
 TCTACATTTC CAGAATCAGC TAATGAAAAG ACTTATTCAG AAAGCCCTTA TGATACAGAC 780
 TGCACCAAGA AATTTATTC AAAAAAAG AGCGTTTCAG CATCAGAGGA TTTGTTGGAA 840
 75 GAAATAGAAT CTGAGCTCTT ATCTACGGAG TTTGCAGAAC ATCGAGTACC AAATGGAATG 900
 AATAAGGGAG AACATGCATT AGTCTGTTT GAAAAGTGTG TGCAAGATAA ATATTGCAG 960
 CAGGAACATA TCATAAAAAA GTTAATTAAG GAAAATAAGA AGCATCAGGA GCTCTTCGTA 1020
 GACATTGTT CAGAAAAAGA CAATTTAAGA GAAGAACTAA AGAAAAGAAC AGAAACTGAG 1080
 AAGCAGCATA TGAACACAA TAAACAGTTA GAATCAAGAA TAGAAGAACT TAATAAGAA 1140
 GTTAAGCTT CCAGAGATCA ACTAATAGCT CAAGACGTTA CAGCTAAAAA TGCAGTTCAG 1200

5 CAGTTACACA AAGAGATGGC CCAACGGATG GAACAGGCOA ACAAGAAATG TGAAGAGGCA 1260
 CGOCAAGAAA AAGAAGCAAT GGTAAATGAAA TATGTAAGAG GTGAGAAGGA ATCTTTAGAT 1320
 CTTCGAAAGG AAAAAGAGAC ACTTGAGAAA AAACCTTAGAG ATGCAAAATA GGAACTTGAG 1380
 AAAAACTACT AAAAAATTA GCAGCTTTCT CAGGAGAAA GACGGTTGCA CCAGCTGTAT 1440
 10 GAAACTAAGG AAGGCGAAAC GACTAGACTC ATCAGAGAAA TAGACAAATT AAAGGAAGAC 1500
 ATTAACCTCT ACGTCATCAA AGTAAAGTGG GCACAAACA AATTAAGC TGAAATGGAT 1560
 TCACACAAGG AAACCAAGA TAACTCAAA GAAACAACA CAAATTAAC ACAAGCAAG 1620
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 45 DHIATSSDK NVGKTPELKE DSCNLFSGNE SSKLENESEK LSLNTDKTLC QPNEHNNRIE 180
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 ESNSLQSQFD KVSCESEQLQ SQCEQMKQTN INLESRLKE EBLRKEBVQT LQAEACRQT 780
 EVKALSTQVE ELKDELVTQR RKHASSIKDL TKQLQARRK LDQVESGSYD KEVSSMGSR 840
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60 SEQ ID NO:252 PB.1 DNA sequence
 Nucleic Acid Accession#: D83760
 Coding sequence: 56-1459 (underlined sequence corresponds to start and stop codon)
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 CACGGCCAGC TACCTCTACT CCCAGGAAG TCCTCTGAG CCAGAGAGTC CCTATCAACA 720
 CTCAGTTGAC ACACCAACCC TGCCCTATCA TGCCACAGAA GCTCTGAGA CCAGAGTGG 780

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CAGGTCTTTC AACCAACAGC TCTTCGCTCA GCTCCTGGCC CAGTCAGTTC ACCACGGCTT 1260
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Protein Accession #: SEQ ID NO:253 PB16 Protein sequence:
NP_005898

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FQPPCSALP PSPSHAFSQS PCTASYPHSP GSPSESPSY QHSVDTPPLP YHATEASETQ 240
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NCNYQHGFHP ATVCKIPSGC SLKVFNNQLF AQLLAQSVHH GFVVYELTK MCTIRMSFVK 420
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SEQ ID NO:254 PB16 DNA sequence

Nucleic Acid Accession#: AB04684

Coding sequence: 472-4377 (underlined sequence corresponds to start and stop codon)

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55 Protein Accession #: SEQ ID NO:255 PB.J8 Protein sequence
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SEQ ID NO:256 PBM1 DNA sequence

Nucleic Acid Accession#: AF111847

Coding sequence: 58-1608 (underlined sequence corresponds to start and stop codon)

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 40 CTGAACACAG AGGCTTCATG TGGGGGAGGA GGAGAGTCT CATGTGACA CATGGGCTCA 1980
 GGGCTGCCAG AATCAGCCGA TGCTGGATGG GCCTGCAGAA ACAACACTCA CCACACACAC 2040
 TTCTTTCAA AGACCAAAAG TGACTGGTGT CTGCTGTGAC AGATTGCTTC ATTTATGTTT 2100
 CTACATAGTA AGGTGACTGC CAAATAATAT TTGAAGTCAT CTGTCTCTTT GTAAATTAAT 2160
 TTATATGACC TATAAATTA AAAATGTTT TCAGTGAGTG CTTTAAACA ACTTAAGCTT 2220
 45 CTGCGCTGCC AAGGAATTA ATGTATCTT GTGAAGGTG TTGCTGTTG AATTGATGAG 2280
 AAATGGAAGA TGAGAACTCC CTAAGAGTTC TCATAATAAA TCATCTATC ACAAAATCAAT 2340
 ACGGTATACA GAGTTAAAGT GGAATGAGGT AAGAAGATAC AGCTACAGAA AATAGTTGCG 2400
 TGTATGGGAG AACAGTCTAT GTAAATGGGT AGTTTGTGTA ATAAATATTT TTAATCTTT 2460
 CTTTCTGAGA ATTACCGAAT GTGTATAAAC AAATAAGAA AAATAATTTA CTGTGTTT 2520
 50 AGACAGCAT AGAATATAT GTTCAGCACA GTAAATATA TTTGAATTT GATAAGCCAA 2580
 AAATGTGTT TTGAATGAAT ATTTGTGAA TCTTTCTTAA AAGCTCAAT TTGTAGACTT 2640
 CTAATAGAA TAAACACTTG CAGCAGAAA AAAAAAAAA AAAAAAAAA AAAAAAAAA 2700
 AAAAAAAAA AAAAAAAAA AAAAAAAAA AAAAAAAAA AAAAAAAAA 2760
 AAAAAAAAA AAAAAAAAA AAAAAAA

SEQ ID NO:257 PBM1 Protein sequence:

PBM1 Protein sequence: CAB76901

60 MGDPSKQDIL TIFKRLRVP TNKVCFCGA KNPSWASITY GVFLCIDCSG SHRSILGVHLS 60
 FIRSTELDSN WSWFQLRMCQ VGGNASASSF FHQHGCTND INAKYNSRAA QLYREKIKSL 120
 ASQATRKHGT DLWLDSCVVP FLSPPPKEED FFASHVSPEV SDTAWASAI AEPSSLTSRPV 180
 ETTLENNEGG QEQGPSVEGL NVPTKATLEV SSIKKKPNQ AKKGLGAKKG SLGAQKLANT 240
 CFNEIEKQAQ AADKMKEQED LAKVVSKEES IVSSLRLAYK DLEIQMEKDE KMNISGKKNV 300
 65 DSDRLGMGFG NCRSVISHSV TSDMQTIEQE SPIMAKPRKK YNDSDDSYF TSSSYFDEP 360
 VELRSSFSF WDDSSDSYWK KETSKDTETV LKTTGYSDRP TARRKPDYEP VENTDEAQKK 420
 FGNVKAISD MYFRQSQAD YETRARLERL SASSSISSAD LFEEPRKQPA GNYSLSSVLP 480
 NAFDMAQFKQ GVRSVAGKLS VFANGVVTSI QDRYGS

SEQ ID NO:258 PBM4 DNA sequence

Nucleic Acid Accession#: D30891

Coding sequence: 1-4032 (underlined sequence corresponds to start and stop codon)

70 ATGGATACTG TCATGAAGCA GACACATGCT GACACACCTG TTGATCATTC TCTATCTGGC 60
 75 ATAAGAAAGT GTAGCAGCAC CTTTAAGCTT AAAAGTGAAG TCAACAAGCA TGAACAGGCC 120
 CTTGAAATGC AGAATOCAAA TTTGAACAAT AAAGAATGTT GTTTCACCTT TACGTTGAAT 180
 GGAAACTCCA GAAATATAGA CCGTAGTGTG TTTACAGCAT ATGGTAAACC CAGCGAGAGT 240
 ATCTACTCAG CCTGAGTGC TAATGACTAT TTCAAGTAAA GGATAAAGAA TCAGTTTAAT 300
 80 AAGAACATTA TTGTTTATGA AGAAAGACA ATAGATGGAC ATATAAATT AGGAATGCCT 360
 CTCAAGTGCC TGCTAGTGA TTCTCATTTT AAAATTACAT TTGTCAAAG AAAGAGTAGC 420

5 AAAGAAGATG GACACATATT ACGCCAATGT GAAAAATCAA ACATGGAATG CATTCTTTTT 480
 CATGTTGTTG CTATAGGAAG GACAAGAAAAG AAGATTGTTA AGATCAACGA ACTTCATGAA 540
 AAAGGAAGTA AACTTTGTAT TTATGCCCTG AAGGGTGAGA CTATTGAAGG AGCCTTATGC 600
 AAGGATGGCC GTTTTCGGTC TGACATAGGT GAATTTGAAT GGAAACTAAA GGAAGGTCAT 660
 AAGAAAAATT ATGGAAAAACA GTCCATGGTG GATGAAGTAT CTGGAAAAAGT CTTAGAAATG 720
 GACATTTCAA AAAAAAAGC ATTACAACAG AAAGATATCC ATAAAAAAT TAAACAGAAT 780
 GAAAGTGCCA CTGATGAAAT TAATCACCAG AGTCTGATAC AGTCTAAGAA AAAAGTCCAC 840
 AAACCAAAGA AAGATGGAGA GAACAAAGAT GTAGAACACA GCAGAGAGCA AATTCTCCCA 900
 10 CCTCAGGATC TAAGCCATTA TATTAAGAT AAAACTGGCC AGACAATTCC CAGGATTAGA 960
 AATTATTACT TTGTAGTTT GCCCGAAAA TATAGGCAAA TAAACTCACA AGTTAGACGG 1020
 AGGCCGATC TGGGTAGCG GTATGCTATT AATCTGGATG TCCAAAAAGG GCAATTAAT 1080
 CTCTTAAAGA ATTATCAAAC GTTGAATGAA GCCATAATGC ATCAGTATCC GAATTTTAAA 1140
 GAGGAGGCAC AGTGGGTAAAG AAAATATTTT CGGGAAGAAC AAAAGAGAAT GAATCTTTCA 1200
 15 CCAGATGATC TAAGCCATTA TATTAAGAT AAAACTGGCC AGACAATTCC CAGGATTAGA 1260
 TCAGTTGCAA CTGCGAACA GCTTACATAT TATAGCAAGT CAGTTGGGT CATGCAATGG 1320
 GACAATAATG GAAACACAGG TAATGCTACT TGCTTTGTCT TCAATGGTGG TTATATTTTC 1380
 ACCGTGCGAC ATGTTGTACA TCTTATGGTG GGTAAAAACA CACATCCAAAG TTGTGGGCA 1440
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 20 GACAAATGGT TTCCGCTTTC GCTTGGCTT AAAGTGTCCA ATGAAAAATC AGATTATGCC 1560
 ATTTTAAAC TAAAGAAAA TGGAAATGCG TTCTCTCCAG GACTATGGCG ACAGATTCTT 1620
 CCTCAACCAT CTACTGGTIT GATTATTTA ATGGTCTATC CTGAAGGCCA GATCAAGAAA 1680
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 CAAGATGGGT TGGTAGATCT CTATGATACC ACCAGTAATG TATAGTGTAT GTTTACCCAA 1800
 25 AGAAGTTTCC TATCAGAGGT TTGGAACACA CACACGCTTA GTTATGATAC TTGTTCTCT 1860
 GATGGGTCTC CAGGCTCCCC AGTGTTAAT GCATCTGCA AATTGGTTCG TTGTCATACC 1920
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 ATGGATTCTT TCTTTGTGA TATTAAAAAG ACAATGAGA GCTTGTATA ATCATTAAAT 2040
 GATGAGAAAC TTGAGACCTA CGATGAAGAG AAAGCCCCGC CCAGGCCAGC CTACCGGCGA 2100
 30 CTAGGATGCT TTCCGCTTTC GCTCTGCTT CCAATACTCG GGACTGGGGA AACCGGGAGA 2160
 ATAGAAGCAG GCAAGGACCG CCGTGGGCAC GGGTCTAGTG AGACAGGGTC CTGCTCGCGG 2220
 CGTCAAGGAG GAGCGCTGTG GGTGTCCCA GCGCAGCCAA TCGGCTTCGG AAGTAGCTGG 2280
 AGCTCTGGAG CCTTCTTTC CTCAAATACG AGCGGGAAT GCGTTGAGCG CTGGATTCCA 2340
 GGCAGATGTC TGGCGAGGCG GCGAGTCTCT AAAGAGCAAC AGAATAATTG CAGTACTTCT 2400
 35 CTAATGAGA TGGATGCTAG AGGAGACCCA AGAGCCACAA CTAATACCCA GGCTCAAAGA 2460
 TTCCATTAC CTAAGAAAAA TCCAGAAGAC CAGACCATGC CCAAAAATAG GACAATATAT 2520
 GTTACCTTGA AGGCTGTGAG AAAAGAGATA GAAACTCACC AAGGCCAAGA AATGCTTTGT 2580
 CGTGGCAGAG AAGGAATTTG AGAGTACATA AACCTTGGAA TGCCCTCAG TTGTTTCCCT 2640
 GAAAGGTGGC AGGTGTGTCAT TACATTTTCC CAAAGTAAAA GTAAGCAGAA GGAAGATAAC 2700
 40 CACATATTGT GCAGGACGGA CAAAGCATCG ACTGAATGTG TCAAATTTTA CATTATGCA 2760
 ATTGGAATTG GGAAGTGTAA AAGAAGGATT GTTAAATGTG GGAAGCTTCA CAAAAAGGG 2820
 CGCAAACTCT GTGTTTATGC TTCAAAGGA GAAACCATCA AGGATGCACT GTGCAAGGAT 2880
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 ATTTTAGAAA GCAOCCAGCC AGTTGATGAA TTAGAAGGCA GATACTTTCA GGTGAGGTT 3000
 45 GAGAAAAGAA TGGTCCCGAG TGCAGCAGCT TCTCAGAATC CTGAGTCAGA GAAAAGAAAC 3060
 AOCCTGTGTG TGAGAGAACA AATCGTGCT CAGTACCCCA GTTTGAAAAA AGAAAGTGAA 3120
 AAAATCATTG AAAACTTCAA GAAAAAATG AAAAGTAAAA ATGGGGAAAC ATTTATTGAA 3180
 TTGCTAGAAA CAACGTTTGG GAAAGTAAAC AAAAATCTCT CTTCGATTAA AGTAGTGAAA 3240
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 50 TACGCCACT CTCTTGTIT TAAAGGATTG TTCAATTTAA CTGTGCGCA TGTAAATAGAT 3360
 AGCATTTGAG GAGACCGAAT AGAGCCAAGT AAGTGGGCAA CCATAATTGG TCAATGTGTA 3420
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 55 ATACATATTA TTGGCCATCC ATATGGAGAA AAAAAAGCAGA TTGATGCTG TGCTGTGATC 3660
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 CCAGAGTATG TCCATATGTA TACTCAAAGA AGTTTCCAGA AAATAGTTCA CAACCTGAT 3780
 GTGATTACCT ATGACACTGA ATTTTCTTT GGGGCTTCCG GCTCCCTGT GTTTGATTCA 3840
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 60 OGATGATCA TTGAGTTTGG CTCTACCAG GAATCCATCC TCTTGATAT TAAGCAAAGA 3960
 CATAAACCAT GGTATGAAGA AGTATTTGTA AATCAGCAGG ATGTAGAAAT GATGAGTGAT 4020
 GAGGACTTGT GAGAAATTCAG TCTACTGGAT TTAAGGGAAT GGCTTATGGA GTTGTATTT 4080
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 65 ACATATGAG ATGGAATATA ACTTGCCCAA ATTTTTTTT TTTTGTAGAC TGAGTCTCAC 4260
 TCTGTGCGCT GGGCTGGAGT ACAGTGGTGC GATCTCAGCT CACTGCAACT TCCACTCCC 4320
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 70 GTGCTGGGAT TACAAGTTTG AGCCACTGCA CCGGCTAAC TTGCCCTATT TTAAGTCAA 4560
 GCAATGGGAA GAATAACAAG ATTATATAGT AATCAGTTTC ATGACACTAA AAGTCATATA 4620
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 CCAAAACTTG TCACTCTCAT GATTCCTTAC ATCTGACATA AGGAAAGTAA GTGCTCAGAA 4740
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 75 AAATGCTTGA TTAGAAATGA TCTCAAAAC TTTTGAATTT TCCAAATCT TCATATTACT 4860
 GAAACTGTGC GAATATATGG GTCTGAAAT TCAGAAGATG ATAGTCACTC TTCCATATT 4920
 TATAGGCTAT TAAGCAAGG GATATCTTAA ACATCATATT ACTTTATTA GATTCTACT 4980
 ACTCCAAAT TAAATATGAT GTATTCTCA TTGTTTACT TCTTCATGGT ATTATGAAGA 5040
 CTATATAGAT GATTCACCA AGCCTGCAAA TCTCCTCTT GTGGAATTCC ACTGGACCCA 5100
 ATCTGTTTTC CATTTCCATT GCAATACTAC TAAAGCCATA CAATATCAAG CAOCCTCCT 5160

CTAGGTCCAG GGAATATCAC AGAAGAAGCA GGCATGTAAG ATTTTAAGGA CTGGTTTCGA 5220
 GGGGTGAGT GTAGGAAAAC AGCCTGTTGC ATTGTAAGAG TGATGTCAAC TTGAAGAGCA 5280
 GCTGGCATGA TGACTGCTGT TTGACTCCTG CATACCAAGA TATTCTGCAG CAATGTCTTT 5340
 AAACAGTGCC GGTAGTACAG ATAACCCCTC ATAAAGATGC TTATCTAACC TCCCAGTGT 5400
 TCAGGTGTTT CACAAGAAAG TCTGAGATAT GACTAGCTAC ACGTTTIGCC AAAAATGCTT 5460
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 TGCTTCTGTT TGTAAATTCC TATTAATGT TCTTCTGAG AAAAAAAAAA A

10 SEQ ID NO:259 PBM4 Protein sequence
 PBM4 Protein sequence: BAB67788

MDTVMKQTHA DTFVDHCLSG IRKCSSTFKL KSEVNHKETA LEMONPNLNN KECCFTFTLN 60
 GNSRKLDRSV FTAYGKPSES IYSALSANDY FSEIKNQFN KNIIVYEKT IDGHINLGMP 120
 15 LKCLPSDSHF KITFGQRKSS KEDGHILRQC ENPNMECLF HVVAIGRTRK KIVKINELHE 180
 KGSKLCIYAL KEGTIEGALC KDGRFRSDIG EFEWKLEKEG KKIYQKQSMV DEVSGKVLEM 240
 DISKKALQQ KDHIKKIKQN ESATDEINHQ SLIQSKKKVH KPKKDGETKD VEHSREQILP 300
 PQDLSHYIKD KTRQITPRIR NYFCSLPRK YRQINSQVRR RPHLGRRYAI NLDVQKEAIN 360
 20 LKKNYQTLNE ADMHQYFNFK EEAQWVRKYF REEQKRMNLS PAKQFNYYKK DRGKMTANSV 420
 SVATCEQLTY YSKSVGFQMW DNNGTNGNAT CFVFNNGYIF TCRHVHLMV GKNTHPSLWP 480
 DIUSKCAKVT FTYTEPCPT DNWFSIEPWL KVSNNENLDYA ILKLKENGNA FPPGLWRQIS 540
 POPSTGLIYL IGHPGGQIKK IDGCTVIPLN ERLKKYFNDC QDGLVDLYDT TSNVYCMFTQ 600
 RSFLSEVVNT HTLSYDTCFS DGSSGSPVFN ASGKLVALHT FGLFYQRFN VHALLIEFGYS 660
 25 MDSILCDIKK TNESLYKSLN DEKLETYDEB KARFRPAYRR LGCFRFRSRF PILGTGETGR 720
 IEAGKDRRGH GVSETGSCSR RQGGALWVSP AQFGRSSW SSGAFASNT SGNCVERWIP 780
 GRVLARRAVS KEGQNNCSTS LMRMESRGDP RATINTQAQR FHSFKKNFED QTMPQNRITY 840
 VTLKVRKEI ETHQGGEMLV RGTEGIKEYI NLGMPLSCFP EGGQVVITFS QSKSKQKEDN 900
 HIFGRQDKAS TECVKFYIHA IGIGKCKRRI VKCGKLHKKG RKLVCYAFKG BTKDALCKD 960
 30 GRFLSFLEND ILESTQPVDE LEGRYQVEV EKRMPVSAAA SQNPSEKRN 1020
 TCVLREQIVA QYPSLKRESE KIENFKKKM KVKNGETLFB LHRTTFGKVT KNSSSIKVVK 1080
 LLVRLSDSVG YLFWDSATTG YATCFVFKGL FILTCRHVID SIVGDGIEPS KWATIGQCV 1140
 RVTFGYEELK DKETNYFFVE FWFIEHNEEL DYAVLKLKEN GQQVPMELYN GITPVLSGL 1200
 35 IHIGHPYGE KKQIDACAVI PQGQRAKKCQ ERVQSKKAE PEYVHMYTOR SFQKIVHNPD 1260
 VITYDTEFFP GASGSPVDS KGSIVAMHAA GFAYTYQNET RSIEFGSTM ESILLDIKQR 1320
 HKPWEYEEVFN NQQDVEMMSD EDL

40 SEQ ID NO:260 PBQ1 DNA sequence
 Nucleic Acid Accession#: NM_015642
 Coding sequence: 489-2489 (underlined sequence corresponds to start and stop codon)

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45	ACATTTCAAA	AAAAATACAT	AGACTGATGT	TTCAGACTTG	TGCAGCATAA	GCCTACAGGG	60
	TACGAAGAAT	GAACTCTGAG	AATGTTTGGA	GAATGTTTCA	TCATTACTAA	CAGGATATTG	120
	CTCATGACAT	TGCTGTCTGA	TCCTTGACCA	TCAGTCTGTG	ACCTGCCCCG	TCTCTTTACA	180
	TGCAGCCGCT	CTCTGTCTCC	TGCCCAATG	AACATCTGCA	CTAGGCCCAA	GCCTTGGAGT	240
50	AATTTACCTG	AAGAGTGACA	CCATTGATTT	TGAAACTACT	GAAGAAACCC	AAGACAGCTG	300
	AAACACAGAA	GGCATCTGAG	GAGAATGAGA	TTACTCAGCC	GGGTGGATCC	AGCGCCAAAG	360
	CGGGCTCTCC	CTGCTGAAC	TTTGAAGCTG	TTTGTCTCC	AGACCCAGCC	CTCATCCACT	420
	CAACACATTC	ACTGACAAAC	TCTCAGCTC	ACACCGGCTC	ATCTGATTGT	GACATCAATT	480
	GCAAGGGGAT	GACCGAGCC	ATTACAGCA	TCAACCTTCA	CAACTTCAGC	AATTCGGTGC	540
55	TCGAGACCTT	CAACGAGCAG	CGCAACCGTG	GCCACTTCTG	TGACGTAAAG	GTGCGCATGC	600
	ACGGGAGCAT	GCTGCGCGCA	CACCGCTGCG	TGCTGGCAGC	CGGCAGCCCC	TTCTTCCAGG	660
	ACAAACTGCT	GCTTGCTTAC	AGCGACATCG	AGATCCCGTC	GGTGTGTGTA	GTGCAGTCAG	720
	TGCAAAAGCT	CATTGACTTC	ATGTACAGCG	CGGTGCTACG	GGTCTGSCAG	TGGGAAGCTC	780
	TGCAGATCCT	CAGGGCCCGC	AGCATCCTGC	AGATCAAAC	AGTCATCGAC	GAGTGCACGC	840
60	GCATCGTGT	ACAGAACGTG	GGCGATGTGT	TCCCGGGGAT	CCAGGACTCG	GGCCAGGACA	900
	CGCCGCGGGG	CATCCCGAG	TCAGGCACGT	CAGGCCAGAG	CAGCGACAG	GAGTGGGGCT	960
	ACCTGCAGAG	CCACCCACAG	CACAGCGTGG	ACAGGATCTA	CTCGGCACTC	TACGCGTGT	1020
	CCATGCAGAA	TGGCAGCGGC	GAGCGCTCTT	TTTACAGGGG	CGCAGTGGTC	AGCCACCCAG	1080
	AGACTGCGCT	CGGCCTGCC	CGCGACCACC	ACATGGAAGA	CCCCAGCTGG	ATCACACGCA	1140
65	TCATGAGCG	CTGCGAGCAG	ATGGAGCGCT	ACCTGTCCAC	CACCCCGGAG	ACCACGCATC	1200
	CGCGCAAGCA	GCCCGGCGCT	GTGCGCATCC	AGAOCCTAGT	GGGCAACATC	CACATCAAGC	1260
	AGGAGATGGA	GGAGGATTAC	GACTACTACG	GGCAGCAAAG	GGTGCAGATC	CTGGAACGCA	1320
	ACGAATCCGA	GGAGTGACAG	GAAGACACAG	ACCAGGCGGA	GGGCACCGAG	AGTGAGCCCA	1380
	AAGGTGAAAG	CTTCGACTCG	GGCGTCAGCT	CCTOCATAGG	CACCGAGCCT	GACTCGGTGG	1440
70	AGCAGCAGTT	TGAGCCTGGG	GCGGCGCGGG	ACAGCCAGCG	TGAACCCACC	CAACCCGAGC	1500
	AGGCTGCAGA	AGCCCCCGCT	GAGGGTGGTC	CGCAGACAAA	CCAGCTAGAA	ACAGGTGCTT	1560
	CCTCTCCGGA	GAGAAGCAAT	GAAGTGGAGA	TGGACAGCAC	TGTTTATCAT	GTGACGAACA	1620
	GCTCCGACAA	GAGCGTCTTA	CAACAGCCTT	CGGTCAACAC	GTCCATCGGG	CAGCCATTGC	1680
	CAAGTACCCA	GCTCTACTTA	CGCCAGACAG	AAACCTTCAC	CAGCAACCTG	AGGATGCCTC	1740
75	TGACCTTGAC	CAGCAACACG	CAGGTCAATT	GCACAGCTGG	CAACACCTAC	CTGCCAGGCC	1800
	TCTTCTACTC	CCAGCCCGCG	GGCAGTGGCC	CCAAAGCCTT	CCTCTTCAGC	CTGCCACAGC	1860
	CCTTGGCAGG	CCAGCAGACG	CAGTTTGTGA	CAGTGTCCCA	GCCCGGTCTG	TGCACCTTTA	1920
	CTGCACAGCT	GCCAGCGCCA	CAGCCCTTGG	CCTCATCCGC	AGGCCACAGC	ACAGCCAGTG	1980
	GGCAAGGCGA	AAAAAGCCTT	TATGAGTGCA	CTCTCTGCAA	CAAGACTTTC	ACCCGCCAAC	2040
80	AGAACTACGT	CAAGCACATG	TTCTGTACAC	CAGGTGAGAA	GCCCCACCAA	TGCAGCATCT	2100
	GTTCGGCGTC	CTTCTCTCTA	AAGGATTACC	TTATCAAGCA	CATGGTGACA	CACACAGGAG	2160

5 TGAGGGCATA CCAGTGTAGT ATCTGCAACA AGCGCTTCAC CCAGAAGAGC TCCCTCAACG 2220
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 TCTCTCACAA GACCTCCTG GAGCGACACG TGGCCCTGCA CAGTGCCAGC AATGGGACCC 2340
 CCGCTGCAGG CACACCCCA GGTGCCCGCG CTGGCCCGCC AGGCGTGGTG GCGTGCACGG 2400
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 10 ATAGTTTTC CAGTCTCCT CGGATGGTGG CCTTAAGGCC TGTAGTGCT TCAAGAGGTC 2760
 CACTGGTTGG ATCTCTAGCT ACTGGCCTCT AAATACAACC CTTCCTTACA AAAAAAAA 2820
 AAAAAAAA

15 SEQ ID NO:261 PBQ1 Protein sequence:
 PBQ1 Protein sequence: NP_056457

20 MTERIHSINL HNFNSVLET LNEQRNRGHF CDVTVRIHGS MLRAHRCVLA AGSFFQDKL 60
 LLGYSDIEP SVVSVQSVQK LIDFMYSGVL RVQSSEALQI LTAASILQIK TVIDECTRIV 120
 SQNVGDVFPQ IQDSGQDTPR GTPESGTSQ SSDTESGYLQ SHPQHSVDRI YSALYACSMQ 180
 NGSGRSFYS GAVVSHHETA LGLPRDHME DPSWIRIHE RSQQMERYLS TIPETIHCCK 240
 QPRFVRIQTL VGNHIKQEM EDDYDYYGQQ RVQILERNES EECTEDTDQA EGTESEPKGE 300
 SFDGVSSSI GTEPDSVEQQ FGPGAARDSQ AEPTQPEQAA EAPAEGGPQT NQLETGASSP 360
 25 ERSNEVEMDS TVITVNSSD KSVLQQPSVN TSIGQPLFST QLYLRQTEIL TSNLRMLTIL 420
 TSNTQVIGTA GNTYLPALFT TQPAGSGFKP FLFSLPQLA GQQTQFVTVS QPGLSTFTAQ 480
 LPAPQLASS AGHSTASGQG EKKPYBCTLC NKTFTAKQNY VKHMFVHTGE KPHQCSICWR 540
 SPSLKDYLK HMVTHTGVR A YQCSICNKRK TQKSSLNVMH RLHRGEKSYE CYICKKKFSH 600
 KTLLEHVAL HSAANGTTPA GTPPGARAGP PGVVACTEGT TYVCSVCPAK FDQIEQFNDH 660
 30 MRMHVSDG

35 SEQ ID NO:262 PBQ8 DNA sequence
 Nucleic Acid Accession#: A1654187
 Coding sequence: 1-612 (underlined sequence corresponds to start and stop codon)

1 11 21 31 41 51
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 40 ATGGTGAAG AGGAAACAGG CATACTTAC ATGGTGGCAG ACAAGGGACA CCTTCTACA 60
 AACTCTACCA CTCTGCGCC GTCTTTTCGA CCATATAAAA ACGACCTATG CGAAGTGGT 120
 CGGAAAACCT CCTCAGCATG TAAACGGAAG ATCAGGAGCA GATTGAAGA ATTACAAGT 180
 GAAATGTGTC CAGTCAGCAT GTCAGAGACA GACCACATAG CCTCTACTTC CTCTGATAAA 240
 AATGTGTGGA AAACACCTGA ATTAAAGGAA GACTCATGCA ACTTGTTTTC TGGCAATGAA 300
 AGCAGCAAT TAGAAAATGA GTCCAACTA TTGTCAITAA ACACGTATAA AACTTATGT 360
 45 CAACCTAATG AGCAZATAA TCGAATTGAA GCCCAGGAAA ATTATATTCC AGATCATGGT 420
 GGAGGTGAGG ATCTTGTGTC CAAACAGAC ACAGGCTCAG AAAATCTGTA ACAAATAGCT 480
 AATTTTCTTA TGGGAAATTT TGCTAAACAT ATTTCAAAAA CAAATGAAC AGAACAGAAA 540
 GTAACACAAA TATGGTGGTA ATTAAGGTCA TCTACATTC CAGAAATCAG TAATGAAAAG 600
 ACTTATTCAG AAGGCCCTTA TGATACAGAC TGCAACAAGA AATTTATTTC AAAAATAAAG 660
 50 AGCGTTTTCG CATCAGAGGA TTTGTGGGAA GAAATAGAAT CTGAGCTCTT ATCTACGGAG 720
 TTTGCAGAAC ATCGAGTACC AAATGGAATG AATAAGGGAG AACATGCATT AGTTCTGTTT 780
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 TTATATAGAT AA

55 SEQ ID NO:263 PBQ6 Protein sequence:
 Protein Accession #: NP_060170

60 MEPKEATGKE NMVTKKKNLA FLRSRLYMLE RRTDITVVE SVSGDHSGLT RRSQSDRTEY 60
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 VQPLRNKIKTD RLDVDSLFSN IESVHQISAK LLSLLEAATT DVEPAMQVIG EVFLQIKQPL 180
 EDIYKIYCYH HDEARSHLES YEKEELKEH LSHCIQSLK

65 SEQ ID NO:264 PB7 DNA sequence
 Nucleic Acid Accession#: NM_014323
 Coding sequence: 662-2725 (underlined sequence corresponds to start and stop codon)

70 1 11 21 31 41 51
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 CCTCAGGCT CCGGAGCCCG GCGCGCGCCA CCGCCCGCGT GCGCGCGCGC CCGCGCGCGC 120
 CTTCGCGCTC GCGTTTGTGT TCTTCGCTC GCGCGCGCGC GCGCGCGCTC GCGCTTTCGA 180
 75 GGGGAGCGAG GCGCGCGCGC CAGCGCGCGC GGGAAAAGCC GCGCGCGCGC GCGCGCGCTG 240
 CCGCGCGGAC CCTCTCTCT CCTCCCGCG TCGCGGTGCC CTCTTGGCT GCGCGCGCGC 300
 GCGCGCTGCG GCGCGCGGAG GAGGTTGCGA GCGCGGTTTG CAGGAGGCGC GCACCTCTTC 360
 GCTCGCGCAC CCGCCCGGAA GGTAGACCGG GAAGGGGAGG CCGCGCGCGC GAGAGGAGAG 420
 AGTGGCGCGA GGTACAGCGA GCGCGCGGCT TGGCTATGTG GGGGGTGGTG CACCCGCGAG 480
 80 TCTAGACAGT CTGATCCGGG CTGGGGGCGT GTACACTCGG CGCACCTGCG AGACTACAGA 540
 GCTTCGGGCC GGCACGTGTG GGGAGTGTGG ACACGTCTGC TCGCGCGCGC TTCTCGCTGC 600

5 TGAGGGGAAG GGAGGGGGCG GGCAGGTGCA CGCGCCGGGC TAGTGGGAGG GGGCGGCGGC 660
 CATGGAGCGG GTGAACGAGC CTTCGTGCGG CCGGTCTGGC TGCTACACAT ACCAGGTGAG 720
 CAGACACAGC ACAGAGATGC TGACAAACCT GAACCAAGCAG CGCAAAACAG CGGGCGCGCTT 780
 CTGCGACGTG CTCTTGCGGG TAGGCGACGA GAGCTTCCCA GCGCACCGCG CCGTGTCTGGC 840
 CGCTGCAGC GAGTACTTTG AGTCGGTGTG CAGCGCCAGT TTGGGCGAGG GGGAGCTGC 900
 GGACGGGGGT CCGGCTGATG TAGGGGGCGC GAGCGCAGCA CCAGGCGGCG GGGCGGGGG 960
 CAGCGGGGAG CTGGAGATGC ACACATATCAG CTCCAAGGTA TTTGGGGACA TTCTGGACTT 1020
 CGCTTACACT TCOCGATCG TGCTGCGCTT GGAGAGCTTT CCCGAACCTA TGACGGCGCGC 1080
 CAAGTTCCGT CTGATGAGGT CGGTATCGA GATCTGCCAG GAAGTCATCA AACAGTCCAA 1140
 10 CGTACAGATC CTGGTACCCC CTGCGCGCGC CGATATAATG CTCTTTGCGC CCGCTGGGAC 1200
 CTCGGACTTG GGCCTTCCCTT TGGACATGAC CAACGGGGCA GCCTTGGCAG CCAACAGCAA 1260
 TGGCATGTGC GGCAGCATGC AGCCAGAGGA GAGGCGAGCT CGGGCGGCTG GTGACGCCAT 1320
 TGCAGGCCAA GCTCTTTGCG CTGTGTATCC TGGGGTGGAG CGCTTGGCCA TGTGGGCTGG 1380
 15 ACCCTTATCC CCGCAACTGC TGACTTCCC ATTCGCCAGT GTGGCATCCA GTGCCCTCC 1440
 CCTGACTGGC AAGCAGGCGC GGGGCCGCCC AAGGAAGGCC AACCTGCTGG ACTCAATGTT 1500
 TGGGTCCCA GGGGGCGTGA GGGAGGCGAG CATCTTCCA TGCGGTCTAT GTGGTAAGGT 1560
 GTTCACTGAT GCCAAGCGCG TCCGGCAGCA CGAGGCGCAG CAGGTGTCA CAGCCCTCCA 1620
 GCTGGGCTAC ATCGACCTTC CTCTCCGAG GCTGGGTGAG AATGGGCTAC CCATCTCTGA 1680
 20 AGACCCGAGC GGGCCCGGAA AGAGGAGCCG GACCAGGAG CAGGTGGCTT GTGAGATCTG 1740
 CGGCAAGATC TTCCGTGATG TGTATCATCT TAACCGGCAC AAGCTGTCCC ACTCTGGGA 1800
 GAAGCCCTAC TCCTGCCCTG TGTGTGGGT CCGGTTCAAG AGAAAAGACC GCATGTCTTA 1860
 CCATGTGGCG TCCCATGATG GGTCCGTGGG CAAGCCTTAC ATCTGCCAGA GCTGTGGGAA 1920
 AGGCTTCTCC AGGCTGATC ACTTGAACGG ACATATCAAG CAGGTGCACA CTCTGAGCG 1980
 25 GCGTCACAA TGTACAGCTT GCAATGCTTC TTTTGCCACC CGAGACCGTC TGGCTTCCA 2040
 CCTGGCTGT CATGAAGACA AGGTGCCCTG CCAGGTGTGT GGGAGTACT TGGCGGCAGC 2100
 ATACATGGCA GACCACTGA AGAAGCACAG CGAGGGGCGC AGCAACTTCT GCATATCTG 2160
 TAAACGAGGT TTCTCTCTCT CCGCTACTT AAAGTCCAT GTTAAACCC ACCAGGTGT 2220
 TCCCTTCTCC CAGGTCTCCA GGCACCAAGG GGCATCTCT AATGGGGGAG CAGCGTTCOA 2280
 30 CTGGCGCAGG GGTCTACCTT TCTCTCTCA GCAGAACATG TCACATCAGG ATCCGATTGA 2340
 GAGCTCTGAC TCCTATGCTG ACCTCTCAGA TCCAGCGGAC CTGAAGACGC CAGAGAAGCA 2400
 GAGTGCCAAAT GGCCTTTTCT CCGTCCGACAT GGCAGTCCCC AAAACAAAA TGGAGTCTGA 2460
 TGGGGAGAG AAGTACCAT GGCCTGAATG TGGGAGCTTC TTCCGCTCTA AGTCTACTT 2520
 35 GAACAAACAC ATCCAGAGG TGCAATGCTG GGCCTCTGGG GGGCCCTGGG GGGACCTGGG 2580
 CCTGCGCAAT GGTCTTTTGA TCTCTCTCA GCAGAACATG TCTCTCTCG AGTCTTTGG 2640
 GTTTCAGATT GTTCAGTGGG CATTTGCTTC ATCTTTAGTA GATCCTGAGG TTGACCAGA 2700
 GCGCATGGGG CCTGAAGGGA AATGAGGCGG CTGCTGTGTC CCCACGGAAA CAACCATCTG 2760
 GGGACTGCTG GGAATGCTG TGAATGCGGA GGAAGTGTAT GTTTGGGTTT TGTAGCTGAG 2820
 AGATTTTAT TCAATTTTAA CTGCCCCCA ACCCACTCC AACTCTCTCT CCACCACTTA 2880
 40 TTCTGCCAAT GGTCTTTTGA AATAGATTTC CATCTGATAT TCTGCAGAAA TATCAATGAG 2940
 ACTTGGTATG GGCAGGGGCG AGAAACACT ACATAGGCGT CCAAGGCAAA ACCAGTCCCA 3000
 GTTCTTTTAA TGGGAAGAG CTGGAATTC TGGTGTCTAA TTCTTAGTGA CCGCAATCT 3060
 ATACCCAAAT CTATGATATT CTGGGACCTC AGTGATTTTG GTCCCCCTCC ACTTCTCTAG 3120
 TTCTGTATCC TCCTTTCCCA TATCTTTCAA AAGAACCACA CTAGGCTCTC CACCTACTTA 3180
 45 TACAATGCGG ATGCCCAACT GTTTTAAAG AAGCCAGAG CATCCCATGG ACCATGGGGT 3240
 GAGTGTCTTC CAAGAGCCCC CTGAGCTCAG CCGTCTGCTT GAGGGGCTCC AGACCTTTCT 3300
 GAGCCCTGCT TGGAGGCGAG CATTTTCACT GCTAGGACAA GCTCAGCTGT TGAAGACACC 3360
 CCCACCCGAA ATTTAGTATT TTACGTGATT TTAACCATTC AACATGCTGT TGGGTTTAA 3420
 TTCTCTAATT ATTATATTAT TTGTATTAT TTTTAGGAC CAGTTGTAGT GAATGCTAC 3480
 50 TGAAGCTAT CCGAGTGTAT ACAGGCTCT TTGTAAACCG CAGTCAACCA TTAGGGTTAG 3540
 TATTAAACTT TGTTTAGATG TACCATAATT AACTTGGCTA GTTGATTGTT TGAAGTCTAT 3600
 GGAAGAAATA GTTTTATGCA AAATTTTAAA AAATGCCAGT CTGGTCAGGG AAGTAGGGGG 3660
 TTTCAATGCT GTTGGGAACC AGGAAGGTGG GACAGCGCGC AGGTAGGGAC ATTGTGTACC 3720
 55 TCAGTTGTGT CACATGTGAG CAAGCCGAGG TTGACCTTGT GATGTGAATT GATCTGATCA 3780
 GACTGTATTA AAAATGTTAG TACATTACTC TA

SEQ ID NO:265 PRY7 Protein sequence:

Protein Accession #: NP_114439

60 MERVNDASCG PSGCYTYQVS RHSTEMLHNL NQQRKNGGRF CDVLLRVGDE SFPRAHRAVLA 60
 ACSEYFESVF SAQLGDGGAA DGGPADVGGTA AAPGGGAGG SRELEMHIS SKVFGDILDF 120
 AYTSRIVVRL ESFPELMTAA KFLLMRSVIE IQEVIKQSN VQILVPPARA DIMLFRPPGT 180
 SDLGFPLDMT NGAALAANSN GIAGSMQPEE EAARAAGAAI AGQASLPVLP GVDRLPMVAG 240
 65 PLSPQLLTSP FPSVASSAPP LTGKRGRGRP RKANLLDSMF GSPGGLREAG ILPCGLGCKV 300
 FTDANRLRQH EAQHGVTSLQ LGYIDLPPR LGENGLPISE DFDGFRKRSR TRKQVACEIC 360
 GKIFRDVYHL NRHKLSHSGE KPYSCPVCLG RFRKRDMSY HVRSHDGSVG KPYCQSCGK 420
 GFSRPDLHNG HIKQVHTSER PHKQCTCNAS FATRDRLSH LACHEDKVPQ QVCGKYLRAA 480
 YIMADHLKKHS EGPNSFCSIC NREGQKCSHQ DPIESSDSYG DLSADSLKT PEKQSANGSF 540
 70 SCDMAVPKNK MESDGEKKYP CPEGGFFRS KSYLNKHIQK VHVRLGGFL GDLGALGSP 600
 FSPQQNMSLL ESFGFQIVQS AFASSLVDFE VDQPFMGPEG K

SEQ ID NO:266 PRY9 DNA sequence

Nucleic Acid Accession #: NM_012429

Coding sequence: 174-1385 (underlined sequence corresponds to start and stop codon)

75 1 11 21 31 41 51
 | | | | |
 CCTACTCCG CCTCTCGGGA TCCTTTAAGA GCGGGGGCTT GGCTGCCAGC TCOCGCGGCC 60
 80 GGGCAAAAGG CTGGGACTTT ACTCCGGGTG GCGGCGAGGA CGAGTCTGTG CTCCATCAGC 120

	TGCGGCACCC	GCCGCCCTCC	GCCCCCAAA	CCCATCCCCG	GGGTGAGCC	ACGATGAGCG	180
	GCAGAGTCGG	CGATCTGAGC	CCCAGGCAGA	AGGAGGCATT	GGCCAAGTTT	CGGGAGAATG	240
	TCCAGGATGT	GCTGCCCGCC	CTGCCGAATC	CAGATGACTA	TTTCTCCTCG	CGTTGGCTCC	300
5	GAGCCAGAAG	CTTCGACCTG	CAGAAGTCGG	AGGCCATGCT	CCGGAAGCAT	GTGGAGTTCC	360
	GAAAGCAAAA	GGACATTTGAC	AACATCATTA	GCTGGCAGCC	TCCAGAGGTG	ATCCACACGT	420
	ATCTGTGAGG	GGGTATGTGT	GGCTATGACC	TGGATGGCTG	CCCAGTCTGG	TACGACATAA	480
	TTGGACCTCT	GGATGCAAG	GGTCTGCTGT	TCTCAGCTTC	CAACAGGAC	CTGCTGAGGA	540
	CCAAGATGCG	GGAGTGTGAG	CTGCTTCTGC	AAGAGTGTGC	CCACCAGACC	ACAAAGTTGG	600
10	GGAGGAAGGT	GGAGACCATC	ACCATAATTT	ATGACTGCGA	GGGGCTTGGC	CTCAAGCATC	660
	TCTGGAAAGC	TGCTGTGGAG	GCCTATGGAG	AGTTTCTCTG	CATGTTTGAG	GAAAATTATC	720
	CCGAAACACT	GAAGCGTCTT	TTTGTGTGTA	AAGCCCCCAA	ACTGTTTCTC	GTGGCCTATA	780
	ACCTCATCAA	ACCTCTCCTG	AGTGAGGACA	CTCCTAAGAA	GATCATGGTC	CTGGGAGCAA	840
	ATTGGAAGGA	GGTTTTACTG	AAACATATCA	GCCCTGACCA	GGTGCTGTG	GAGTATGGGG	900
15	GCACCATGAC	TGACCTTGAT	GGAAACCCCA	AGTGCAATC	CAAGATCAAC	TACGGGGGTG	960
	ACATCCCATG	GACATATTAC	GTGCGAGACC	AGGTGAAGCA	GCAGTATGAA	CACAGCGTGC	1020
	AGATTTCCTG	TGCTCTCTCC	CACCAAGTGG	AGTATGAGAT	CCTCTTCCCT	GGCTGTGTCC	1080
	TCAGGTGCTC	GTTTATGTGA	GATGGAGCGG	ATGTTGGTTT	TGGGATTTTC	CTGAAGACCA	1140
	AGATGGGAGA	GAGGCAGCGG	GCAGGGGAGA	TGACAGAGGT	GCTGCCCAAC	CAGAGGTACA	1200
20	ACTCCCACTT	GGTCCCTGAA	GATGGGACCC	TCACCTGCGA	TGATCTCTGG	ATCTATGTCC	1260
	TCTGGTTTGA	CAACACCTAC	AGCTTCAATC	ATGCCAAGAA	GGTCAATTTT	ACTGTGGAGG	1320
	TCTCTGCTCC	AGACAAAGCC	TCAGAAAGAGA	AGATGAAGCA	GCTGGGGGCA	GGCACCCCGA	1380
	AATAACACCT	TCTCTTATAG	CAGGCTGGC	CCCCTCAGTG	TCTCCCTGTC	AAITTTCTACC	1440
	CCTTGATGCA	GTCATTTTTC	CACAACCTTG	AAGCCCAAG	AAACTGGGCT	GGAGGACAGA	1500
25	CCTCAGGAGC	TTTCAATTTA	GTTAGGCAGA	GGAAGAGCGA	CTGCAGTGGG	TCTCCGTGTC	1560
	TATCAAAATC	TTAGCACTGA	CCCAGGAGCT	GGCTGGCCAT	CGTGATAGGA	TCTGTCTGTC	1620
	CTGTAAACTG	TGCCAACTTC	ACCTGTCCAG	GGACAGCGAA	GCTGGGGGTG	CGCGGGGGCA	1680
	TGTATCCAGC	GGTGCCAGCA	GGGAAAAAAA	TTAGAAAAAG	GTGAAGATT	GGGACTTAAC	1740
	ACTTCAGGGA	AGTCAGCTGC	CGGGGAGAAA	CTTGCTCCTA	AATGAACACA	TAAGTTTAGA	1800
30	TGCCAATGAG	GAGTAGCAGG	GTAGCTGGTT	GCTAGAGTTA	CGGTGGGGAT	CAGAACTCT	1860
	TCCAAACATT	CTAGCACTGT	GGCTGGGGTA	GCTTTTGGCT	TTTCCAGAGT	CTCAGGAGGT	1920
	GGCCTGAGTC	AGCACACATC	TTCCCACTCG	GTAGACAGGC	TGGCCTCTCC	CTCACTTTGA	1980
	GACTTTGGCA	ACTCTTGGGC	CACACGGCCT	GCCTCTTTGA	TTACTAATGA	TTGTCACTGA	2040
	CTCAGAGCTT	CCTGGGACTT	CGGGTACCCA	CCCCTGTGTC	TCCATGCAAA	CAAGCGCCA	2100
35	GGGAATGAC	CCACAGGAT	CGCAGCTGCA	GGGAGGGCCA	GGGAGGTTGG	GGGTGGGAGT	2160
	GAATGCTAAA	CTAGAGATCT	CCAGTGCCCT	TTTCAGTGCT	ACCGGCTCT	CACCAAGCAG	2220
	TCTCTCATGT	GAGCAACCCC	GAGACAAAAA	TGCTAAGTGG	GATCAAGAGA	GCAGCACTCG	2280
	GAGAGGGTGT	TTGCCAGTCT	GAGTGTCCCG	CGGTGCCCGC	CAACCCGCTT	CCTGACTGAC	2340
	CTGAGCAAGG	TCTTACTAAG	CAGTCCATC	TCTGTGGGAG	GCATGCAACG	CGTGCAAGGA	2400
40	GTTCAGGTGC	CGGTCCGGCT	AGCCAGGCCT	GGAGGCCCCC	CAGCAGGAG	GCGGCCAAAA	2460
	GGCGGGGGCG	GGGTCTCGCA	GACTAGGGGC	TGGGGGGGGC	CACAGACGGC	CTCGAAACCA	2520
	CAGCCCTTAC	CCCAATCCCA	CGAGCCCCGC	CAACGAACCA	CAGGTGCTGG	GCTTTAGAGA	2580
	ACATGGGAGG	CGGGCCCCAG	ACCTGGCGGG	AACGCCCTTC	CCTCAGAGCC	AGGCCCGGGC	2640
	CCCGTCTGGG	AAGCTCATCT	TGCGAAGCTG	AGGGAGCTCA	GGGCAAGGC	CAGGCTAGCG	2700
45	CGGACCGGAA	GGGGCCGAGG	CTGCACGGGC	CTCTGCCAGA	ACGCTCAGGA	CATCCCGGGC	2760
	TGGGTTTACA	ACGCTGTTAG	GAAAAATTAC	CAATGAATAA	AGCAACGTTT	AGTGCGCA	

SEQ ID NO:267 PBY9 Protein sequence:

Protein Accession #: NP_036561

50	MSGRVGDLSR	RQKEALAKFR	ENVQDVLPAL	FNPDYFLLR	WLRARSFDLQ	KSEAMLRKHV	60
	EFKQKQKIDN	HSWQPEVI	QYVLSGGMCG	YDLGCPVWY	DIHPLDAKG	LLFSASKQDL	120
	LRTKMRECEL	LLQECAHQTT	KLGRKVVETIT	IYDCEGLGL	KHLWKPAVEA	YGEFLCMFEE	180
55	NYPETLKRLE	VVKAPKLPV	AYNLKPFLLS	EDTRKKIMVL	GANWKEVLLK	HISPDQVPVE	240
	YGGTMDPDG	NPCKSKINY	GGDIPRKYV	RDQVQKQYEH	SVQISRGS	SHQVEYELFPG	300
	CVLRWQFMSD	GADVGFGLF	ETKMGERQRA	GEMTEVLFNQ	RYNSHLVED	GLTCSDFGI	360
	YVLRFDNTYS	FIHAKKNFT	VEVLLFDKAS	EEKMKQLGAG	TPK		

SEQ ID NO:268 PBY9 DNA sequence

Nucleic Acid Accession #: XM_009756

Coding sequence: 301-1440 (underlined sequence corresponds to start and stop codon)

65	1	11	21	31	41	51	
	GTGGGGACAG	CCGAGCCCGG	CCGGGCCCTT	GGACGGCGTC	GCCAAGGAGC	TGGGATCGCA	60
	CTTGCTGCAG	ACTTTGGATG	GATTTGTGTT	TGTGGTAGCA	TCTGATGGCA	AAATCATGTA	120
	TATATCCGAG	ACCGCTCTTG	TCCATTTAGG	CTTATCCCA	GTGGAGCTCA	CGGGCAACAG	180
70	TATTTATGAA	TACATCCATC	CTTCTGACCA	CGATGAGATG	ACCGCTGTCC	TCACGGCCCA	240
	CCAGCCGCTG	CACCAACACC	TGCTCCCAAG	TATGAGATAG	AGAGGTCTGT	CTTTCTTCGA	300
	ATGAATGTG	TCTTGGCGAA	AAGGAACGGG	GGCCTGACCT	GCAGCCGATA	CAAGGTTCATC	360
	CATGTCAGTG	GCTACTGTAA	GATCAGGCAG	TATATGCTGG	ACATGTCCTT	GTACGACTCC	420
	TGCTAACAGA	TTGTGGGGCT	GGTGGCCGTT	GGCCAGTCCG	TGCCACCCAG	TGCCATCACC	480
	GAGATCAAGC	TGTACAGTAA	CATGTTTCAT	TTACGGGCCA	GCTTTGACCT	GAAGCTGATA	540
75	TTCTGAGATT	CCAGGGTGC	CGAGGTGAGC	GGGTACGAGC	CGCAGGACCT	GATCGAGAAG	600
	ACCTATATCC	ATCAGCTGCA	CGGCTGCGAC	GTGTTCCACC	TCCGCTACGC	ACAACCACTC	660
	CTGTGGTGA	AGGGCCAGGT	CAACCAACAG	TACTACCGGC	TGCTGTCCAA	CGGGGGGGGC	720
	TGGGTGTGGG	TGCAGAGCTA	CGCCACCGTG	GTGCACACAA	CGCGCTCCCT	CGGGGCCAC	780
80	TGCATCGTGA	GTGTCAATTA	TGTACTCAGC	GAGATTGAAT	ACAAGGAAC	TCAGCTGTCC	840
	CTGGAGCAGG	TGTCCACTGC	CAAGTCCACG	GACTCTTGGG	GGACCCGCTT	GTCTACCTCA	900

5 CAAGAACTA GGAATTAGT GAAACCCAAA AATACCAAGA TGAAGACAAA GCTGAGAACA 960
 AACCCCTACC CCCACAGCA ATACAGCTCG TTCCAAATGG ACAAACTGGA ATGCGGCCAG 1020
 CTGCGAAACT GGAGAGCCAG TCCCCCTGCA AGCGCTGCTG CTCTCCAGA ACTGCAGCCC 1080
 CACTCAGAAA GCAGTGACCT TCTGTACAGG CCATCCTACA GCGTGCCCTT CTCTTACCAT 1140
 TACGGACACT TCCCTCTGGA CTCTCACGTC TTCAGCAGCA AAAAGCCCAAT GTTCCCGGCC 1200
 AAGTTCGGGG AGCCCCAAGG ATCCCTTGT GAGGTGGCAC GCTTTTCTCT GAGCACACTG 1260
 CCAGCCAGCG GTGAATGCCA GTGGCATTAT GCCAACCCCC TAGTGCTTAG CAGCTCCTCT 1320
 CCAGCTAAAA ATCCTCCAGA GCCACCGGCG AACACTGCTA GGCACAGCCT GGTGCCAAGC 1380
 TACGAAGGCA AGCAGATGTC CTCTGCGGAG ATACCGCCAG CTCCCCAGGA CGCAGACTGA 1440
 10 CTCTGTTTG CTGCTGGAC CAAC

SEQ ID NO:269 PBH8 Protein sequence:
 Protein Accession #: NP_005060

15 MKEKSKNAAK TRREKENGFE YELAKLLPLP SAITSQLDKA SIIRLTTSYL KMRAVFPEGL 60
 GDAWGQPSRA GFLDGVAKEL GSHLLQTLDG FVFVVASDGK IMYISETASV HLGLSQVELT 120
 GNSIYEYIHP SDHDEMIAVL TAHQPLHHHL LQYEIERSF FLRMKCVLAK RNAGLTCSGY 180
 20 KVIHCSGYLK IRQYMLDMSL YDSCYQIVGL VAVGQSLPPS AITEIKLYSN MFMFRASLDL 240
 KLIFLDSRVT EVTVPEPDL IEKILYHIVH GCDVFHLRYA HHILLVKGOV TTKYRLLSK 300
 RGGVWVWQSY ATVVHNSRSS RPHCIVSVNY VLTEIEYKEL QLSLEQVSTA KSQDSWRTAL 360
 STSQETRLV KFKNTKMKTK LRTNPYPFQQ YSSQMDKLE CGQLGNWRAS PPASAAAPPE 420
 LQPHSESSDL LYTPSYSLPF SYHYGHFPLD SHVFSKKKPM LPAKFGPQSG SPCEVARFFL 480
 25 STLPASGEQY WHYANLPVS SSSPAKNPPE PFANTARHSL VPSYEAFAAA VRRFEDTAP 540
 PSFSGHYR BEPALPKA ARQAARDGAR LALARAAPEC CAPTPEAPG APAQLFVLL 600
 NYHRLVLRG PLGGAAPAS GLACAPGGPE AATGALRLRH PSPAATSPFG APLPHYLGA 660
 VIITNGR

30 SEQ ID NO:270 PBH8 DNA sequence:
 Nucleic Acid Accession#: AA760894

GGCAGGAGGA GAAGATGTGG CTTGCTCATG CTTGACTTCT GCCATGGTTG TGAGGCCTCC 60
 35 CCAGCCATGT GGAACGTGTT TCAGGTGCTG GTTCCATGGC TCTTCTGAG CCGAAATAAA 120
 GGAAACTCCA TAGACCTTGT CCACTGGAAC TCGTTCCTAT CTACCTCCA CTCTATCCAG 180
 GGTGATGGAT CTCTGCAGTA AGTGAAGAG TTCTTCATGG CCCCCAAGT TATATCCATC 240
 TAGAACTTCA GCAGCTAATT TCATCTGGAA ATAGTGCTTT TGTGGATATA AGTTAGGTAA 300
 AACTGAAGAT GAGATCATAC TGGATTAGGA TGGGATCTAA ATCCAATGAA AATGTCTTCA 360
 40 TAAAAACAG GAAAGAACCC ATAGAAACAC AAGGAAGAAG GTCATGTGAA GATGGAGGCA 420
 GAGATTGGAG GGATGCAGCC ACCGGCCAG GAATGCCAGC AGCCACCCAG AAGCTGGAAG 480
 GAAATGAGGG ATTCTCTCTT AGAACCTTGA GAGAGRACAT GGTCTGTGTA ACAGCTTGAT 540
 TTTGGACTTG CCCATAGCTT GTATACCTTT ACTTTGGATA CAATTTTATC CAAACTTGGC 600
 TAAACAGTIT CTCAGCTAT GGAAATTTA AAATGGAGAA GATTCAACTC GATTTCTTCA 660
 45 GATTCAAGC AAGAAAAA TGGGAACATA GGAGGAGACC AAGAAAGCCT ATAAAAAGCA 720
 AAAATATGAA GTGAACATTG TGGTAGCTTT AAGATGTTA GTGTAGCTGC AGGCACCCTA 780
 TACACATGAA AACCCCCAAG GGGAAATCCC ATATCACAGT GTAGTGTGAT ATTGACATT 840
 YGTGATCATY TAGAGATGTA CAGAAAGGT GAATCTGTGT TCTGTATATT CTGCCTAAGG 900
 CAAAGAAATG TTTAGCTYTC TTTAAAAA TAG TTCCATAATT TTTTAAAA AGCTTTGCTT 960
 50 GAAACCTGTA AGCTTCCAT ATCTGGAGCA TTTCACCTTA AATATTGGA TAAATATGTT 1020
 ATCTTCTTAC TTGGACATTT CATGTGTTA GGGATTGTYT TYTAAATCT TCTAATTCA 1080
 TATAGCTGCT AACACTCCC GCAGAGCTAA ACCATTACG ANTATGAAAT AAAGACCCTA 1140
 TTGATTTGAA CTAAAAAAA AAAAMAMAAA AAAAAAAAAA AAAAAAAAT GA

55 SEQ ID NO:271 PBQ4 DNA sequence
 Nucleic Acid Accession#: AA148578
 Coding sequence: 1-1363 (underlined sequence corresponds to start and stop codon)

1 11 21 31 41 51
 60 ATGGAATCAA TCTCTATGAT GGAAGCCCT AAGAGCCTTA GTGAACTTGT TTTACCTAAT 60
 GGCATAAATG GTATCAAAGA TGCAAGGAAG GTCACGTGAG GTGTGATTGG AAGTGAGAT 120
 TTTGCCAAAT CCTTGACCAT TCGACTTATT AGATGCGGCT ATCATGTGGT CATAGGAAGT 180
 AGAAATCCTA AGTTTGCTTC TGAATTTTTT CCTCATGTGG TAGATGTCAC TCATCATGAA 240
 65 GATGCTCTCA CAAAGACAAA TATAATATTT GTTGCTATAC ACAGAGAACA TTATACCTCC 300
 CTGTGGGACC TGAGACATCT GCTTGTGGGT AAAATCCTGA TTGATGTGAG CAATAACATG 360
 AGGATAAACC AGTACCCAGA ATCCAAATGCT GAATATTTGG CTTCATTTAT CCCAGATTCT 420
 TTGATTGTCA AAGGATTTAA TGTGTCTCA GCTTGGGCAC TTCAGTTAGG ACCTAAGGAT 480
 GCCAGCCGCG AGGTTTATAT ATGCAGCAAC AATATTCAG CCGACACAAC GGTATTTGAA 540
 70 CTGTCCCGCC AGTTGAATTT CATTCOCATT GACTTGGGAT CCTTATCATC AGCCAGAGAG 600
 ATTGAAATTT TACCCTACG ACTCTTTACT CTCTGGAGAG GGCCAGTGGT GGTAGCTATA 660
 AGCTTGCCCA CATTTTTTTT CTTTTATTCC TTTGTCAGAG ATGTGATTCA TCCATATGCT 720
 AGAAACCAAC AGAGTGACTT TTACAAAATT CCTATAGAGA TTGTGAATAA AACCTTACCT 780
 ATAGTTGCCA TTAATTGCT CTCCCTAGTA TACCTGCGAG GTCTTCTGGC AGCTGCTTAT 840
 75 CAACTTTATT ACGGACCAAA GTATAGGAGA TTTCCACCTT GGTGGAAAC CTGGTTACAG 900
 TGTAGAAAC AGCTTGAAT ACTAAGTTTT TTCTTGGCTA TGGTCCATGT TGCTTACAGC 960
 CTCTGCTTAC CGATGAGAAG GTCAGAGAGA TATTTGTTTC TCAACTGGC TTATCAGCAG 1020
 GTTCATGCAA ATATTGAAA CTCTTGGAAAT GAGGAAGAAG TTTGAGAAAT TGAATGTAT 1080
 ATCTCTTTC GCATAATGAG CCTTGGCTTA CTTTCCCTCC TGGCAGTCAC TTCTATCCCT 1140
 TCAGTGAGCA ATGCTTTAAA CTGGAGAGAA TTCAGTTTTA TTCAGTCTAC ACTTGGATAT 1200

GTCGCTCTGC TCATAAGTAC TTTCATGTT TTAATTEATG GATGGAAACG AGCTTTTGAG 1260
 GAAGAGTACT ACAGATTGTA TACACCACCA AACTTTGTTT TGTCTCTTGT TTTGCCCTCA 1320
 ATTGTAATTC TGGATCTTTT GCAGCTTTGC AGATACCCAG ACTGA

5 SEQ ID NO:272 PBQ4 Protein sequence:
 Protein Accession #: none

10 1 11 21 31 41 51
 MESISMGGSP KSLSETCLFN GINGIKDARK VTGVVIGSGD FAKSLTIRLI RCGYHVIGS 60
 RNPKFASFPF PHVVDVTHHE DALTKTNIIF VAIHREHYTS LMDLRHLLVG KILIDVSNM 120
 RINQYFESNA EYLASLPFDS LIVKGFNVVS AMALQLGPKD ASRQVYICSN NIQARQQVIE 180
 LARQLNFIPI DLGSLSSARE IENLPLRLFT LWRGPFVVVAI SLATFFFLYS FVRDVIHPYA 240
 RNQGSDFYKI PIEIVNKTLP IVAITLLSLV YLAGLLAAAY QLYYGTQYRR FPPWLETWLQ 300
 CRKQLGLLSF PFMVHVAVS LCLFMRRSER YLPLRMAYQQ VHAHENSNN EEEVWRIEM 360
 ISFGIMSLGL LSLAVTSIP SVSNALNWRB FSPFIQSTLGY VALLISTFHV LIYGWKRAFE 420
 BEYYRYFTPP NFVLALVLPV IVIDLLQLC RYPD

20 SEQ ID NO:273 PBQ5 DNA SEQUENCE
 Nucleic Acid Accession#: NM_001973
 Coding sequence: 150-1445 (underlined sequence corresponds to start and stop codon)

25 1 11 21 31 41 51
 CCGCCGCGCTT CTACTCCGCC GCGGGGGTCC CAGCGGCTGC CGCGCCGTCC TCGAGTTTCC 60
 AGCGTGAGGA GGAGGCTGAG GCGGAGAGGG CGCATCGTGT TCGAGGCGGA GACCGAGGGG 120
 GAGCCGCCCG CGCGGCGTCC CTCAATGCTA TCGACAGTGC TATCACCCCTG TGGCAGTTCC 180
 TTCTTCAGCT CCTGCGAAGG CCTCAGAACA AGCACATGAT CTGTTGGACC TCTAATGATG 240
 GGCAGTTTAA GCTTTTTCAG GCAGAGAGGG TGGCTCGTCT CTGGGGGATT CGCAAGAACA 300
 AGCCTAAGCAT GAATTATGAC AAACCTCAGCC GAGCCCTCAG ATACTATTAT GTAAAGAATA 360
 TCATCAAAAA AGTGAATGCT CAGAAGTTTG TGTACAAGTT TGTCTCTTAT CCAGAGATTT 420
 TGAACATGGA TCCAAATGCA GTGGGCAGGA TTGAGGGTGA CTGTGAAAGT TTAACCTTCA 480
 GTGAAGTCAG CAGCAGTTCC AAAGATGTGG AGAATGGAGG GAAAGATAAA CCACCTCAGC 540
 CTGGTGCCAA GACCTCTAGC CGCAATGACT ACATACACTC TGGCTTATAT TCTTCATTAA 600
 CTCTCAACTC TTGTAACTCC TCCAATGTAA AGCTTTTCAA ATTGATAAAG ACTGAGAATC 660
 CAGCCGAGAA ACTGGCAGAG AAAAATCTCT CTCAGGAGCC CACACCATCT GTCATCAAT 720
 TTGTCAACAG ACCTTCCAAA AAGCCACCAG TTGAACCTGT TGCTGCCACC ATTTCAATTG 780
 GCCCAGTAT TTCTCCATCT TCAGAAGAAA CTATCCAAGC TTGGAGACA TTGGTTTCCC 840
 CAAAACCTGC TTCCCTGGAA GCCCAACCT CTGCTCTTAA CGTAATGACT GCTTTTGCCA 900
 CCACACCAAC CATTTCTGCC ATACCCCTTT TGCAGGAACC TCCAGAACCA CCTTCACCAC 960
 CACTGAGTTC TCACCCAGAG ATCGACACAG ACATTGATTC AGTGGCTTCT CAGCCAATGG 1020
 AACTTCCAGA GAATTGTCT CTGGAGCCTA AAGACCAGGA TTCACTCTTG CTAGAAAAGG 1080
 ACAAAATGAA TAAATTCATCA AGATCCAAGA AACCCAAAGG GTTAGGACTG GCACCCACCC 1140
 TTGTGATCAC GAGCAGTGAT CCAAGCCAC TGGGAATACT GAGCCCATCT CTCCCTACAG 1200
 CTCTCTTAC ACCAGCATT TTTCACAGA CACCCATCAT ACTGACTCCA AGCCCTTGC 1260
 TCTCCAGTAT CCATCTTGG AGTACTCTCA GTCTGTGTG TCCCTAAGT CCAGCCAGAC 1320
 TGCAAGGTGC TAACACACT TTCCAGTTTC CTCTGTACT GAACAGTCAT GGGCCATTCA 1380
 CTCTGTCTGG GCTGGATGGA CCTTCCACCC CTGGCCCAT TTCCCCAGAC CTACAGAAGA 1440
 CATTAACCTAT GCATCTGTGG AATGAGAGAA CCGAGGAACG AAGAAGCAGA CATTCAACAT 1500
 GATTGCATTG GAAATGAGCA ATTGATAGTT CTACAATGCT GATAATAGAC TATTGTGATT 1560
 TTTGCCATTG CCAATGAAA ACATCTTTT AGGATCTCT TGAATAGGA CTCAGTTGG 1620
 ACTATATGTA TAAAAATGCC TTAATTGGAG TCTAACTCC ACCTCCCTCT GTCTTTTCT 1680
 TTTCTTTTTC TTTCCTTCT TCTTTTCTT TCTCTTTTA AAAATATTT GAGCTTTGTG 1740
 CTGAAGAAGT TTTTGTGGG CTTTGTGAC TGTGCTTGC AAAAGCAAT AAGAACAAG 1800
 TTAATCTCTC TGGCTATTGG GACCTTTGG CCAGGAAAAA TTAATGCTTAG AATCTATTAT 1860
 TTAAGAAGT ATTTGTGAAA TGAACAAAAA AAAAAAAA AAAAAAAA AAAAAAAA 1920
 AAAAAAAA AAA

60 SEQ ID NO:274 PBQ5 Protein sequence:
 Protein Accession #: NP_001984

65 MDSAITLWQF LLQLLQKPQN KHMICWTSND GQFKLLQAE VRLWGIRKN KPNMNYDKLS 60
 RALRYYYVKN IKKVNGQKF VYKFVSYPEI LNMDPMTVGR IEGDCESLNF SEVSSSSKDV 120
 ENGGKDEPPQ PGAKTSSRND YHSGLYSSP TLNSLNSSNV KLFKLIKTN PAEKLAEEKS 180
 PQEPTPSVIK FVTTPSKPP VEPVAATSI GPSISPSSE TQALETLS PKLPSLEAPT 240
 SASNVMTAFA TPTPISSIP LQEPPTSP PLSSHPOIDT DIDSVASQPM ELPENISLEP 300
 KDQDSVLEK DKVNNSSRSK KPKGGLAPT LVITSSDFSP LGILSPSLPT ASLTPAFSQ 360
 TPILLTPSL LSSHFWSL SPVAPLSPAR LQGANTLFQF PSVLNSHGPF TLGSLDGPST 420
 PGFPFDLQK T

75 SEQ ID NO:275 PBQ5 DNA SEQUENCE
 Nucleic Acid Accession#: AB040621
 Coding sequence: 131-2560 (underlined sequence corresponds to start and stop codon)

1 11 21 31 41 51

	AATCAGGAAC	AGATCATATA	TTGACCGAGA	TTCTGAGTAT	CTCTTGCAAG	AAAAAGAAC	60
	AGATGGAACT	TTAGACCAAA	AATTATTGGA	AGATTACAA	AAGAAAAAA	ATGACCTTCG	120
	GTATATTGAA	ATGCAAGCATT	TCAGAGAAAA	GCTGCCCTCG	TATGGAATGC	AAAAGGAATT	180
5	GGTAAATTTA	ATTGATAAACC	ATCAGGTAAC	AGTAATAAGT	GGTGAAACTG	GTGTGGCAA	240
	AACCACTCAA	GTTACTCAGT	TCATTTTGGG	TAACATACAT	GAAGAGAGAA	AAGGATCTGC	300
	TTGCAGAAAT	GTTTGTACTC	AGCCAAGAAG	AATTAGTGCC	ATTTAGTTTG	CGGAAAGAGT	360
	AGCTGCAGAA	AGGGCAGAA	CTTGTGGCAG	TGGTAATAGT	ACTGGATATC	AAATTCGTCT	420
	CCAGAGTCGG	TTGCCAAGGA	AACAGGGTTC	TATCTTATAC	TGTACAACAG	GAATCATCCT	480
10	TCAGTGGCTC	CAGTCAGACC	CGTATTTGTC	CAGTGTATGT	CATATCGTAC	TTGATGAAAT	540
	CCATGAAAGA	AATCTGCAGT	CAGATGTTTT	AATGACTGTT	GTTAAAGACC	TTCTCAATTT	600
	TCGATCTGAC	TTGAAAGTAA	TATTGATGAG	TGCAACATTC	AATGCAGAAA	AGTTTTTCAGA	660
	ATATTTTGGT	AATGTCCTAA	TGATACATAT	ACCTGGTTTT	ACCTTTCCGG	TTGTGGAATA	720
	TCCTTTTGGAA	GATGTAATTT	AAAAAATAAG	GTATGTTCCA	GAACAAAAAG	AACACAGATC	780
	CCAGTTTAAAG	AGGGGTTTCA	TGCAAGGGCA	TGTAAATAGA	CAAGAAAAAG	AAGAAAAAGA	840
15	AGCAATAAT	AATGCAACGT	GGCCAGATTA	TGTAAGGGAA	CTCGCAAGAA	GGTATTCCTG	900
	AAGTACTGTA	GATGTTATAG	AAATGATGGA	GGATGATAAA	GTTGATCTGA	ATTGATTGTT	960
	TGOCCTCATC	CGATACATTG	TTTTGGAAGA	AGAGGATGGT	CGGACTCTGG	TCTTCTTGCC	1020
	AGGCTGGGAC	AATATCAGCA	CTTTACATGA	TCTCTTATAG	TCACAGTAA	TGTTTAAATC	1080
20	AGATAAATTT	TTAATATATC	CTTTACATTC	ACTGATGCTT	ACAGTTAAAC	AGACACAGGT	1140
	GTTTAAAGAA	ACCCCTCCTG	GTTGTCGGA	AATAGTAATT	GCTACCAACA	TTGCGGAGAC	1200
	TAGCATTTACC	ATAGATGATG	TCGTTTATGT	GATAGATGGA	GGAAAAATAA	AAGAGACGCA	1260
	TTTTGATACT	CAGAACAATA	TCAGTACAAT	GTCCGCTGAG	TGGGTTAGTA	AAGCTAATGC	1320
	CAAAACAGAA	AAAGGTCGAG	CTGGAAGAGT	TCAACCTGGT	CATTGCTATC	ATCTGTATAA	1380
25	TGGTCTTAA	GCAAGTCTTC	TAGATGACTA	TCAACTGCCA	GAATTTTGA	GAACCTCTTT	1440
	GGAAGAACTT	TGTTTACAAA	TAAAGATTTT	AAGGCTAGGT	GGAATGCTTT	ATTTTCTGAG	1500
	TAGATTAAAT	GACCCACCAT	CAATGAGGOC	AGTGTTACTC	TCCATAAGAC	ACCTGATGGA	1560
	GCTGAACGCT	TTGGATAAAC	AAGAAGAAAT	GACACCTCTT	GGAGTCCACT	TGGCACGATT	1620
	ACCCGTTGAG	CCATCATATT	GAAAAATGAT	TCTTTTGGGA	GCACTGTCTT	GCTGCTTAGA	1680
30	CCAGTACTCT	ACTATTGCTG	CTAGTCTCAG	TTTCAAAGAT	CCATTGTGCA	TTCCACTGGG	1740
	AAAAGAAAG	ATTGCAAGAT	CAAGAAGAAA	GGAATTGGCA	AAGGATCTA	GAAGTATCTA	1800
	CTTAAACATT	GTGAATGCGT	TTGAGGGCTG	GGAAGAGGCT	AGGCGACGTG	GTTTCAGATA	1860
	CGAAAAGGAC	TATTGCTGGG	AATATTTTCT	GTCTTCAAAC	ACACTGCAGA	TGCTGCATAA	1920
	CATGAAGAGA	CAGTTTGTCT	AGCATCTTCT	TGGAGCTGGA	TTTGTAAAGCA	GTAGAAATCC	1980
35	TAAAGATCCA	GAATCTAATA	TAAATTCAGA	TAATGAGAAG	ATAATTAAG	CTGTCTCTG	2040
	TGCTGGAATTT	TATCCCAAG	TTGCTAAAT	TCGACTAAAT	TTGGTAAATA	AAAGAAAAAT	2100
	GGTAAAGATT	TACACAAAA	CCGATGGCCT	GGTGTCTGTT	CATCTAAAT	CTGTTAATGT	2160
	GGAGCAAAAC	GACTTTCACT	ACAACCTGGT	TATCTATCAC	CTAAGATGA	GAACAAGCAG	2220
40	TATATACTTG	TATGACTGCA	CAGAGGTTTC	CCCATACTGT	CTCTTGTGTT	TTGGAGGTGA	2280
	CATTTCCTCA	CAGAAGGATA	ACGATCAGGA	AACTATTGCT	GTAGATGAGT	GGATTGTATT	2340
	TCAGTCTCCA	AACAATTTTC	CCCATCTTGT	TAAGGAATTA	AGAAAGGATA	TAGATATTCT	2400
	TCTGCAAGAG	AAGATTGAAA	GTCCTCATCC	TGTAGACTGG	AATGACACTA	AATCCAGAGA	2460
	CTGTGCAGTA	CTGTGACGTA	TTATAGACTT	GATCAAAACA	CAGGAAAGG	CAACTCCAG	2520
	GAACCTTTCCG	CCAGATTTCC	AGGATGGATA	TTACAGCTGA	CAGCTTTTCA	GGGGTGGTCT	2580
45	GAAGAGCCAG	TTTGACAGCC	ATTCTTCACT	ATTGTTTAAA	TTTTGGCTGG	ATGCCAAACC	2640
	CTGGGACATG	AACAATTTTC	ATGTTTAAGG	TAGAAGCCTT	CAGTAGGTAG	TAAAGACTTA	2700
	ATGTGCATGA	CTTGATGTTA	TATGTAGAGA	TATATATATA	TATATATATA	CCATATAAGC	2760
	AATATGTTCT	CTGATCATAT	ACTCTGCTGT	GOTCATGCC	ACTCTTTGGG	AGTATATTC	2820
	CTTATGATAT	ATTAGATATT	GTACCACTTG	AGAAATTCCT	TTGTTCTGTT	ATACAAAAAT	2880
50	AATCTTTCTG	CTCATATATG	TTGATGATAC	CACCACTAAA	AATAGGATGT	TTACCCCAAA	2940
	ACAAGTGTCA	ATTAAGAAAT	TGAACACAAC	CACATTTTTT	AAAAAGAAC	TTCTATCGGA	3000
	AGTAATATTA	TTTGTGTGAA	TAAAGTCCAG	TATTTAATAA	AATGTACAA	GTTAAATCTC	

SEQ ID NO:276 PBYS Protein sequence:

Protein Accession #: BAA96012

55	IRNRSYIDRD	SEYLLQENEF	DGTLDDQKLE	DLQKKNDLR	YIEMQHREK	LPSYGMQKEL	60
	VNLIDNHQVT	VISQETGCGK	TTQVTQFILD	NYIERGKGS	CRIVCTQPRR	ISAISSAERV	120
	AAERAESCGS	GNSTGYQIRL	QSRLPRKQGS	ILYCTTGHL	QWLQSDPYLS	SVSHIVLDEI	180
60	HERNLQSDVL	MTVVKDLNLF	RSDLKVLMS	ATLNAEKFS	YFGNCPMIH	PGFTFFVVEY	240
	LLEDVIEKIR	YVPEQKEHRS	QFKRGFMQGH	VNRQKEEKE	AIYKERWPDY	VRELRRYSA	300
	STVDVIEEME	DDKVDNLNIV	ALIRYVLEB	EDGAILVFLP	GWDNISTLHD	LLMSQVMFKS	360
	DKFLIPLHS	LMPTVNQTVQ	FKRTPPGVRK	IVATINAEI	SITIDVVVYV	IDGGKIKETH	420
	FDTONNISM	SAEWSKANA	KQRKGRAGRV	QPGHCYHLN	GLRASLDDY	QLPELRITPL	480
65	EELCLQIKIL	RLGGLAYFLS	RLMDPPSNEA	VLLSIRHLMS	LNALDKQEL	TPLGVHLARL	540
	PVEPHIGKMI	LFGALFCCLD	PVLTAASLS	FKDPPVPLG	KEKIDARRK	ELAKDTRSDH	600
	LTVVNAFEGW	EBARRRGFRY	EKDYCWEIFL	SSNTLQMLHN	MKGQFAEHL	GAGFVSSRNP	660
	KDPESNINS	NEKIKA VIC	AGLYPKVAKI	RLNLGKKRKM	VKVYTKTDGL	VAVHPKSVNV	720
	EQDIFHYNWL	IYHLKMRSTS	IYLYDCTEVS	PYCLLFFGGD	ISIQKNDND	TIADVEWTVF	780
70	QSPARIAHLV	KELRKELDIL	LQEKIESPHP	VDWNDTKSRD	CAVLSAIDL	IKTQEKATFR	840
	NFFRFQDGY	YS					

SEQ ID NO:277 PBYS DNA SEQUENCE

75	Nucleic Acid Accession#: AA464018
	Coding sequence: 64-1669(underlined sequence corresponds to start and stop codon)

GATTTTATCC TGGAACATTA CAGTGAAGAT GGCTATTTAT ATGAAGATGA AATTGCAGAT 60
 CTTATGATC TGAGACAAGC TTGTGGAGC CCTAGCCGG ATGAGGCCGG GTTGGAACTG 120

5 CTGATGACAT ACTTCATCCA GCTGGGCTTT GTGAGAGATC GATTCTTCCC GCCACACGG 180
 CAGATGGGAC TCTGTTCAC CTGGTATGAC TCTCTCACCG GGGTTCGGT CAGCCAGCAG 240
 AACCTGCTGC TGGAGAAGGC CAGTGTCTGT TTCAACACTG GGGCCCTCTA CACCCAGATT 300
 GGGACCCGGT GTGATGGGCA GACGCAGGCT GGGCTGGAGA GTGCCATAGA TGCCCTTCAG 360
 10 AGAGCCGAG GGGTTTTAAA TTAOCTGAAA GACACATTA CCCTACTOC AAGTTACGAC 420
 ATGAGCCCTG CCATGCTCAG CGTGCTCGTC AAAATGATGC TTGCACAAGC CCAAGAAAGC 480
 GTGTTGAGA AAATCAGCCT TCTGGGATC CGGAATGAAT TCTTCATGCT GGTGAAGGTG 540
 GCTCAGGAGG CTGCTAAGGT GGGAGAGGTC TACCAACAGC TACACGCAGC CATGAGCCAG 600
 GCGCCGGTGA AAGAGAACAT CCOCTACTOC TGGGCCAGCT TAGCCTGCGT GAAGGCCAC 660
 CACTAOCGGG CCOCTGGCCA CTACTCACT GCCATCTOC TCATOGACA CCAGGTGAAG 720
 CCAGGCACGG ATCTGGACCA CCAGGAGAAG TGCCTGTCC AGCTCTACGA CCACATGCCA 780
 GAGGGGCTGA CACCTTTGGC CACTCTAAG AATGATCAGC AGCGCCGACA GCTGGGGAAG 840
 TOCCACTTGC CAGAGCCAT GGCTCATCAC GAGGAGTCGG TGGGGAGGC CAGCCTCTGC 900
 15 AAGAAGCTGC GGAGCATTGA GGTGCTACAG AAGGTGCTGT GTGCCGACA GGAACGCTOC 960
 CGGCTCAGT ACGCCAGCA CCAGGAGGAG GATGACCTGC TGAACCTGAT CGACGCCGCC 1020
 AGTGTGTTG CTAAAACTGA GCAAGAGGTT GACATTATAT TGCCCAAGTT CTCCAAGCTG 1080
 ACAGTCACGG ACTTCTTCCA GAAGCTGGGC CCCTTATCTG TGTTTTCCGC TAACAAGCGG 1140
 TGGACGCTC CTGAGAGCCAT CCGCTTCACT GCAGAAGAAG GGGACTTGGG GTTCACTTGT 1200
 20 AGAGGGAACG CCCCCTTCA GGTTCACITC CTGATCTCT ACTGCTCTGC CTGCTGGCA 1260
 GGAGCCCGGG AAGGAGATTA TATTGTCTCC ATTCAGCTTG TGGATTGTAA GTGGCTGAGC 1320
 CTGAGTGAGG TTATGAAGCT GCTGAAGAGC TTTGGCGAGG ACGAGATCGA GATGAAAGTC 1380
 GTGAGCCTCC TGGACTCCAC ATCATCCATG CATAATAAGA GTGCCACATA CTCCGTGGGA 1440
 ATGCAAAAAA CGTACTCCAT GATCTGCTTA GCACTTGATG ATGACGACAA AACTGATAAA 1500
 25 ACCAAGAAAA TTCTCAAGAA GCTTTCCTTC CTGAGTTGGG GCACCAACAA GAACAGACAG 1560
 AAGTCAGCCA GCACCTTGTG CTOCCATCG GTGCGGGCTG CACGGCCTCA GTCAAGAAG 1620
 AAGCTGCCCT CCOCTTTCAG CTTCTCAAC TCAGACAGTT CTGGTACTAA

30 SEQ ID NO:278 PB8 Protein sequence
 Protein Accession #: NP_149094

35 DFILEHYSED GYLVEDEIAD LMDLRQACRT PSRDEAGVEL LMTYFIQLGF VESRFFPPTR 60
 QMGLLFVYD SLTGVFVSQ NLLEKASVL FNTGALYQI GTRCDRQQA GLESAIDARQ 120
 RAAGVINYLK DFTHTPSYD MSPAMLSVLV KMMLAQAES VFEKISLPGI RNEFFMLVKV 180
 40 AQEAAKGVGV YQQLHAAMSQ APVKENIPYS WASLACVKAH HYAALAHYFT ALLIDHQVK 240
 YGDLHDHQEK CLSOLYDHMP EGLTFLATLK NDQRRQLGK SHLRRAHAH EESVREASLC 300
 KKLSEVQLQ KVLCAAQERS RLTYAQHQUE DDLNLIDAP SVVAKTEQEV DILPQFSKL 360
 TVIDFQKLQ PLVSFSANKR WTPRSIRFT AEEGDLGFTL RGNAPVQVHF LDPYCSASVA 420
 45 GAREGDYVS IQLVDCRWLT LSEVMKLLKS FGEDEIEMKV VSLLDSTSSM HNSATYSVG 480
 MQKTSYMICL AIDDDDKTDK TKKISKLSF LSWGINKNRQ KSASTCLPS VGAARPQVK 540
 KLPSPFSLN SDSSWY

45 SEQ ID NO:279 PB8 DNA SEQUENCE
 Nucleic Acid Accession#: AF107493
 Coding sequence: 125-656 (underlined sequence corresponds to start and stop codon)

50 1 11 21 31 41 51
 GAATTCGGCA CGAGCCTTGT TGGAGGTTCT GGGGCGCAGA ACCGCTACTG CTGCTTCGGT 60
 CTCTCCCTGG GAAAAATAA AATTGGAACC TTTTGGAGCT GTGTGCTAAA TCTTCAGTGG 120
 GACATGGGTT TCAGACAAA GAGTGAGTAG AACAGAGCGT AGTGGAGAT ACGGTTCCAT 180
 CATAGACAGG GATGACCGTG ATGAGCGTGA ATCCCGAAGC AGGCGGAGGG ACTCAGATTA 240
 55 CAAAAGATCT AGTGATGATC GGAGGGGTGA TAGATATGAT GACTACCGAG ACTATGACAG 300
 TCAGAGAGAG GAGCGTGAAG GAAGGAACAG TGACCGATCC GAAGATGGCT ACCATTACAG 360
 TGGTGACTAT GGTGAGCAGC ACTATAGGCA TGACATCAGT GACGAGAGGG AGAGCAAGAC 420
 CATCATGCTG CGCGGCCCTC CCATCACCAT CACAGAGAGC GATATTGAGG AATGATGGA 480
 GTCTTTCGAA GGCCTTCAGC CTGCGGATGT GAGGCTGATG AAGAGGAAAA CAGGTGAGAG 540
 60 CTTGCTTAGT TCTGATATT ATTGTTCTCT TCCCATTTCC CACCTCAGTC CCTAAGAAC 600
 ATCTGATTC CCGCAGTCTT CAAGCACATG AATTCAGAA GAAAGGTTTG CCATGGCTAA 660
 GGAATGTGAC TCTTTGAAAA CCATGTTAGC ATCTGAGGAA CTTTTTTAAA CTTTGTTTTA 720
 GGGACTTTT TTTCTTAGG TAAGTAATGA TTTATAAACT CTTTTTTTTT TTTGACTATA 780
 GTCGGTTGCA TGGTACTTTT AAGCGTGGAA TCAATGGAG TGGCATTAG TTCAGGCGGC 840
 65 TTGTCTCTTG CCATGGCAAA GTATCAAGAA GATCCCAAG TCAAGTCACA TTTGTAAGC 900
 TGCTTCCCAA TTGGCTTTGT CACGCAGTGT TGAAGCAGTG GGAGAGAGAT TCACCTGTTA 960
 TAAAGGAAGT GACTAACACA AGTATCCCGT CTATATCTGA ATGCTGTCTC TAGGTGTAAG 1020
 CCGTGTGTTT GCCTTCGTGG AGTTTATCA CTGCAAGAT GCTACCAGCT GGAATGGAAG 1080
 CAATCAGGTT GCTTCACTCA CCAAGTCTAG ATATTCATGA AAATGGAACA AGTCTGTACA 1140
 70 ATTTTAAAAA AAGGTTGAAG GAGTGGTTTG TTCCAAAGGA GTGACTTTTT TTTAAAAAAA 1200
 AAGCTTTGTA TATATTAAAA TTGATGTTAC TAGAATAAGT ACAGTACCAA GGACTTCATT 1260
 ATAGAAATTT TCTGCTCTTT AAACATGGCT ACCTACCTGG CAGGGCTTTG TTAAGTACTG 1320
 AATACCTGTC TGTATATCAC TAAACATCT TTAGTGTTC CTTTTTTCTA GTTGTGTATA 1380
 75 TTCTATTAT GTCCATTGAG AGTAAGCTTA GTATATCAAA CTCCTCATTT GACAGTGAAG 1440
 AGAACATAGT GAAAGTCTGT GCGGCATTT TTATAAGTAA TTCTTTATTT CTGCTGTAAG 1500
 ACCACAAAGC CTCTCGGAGG CGTAACCTGT CAGACCGGTC TTCAGGGAAT ATTTAAGGAC 1560
 TTAGTGAATG TTAGTGAACA TAAGTCTGAT GAGATTAGCC TGGGAGTGGT GTCTCCGAGC 1620
 TGCTTAATCT AGAGTGGCAT TAACATTCTA ATCTOCTTGA GAATGCCTTT TATAGTCTGT 1680
 TCAAGCAAG TCATTGATGG TTCTTCGAGG TAGTGTAAAC TGAAGTGTTC TTCAGTTTGT 1740
 CAGATAATG TTCAGTGCTT GGCACCTAAA TAACATTTTT TGCAAGAACT CCAAGGCACA 1800

5 TTATTGAATG CCTTTAACCA AGTGCATTCT GGGAAAGTTG CTTGACTCAT TATCTTGCTT 1860
 TTCTGCAGCA TTCTGTGATT TGAGTCATCC ATGAATCCAT GAATAAAAGT TACATTCTTT 1920
 GATTGGTAAT ATTGCCATTT ATACCAAGAC TCACTAATGA GGGTATCACT TTGACTGACT 1980
 GATTGTGTAA AGTTTTTAAAG CCTCTCATTT TCCTAACCCA GAAATCACAG CCTGATTTTA 2040
 10 TTAAGAGTAG AGCTTTCATTC ATTTCATACC ATAGATACCA TCCTAGTAAA TCCAGAACAT 2100
 ATACAGGTTT CATGTGAGTC TGCTTTCTTG ACATGATAGC ATTGTTTGAT GCAGTGGATA 2160
 TGTCAGAATG ACTAACCTAG GAGTTTGAAG CTCTTAAGAA ACTAAAACCT GTAAGACATT 2220
 TAAAGTGCTC CACAATTTTA ATGTATACAA AGCTATGTTA CTGTGTAAAC CATTCAGATT 2280
 CAAATTCACCT CCAAGAAATAA AAGGCCAGTA GGATTAGGGA CTCACTGGTA GTTTGGAGTC 2340
 15 TCCAGCACCA CATCCCTCCT AGTGGGATGA TCTATTACCA TATCTCCAG CTTTTTTATT 2400
 TTGCTCTCTG TATATCAGAG TGAGTGGATG GCGCTTCAGC TTTTCTCTCT CTGCGCAGAC 2460
 ATGCAGTCTT GCGTTTAGAT ATGCGCAGAG CAAAATTCAC AGCATGTCTT AAATCTTCCA 2520
 GGATTTCGAA GAACCAAAAT GCTCAACAGT ATGTATGTTT AGAGGGGTTA GACTCTCTTT 2580
 TAAATCTGG ATATCTAAC ACCTACTTAA ATCTGTTTGA TAGTGTCAAA CCACCCCCAC 2640
 CCTTGATCCT CCCACCCCA AAAAAAAAA AAAA

SEQ ID NO:280 PBV8 Protein sequence
 Protein Accession #: XP_003261

MGSDKRVSR ERSRGYSII DRDDRDERES RSRRRSDYK RSSDDRRGDR YDDYRDYDSP 60
 ERERERRNSD RSEDGYHSDG DYGEHDYRHD ISDERESKTI MLRGLPTTIT ESDIREMMES 120
 FEGPQPADVR LMKRKTGESL LSS

SEQ ID NO:281 PC12 DNA SEQUENCE

Nucleic Acid Accession#: AF208281
 Coding sequence: 109-3705 (underlined sequence corresponds to start and stop codon)

30 1 11 21 31 41 51
 CGGCCGCTTT TTTCTCAAGA TGGCAGATTC CCACTGAGGC TGAGGGGGCC GAGCTGGGCG 60
 GCGCGGTTC CTCTCCCGTT GGCATGAACC GCGGACACCC CGGCCCCGAT GGCCCCCGTG 120
 35 TACGAAGGTA TGGCCTCACA TGTGCAAGTT TTCTCCCTCC ACACCTCTCA ATCAAGTGCC 180
 TTCTGTATGT TGAAGAAATC AAAAGTAGAG CCAAGTTCCA ACTGGGACAT GACTGGGTAC 240
 GGCTCCACCA GCAAGGTGTA CAGCCAGAGC AAGAACATAC CACCTTCTCA GCCAGCCTCC 300
 ACACCGGTCA GCACCTCTCT GCGCGTCCCA AACCCAAAGCC TACCTTACGA GCAGACCATC 360
 GTCTTCCAG GAAGCAACGG GCACATCGTG GTCACTCAG CAAGCAGCAC TTCTGTACCC 420
 40 GGGCAAGTCC TCGCGGAGC ACACAACCTA ATGCGTGGAA GCACTGTGAG CCTCTTGAT 480
 AACTACCAA AATGTGGACT CAAGCGTAAG AGCGAGGAGA TCGAGAACAC AAGCAGCGTG 540
 CAGATCATCG AGGAGCATCC ACCCATGATT CAGAATAATG CAAGCGGGGC CACTGTCCGC 600
 ACTGCCACCA CGTCTACTGC CACCTCCAAA AACAGCGGCT CCAACAGCGA GGGCGACTAT 660
 CAGCTGGTGC AGCATGAGGT GCTGTGCTCC ATGAACAACT CCTACGAGGT CTTAGAGTTC 720
 45 TTGGGCGGAG GGAAGTTTGG ACAAGTGGTC AAGTGTGGAA AACGGGGCAC CAATGAGATC 780
 GTAGCCATGA AGATCTCTGA GAACCGCCCA TCCTATGCCC GACAAGGTCA GATTGAAGTG 840
 AGCATCTGG CCCGGTTGAG CACGGAGAGT GCCGATGACT ATAACTTCTG CCGGGCCTAC 900
 GAATGCTTCC AGCACAAGAA CCACAGTGC TTGGTCTTCG AGATGTTGGA GCAGAACCCT 960
 TATGACTTTC TGAAGCAAAA CAAATTTAGC CCGTTGCCCC TCAATATACAT TCGCCAGATT 1020
 50 CTCCAGCAGG TAGCCACAGC CTTGATGAAA CTCAAAAGCC TAGGCTCTAT CCACGCTGAC 1080
 CTCAAAACCA AATACATCAT GCTGGTGGAT CCATCTAGAC AACCATACAG AGTCAAGGTC 1140
 ATGCACTTTG GTTCAGCCAG CCACGCTCTC AAGGCTGTGT GCTCCACCTA CTTGCACTCC 1200
 AGATATTACA GGGCCCTCGA GATCATCCTT GPTTTACCAT TTTGTGAGGC AATTGACATG 1260
 TGCTGCTTGG GCTGTGTTAT TGCAGAAATG TTCTGGGTTT GGCCGTTATA TCCAGGAGCT 1320
 55 TCGGAGTATG ATCAGATTGT GTATATTICA CAAACACAGG GTTGTGCTGC TGAATATTTA 1380
 TTAAGCGCGC GGACAAAGAC AACTAGGTTT TTCAACCGTG ACACGGACTC ACCATATCCT 1440
 TTGTGGAGAC TGAAGACACC AGATGACCAT GAAGCAGAGA CAGGSATTAA GTCAAAGAA 1500
 GCAAGAAAGT ACATTTTCAA CTGTTTAGAT GATATGGCCC AGGTGAACAT GACGACAGAT 1560
 TTGGAAGGGA GCGACATGTT GGTAGAAAAG GCTGACCGGC GGGAGTTTAT TGACCTGTTG 1620
 60 AAGAAGATGC TGACCATTGA TGCTGACAG AGAATCACTC CAATCGAACC CCTGAACCAT 1680
 CCTTGTGCA CCAATGACACA CTTACTCGAT TTTCCCCACA GCACACAGCT CAAATCATGT 1740
 TTCCAGAAAC TGAGATCTGT CAAGCGTCCG GTGAATATGT ATGACACGGT GAACAGAGC 1800
 AAAACCCCTT TCATCAACCA CGTGGCCCCC AGCACGTCCA CCAACCTGAC CATGAOCTTT 1860
 AACACCCAGC TGACCACTGT CCACAACCA GCTCCCTCCT CTACCACTGC CACTATTTC 1920
 65 TTAGCCAATC CCGAAGTCTC CATACTAAAC TACCATCTA CACTCTACCA GCGCTCAGCG 1980
 GCATCCATGG CTGCACTGGC CCAGCGGAGC ATGCCCTGTC AGACAGGAAC AGCCAGATT 2040
 TGTGCCCGGC CTGACCGCTT CCAGCAAGCT CTCTGTGTGT GTCCCCCGG CTTCCAGGC 2100
 TTGCAAGCCT CTCCCTCTAA GCACGCTGGC TACTCGGTGC GAATGAAAAA TGCAGTTCC 2160
 ATGCTCACTC AAGCCCAAGG AGCTCAGCCT CTTCAGATCC AACCAAGTCT GCTTGCCAG 2220
 70 CAGGCTTGGC CAAAGTGGAC CCAGCAGATC CTGCTTCCCG CAGCATGGCA GCAACTGACT 2280
 GGAGTGGCCA CCACACATC AGTGCAGCAT GCCACCGTGA TTCCCGAGAC CATGGCAGC 2340
 ACCAGCAGC TGGCGGACTG GAGAAATACG CATGCTCAGC GAAGCCATTA TAATCCATC 2400
 ATGCAAGCAG CTGCACTATT GACCGGTCAT GTGACCTTC CAGCAGCACA GCGCTTAAAT 2460
 TGGGTGTGG GCGCATGTAT GCGGCAGCAG CCAACAGCA CCACCTCTC CCGAAGAGT 2520
 75 AAGCAGACCC AATCATCTGT GAGAAATGTC TOCACTGTG AGGTGTCTCT CTCTCAGGCC 2580
 ATCAGCTCCC CACAGCGATC CAAGCGTGTG AAGGAGAACA CACCTCCCG CTGTGCCATG 2640
 GTGCACAGTA GCGCGCCTG CAGCACTCG GTCACTGTG GGTGGGGCGA CGTGGCCTC 2700
 AGCACCACCC GGAAGGGCA GCGGCAGACA ATGTCTATT CCGACACTCC CAGCCCCAG 2760
 TCAAGCTCA TCACCATCAG CAGTGACAG GACGAGGAGG AGGAACAGAA ACACGCCCC 2820
 80 ACCAGCACTG TCTCCAAGCA AAGAAAAAC GTCATCAGCT GTGTCAAGT CCACGACTCC 2880
 CCTACTCCG ACTCTCCAG CAACACCAG CCTACTCCG TGCAGCAGC TGCTGGGCAC 2940

5 AACAAATGCCA ATGCGCTTTGA CACCAAGGGG AGCCTGGAGA ATCACTGCAC GGGGAACCCC 3000
CGAACCATCA TCGTGCACCC CCGTGAACAC CAGGCCAGCG AAGTATTTGGT GGAGTGTGAT 3060
AGCCTGGTGC CAGTCAACAC CAGTCACCAC TCGTCTCTCT ACAAGTCCAA GTCCTCCAGC 3120
AACGTGACCT CCACCAGCGG TCACCTCTCA GGGAGCTCAT CTGGAGCCAT CACCTACCGG 3180
CAGCAGCGCG CGGGCCCCCA CTTCACAGCAG CAGCAGCCAC TCAATCTCAG CCAGGCTCAG 3240
CAGCACAATCA CCACGGACCG CACTGGGAGC CACCGAAGGC AGCAGGCCA CATCACTCCC 3300
ACCATGGCCC AGGCTCCGTA CTCCTTCCCG CACAACAGCC CCAGCCACGG CACTGTGCAC 3360
CCGCATCTGG CTGCAGCCCG TGCCGCTGCC CACCTCCCCA CCCAGCCCA CCTCTACACC 3420
TACACTGCGC CGGCGGCCCT GGGCTCCACC GGCACCGTGG CCCACCTGGT GGCGCTGCAA 3480
GGCTCTGCGC GCCACACCGT GCAGCACACT GCCTACCCAG CCAGCATCGT CCACCCAGTC 3540
CCCGTAGGCA TGGGCCCCCG GGTCTCTGCC TCGCCACCA TCACCCCGAG TCAGTATCCA 3600
GCCCAATTTC CCACACAGAC CTACATCAGC GCCTCGCCAG CCTCCACCGT CTACACTGGA 3660
TACCCACTGA GCCCGGCCAA GGTCAACAG TACCTTACA TATAAACACT GGAGGGGAGG 3720
GAGGAGGGA GGGAGGGAGA GAATGGCCCG AGGGAGGAGG GAGAGAAAGG GGGAGGCGCT 3780
15 CCTGGGAGG GGGGCGCTGG CCTTTTATAC TGAAGATGCC GCACACAAC AATGCAAAAC 3840
GGGCAGGGC GGGGGGGGGG GGGGCAGAGG GCAGGGGGAC GGGTCGGGAC ACCAGTAAA 3900
CTTGAACCGG GAAGTGGGAG GACGTAGAGC AGAGAAGAGA ACATTTTAA AAGGAAGGGA 3960
TTAAGAGGG TGGGAATCT ATGGTTTTTA TTTTAAAAA

20 SEQ ID NO:282 PCT2 Protein sequence:
Protein Accession #: NP_073577

25 MAPVYEGMAS HVQVSPHIL QSSAFCSVKK LKVEPSSNWD MTGYGSHSKV YSQSKNIPPS 60
QPASTTVSTS LPVNPSPSLPY EQTIVFPGST GHIVVTSASS TSVTGQVLGG PHNLMRRSTV 120
SLLDITYQKCG LKRSKEEEN TSSVQIEEH PPMIQNNASG ATVATATST ATSKNSGNS 180
EGDYQLVQHE VLCSMTNTYE VLEFLOROTF GQVVKCWKRG TNEIVAAIL KNRPSYARQG 240
QIEVSLARL STESADDYFN VRA YECFQHK NHTCLVFEML HQNLYDFLKQ NKFSPLPKY 300
30 RPYVLOQVAT ALMKLKSGL IHADLPENI MLVDPSPQPY RVKVIDFGSA SHVSKAVCST 360
YLQSRYYRAP EILGLPFCE AIDMWSLGCV IAEFLGWPL YPGAseyDQI RYISQTQGLP 420
AEYLLSAGTK TTRFRNRD TD SPYPLWRLKT PDDHEAETGI KSKEARKYIF NCLDDMAQVN 480
MTTDLGSDM LVEKADREF IDLLKKMLTI DADKRITPIE TLNHPFVMT HLLDFPHSTH 540
VKSCFQNM EI CKRRVNMVDY VNQSKTPIET HVAPSTSTNL TMIFNNQLIT VHNQAPSTTS 600
35 ATISLANPEV SILNYSTLY QPSAASMAA V AQRSMPLQTG TAQICARPD PQQALIVCFP 660
GFQGLQASPS KHAGYSVRME NAVPIVTPAQ GAQPLQIQPG LLAQQA WPSG TQQLLPFAW 720
QQLTGVAITH SVQHATVIFE TMAGTQQLAD WRNTHAGSH YNPIMQFAL LTGHVTLPA 780
QPLNVGVAHV MRQOPTSTTS SRKSKQHQS VNRVSTCEVS SSQALSSPQR SKRYKENTFP 840
RCAMVHSSPA CSTSVTCGWG DVASSTTRER QRQITVIFDT PSPTVSVITI SSDTDEEEQ 900
40 KHAPSTVSK QRKNVISCVT VHDSPYSDSS SNTSPYSVQO RAGHNNANAF DTKGSLNHC 960
TGNRTYVAP PLKTLQASEVL VECDSLVPVN TSHSSSYKS KSSNVSTTS GHSSGSSGA 1020
ITYRQORPFG HROQQQPLNL SQAQQHITD RTGSHRRQQA YTIPTMAQAP YSFFHNSPSH 1080
GTVHPHLLAA AAAAHLPTQP HLYTYTAPAA LGSTGTVAHL VASQGSARHT VQHTAYPASI 1140
VHQVPSMGP RVLPSPTIHP SQYPAQFAHQ TYISASPAST VYTGYLSPA KYNQYPI

45 SEQ ID NO:283 PB1 DNA SEQUENCE
Nucleic Acid Accession#: NM_017700
Coding sequence: 147-806 (underlined sequence corresponds to start and stop codon)

50 1 11 21 31 41 51
AGTCACAGCC AGGTAACCCCT GGAGTGAAGC GGTTTAGTTA GAAGGGAGCA GATAAACTCG 60
TCACTCTAGT AGCTTTAACC CTCACCCCTGA GGCACCTTAG CAATCAGCCA TTGCTGCAA 120
GCTTCAAAAG CTGTCTTTTG CCTAATATGG AGCCCAAAAGA AGCCACTGGG AAAGAAAACA 180
TGGTCAACCA GAAAAAGAT CTGGCCCTCT TGAGGTCTAG ACTCTATATG CTGGAGAGAA 240
55 GGAAGACTGA CACTGTGCTT GAGAGCAGTG TTTCTGGGGA CCACCTGGCC ACCTTGAGGA 300
GGAGCCAATC TGACAGGACC GAATACAACC AGAAATTACA AGAAAGATG ACTCCACAGG 360
GTGAGTGTC TGTAGCTGAG ACCTTAACCC CAGAGGAAGA GCATCATATG AAGAGGATGA 420
TGGCAAGAGC GGAAGAGATC ATTAAGGAGC TGATACAGAC AGAAAGGAT TATCTCAATG 480
60 ATCTAGAGCT GTGTGTAGG GAAGTGGTTC AGCCCTGAG AAATAAAAG ACTGATAGGC 540
TGGATGTGGA TAGCTGTGTT AGCAACATTC AGTCCGTGCA TCAGATATCA GCCAAGCTGC 600
TGTCTGTGTT GGAAGAGGCC ACAACAGAGC TGGAAACCGC CATGCAAGTA ATTGGAGAAG 660
TATCTTGCA GATTAAAGGG CCACTGGAAG ATATTTATAA AATCTACTGC TATCACCATG 720
ATGAAGCACA TAGTATACTG GAGTCCCTATG AAAAGGAAGA AGAGCTGAAG GAACATTTGA 780
65 GCCACTGTAT CAGTCTCTTA AAGTAAGGCC TTTTCAAAATG ATGATCCCA TCTCCTCTCA 840
GTTGCCCTAGC AGGGAACATC TTAATGGAT GTAGATGAAA GGTCTCACAT AAATCCTATG 900
TTTATGAGA CTGTCTGGGA GCTCTGCTTT GCATTCCTTT TATAAAAGC TGACATGCCA 960
GAAGCCCTGA TTGACTTTTT TTCCCTCTGC GAGAATGACT AAAAATAACA TGGAGAAGA 1020
TTTAGAGCTC TGCAGCGATT GAAAAATGCA ATATCAAAAT ATAAATGTG GAAGAAAAGC 1080
70 CTCTTCTTAA AGCTATTTGA ACTTGCTGG CCCACAGTAG TTCAAGGAT ATGTGAGATA 1140
ACACGTGGCC CCATGACCAT TGGAGCACAT GGGTTAATGG AGTTAGGGGA ATGGCTTACA 1200
ACTCTGCATG GCCCTCTTCT TTCCCAAAAC TCACTGTGGG GAGATGGGG AAGACAAGTC 1260
AGGCCTTGT AAAGTTAGTT TCAGAACAA TACTCATGCC TTCTTTCTC ATCCCTAAA 1320
CATGTGTGG GAGCTACAC AATGTACTTT TCTTTTCTTA GAGGAAGTAT CTATTCACTG 1380
75 TGAATACTCT AAAAAATATA CAAAGTATGT GTAAGATAA AACCCCTTGC TATTTCAAA 1440
AAAAAAAAA AAAAAAAAAA AAAA

80 SEQ ID NO:284 PB1 Protein sequence:
Protein Accession #: NP_060170

1 11 21 31 41 51

MEPKKATGKE NMVTKKKNL FLRSRLYMLE RRTDTTVVES SVSGDHSGLT RRSQSDRTEY 60
NQKLQEKMTD QGECSSVAETL TPEEKHEMKR MMAKREKIK ELIQTEKDYI NDLELCVREV 120
VQPLRNKRTD RLDVDSLPSN IESVHQISAK LLSLEEAAT DVEPAMQVIG EVFLQIKGFL 180
5 EDIYKIYCYH HDEAHSILES YEKEELKEH LSHCIQSLK

SEQ ID NO:285 PBQ9 DNA SEQUENCE

Nucleic Acid Accession#: X66534

Coding sequence: 523-2676 (underlined sequence corresponds to start and stop codon)

1 11 21 31 41 51
15 CCCTTATGCG GATTGGGGCG CTGCAGAGAC CAGGACTCAG TTCCCTTGCC CTAGTCTGAG 60
CCTAGTGGGT GGGACTCAGC TCAGAGTCAG TTTTCAGAA CAGGTTTCAG TTGCAGAGTT 120
TTCTTACACT TTCTCTGGCG TAGAGCAGCG AGCAGCCTGG AACAGACCCA GGGGAGGAC 180
AOCCTGTGGG GAGGAGAGCG CTGGAGGAGC TTAGAGACCC CAGCCGGGCG TGATCTCACC 240
20 ATGTGCGGAT TTGCGAGCGC CGCCCTGGAG CTGCTAGAGA TCCGGAAGCA CAGCCCGGAG 300
GTGTGGGAAG CCACCAAGAC TCGGCTCTT GGAGAAAGCG TGAGCAGGGG GCCACCGCGG 360
TCTCCGGCCT GTCTGCACCC TGTGCGCTGA GCTGCTGAC AGTGACAATG ACATCCAGT 420
TACCAGTGTG CTTGATTTGA TAGTGGCTTC TGTGTGTCAG TCTCATATAA GAATCAGAGC 480
TCATCAGGAG GAGATCGCAG CAGGGTAAGA GACACCAACA CCATGTTCTG CACGAAGCTC 540
25 AAGGATCTCA AGATCAGAGG AGAGTGTCTT TCTCTCTTAC TGGCACCAGG TCAAGTTCTT 600
AAGGATCTCT CAGAGGAGGC AGCAGGAAGC TCAGAGAGCT GCAAGCAAC CGTGGCCATC 660
TGTCAAGACA TTCTTGAGAA GAACATACAA GAAAGTCTTC CTCGAAGAAA AACCAGTCCG 720
AGCCGAGTCT ATCTTCACAC TTTGGCAGAG AGTATTGTGA AACTGATTTT CCCAGAGTTT 780
GAACGGCTGA ATGTTGCTCT TCAGAGAACA TTGGCAAAAG ACAGAAATAAA AGAAGCAGG 840
30 AAATCTTTGG AAAGAGAAGA CTTTGAAAAA ACAATGTGAG AGCAAGCAGT GCAGCAGAGT 900
CCAGTGGAGT TATCAAGAAG TCTCTTGGTG AAGAGGTTT TAAAAATATG TACGAGGAAG 960
ATGAAACATC CCTTGGGGTG GTTGAGGCA CCCTTAAAGA TTTTAAACA GCTTCAATAC 1020
CCTTCTGAAA CAGAGCAGCC ATTGCCAAGA AGCAGGAAAA AGGGGCGAGT TGAGGACGCC 1080
TCCATCTCAT GCGCTGATAA GGAGGATGAT TTTCTACATG TTTACTACTT CTTCCTTAAG 1140
35 AGAACCACCT CCCTGATCTT TCCCGGCATC ATAAAGGCGC CTGCTCACGT ATTATATGAA 1200
ACGGAAGTGG AAGTGTCTGT AATGCTCCG TGCTTCCATA ATGATTGCAG CGAGTTTGTG 1260
AATCAGCCCT ACTTGTGTGA CTCCGTTTAC ATGAAAAGCA CCAAGCCATC CTTGTCCCCC 1320
AGCAAAACCC AGTCTCTGCT GGTGATTCCT ACATCGCTAT TCTGCAAGAC ATTTCCATTC 1380
CATTTCTATG TTGACAAAGA TATGACAATT CTGCAATTTG GCAATGGCAT CAGAAGGCTG 1440
40 ATGAACAGGA GAGACTTTCA AGGAAAGCCT AATTTGAAAT ACTTTGAAAT TCTGACTCCA 1500
AAAATCAAGC ATGCGCTTAG CGGATCATG ACTATGTTGA ATATGCAATT TGTGTACGA 1560
GTGAGGAGAT GGGACAACCT TGTGAAGAAA TCTTCAAGGG TATGCACTT CAAAGGCCAA 1620
ATGATCTACA TTGTTGAATC CAGTGCAATC TTGTTTTTGG GGTCAACCTG TGTGGACAGA 1680
TTAGAAGATT TTACAGGACG AGGGCTCTAC CTCTCAGACA TCCCAATTCA CAATGCACCTG 1740
45 AGGGATGTGG TCTTAATAGG GGAACAAGCC CGAGCTCAAG ATGGCCTGAA GAAGAGGCTG 1800
GGGAAGCTGA AGGCTACCTT TGAGCAAGCC CACCAAGCCC TGGAGGAGGA GAGAAAAAG 1860
ACAGTAGACC TTCTGTGCTC CATATTCTCC TGTGAGGTTG CTGAGCAGCT GTGGCAAGGG 1920
CAAGTTGTGC AAGCCAAGAA GTTCAGTAAT GTCCACATGC TCTTCTCAGA CATCGTTGGG 1980
TTCAGTCCCA TCTGCTCCCA GTGCTCACC GTGCAAGTCA TCACCATGCT CAATGCACCTG 2040
50 TACACTCCCT TGACACAGCA GTGTGGAGAG CTGGATGTCT ACAAGGTGGA GACCATTTGG 2100
ATGCTTATGT TGTGCTTTGG GGGATTACAC AAAGAGAGTG ATACTCATG TGTTCAGATA 2160
GCGCTGATGG CCCTGAAGAT GATGGAGCTC TCTGATGAAG TTATGTCTCC CCATGGAGAA 2220
CCTATCAAGA TGGGAATGG ACTGCACCTT GGTACAGTTT TTGCTGGCGT CCGTTGAGTT 2280
AAAATGCCCC GTTACTGTCT TTTTGGAAAC AATGTCACCT TGCTAAACAA ATTTGAGTCC 2340
TGCAGTGTAC CAGGAAAAAT CAATGTCAGC CCAACAACCT ACAGATTACT CAAAGACTGT 2400
55 CTTGTTTGG TGTTTACCCC TCGATCAAGG GAGGAACCTC CACCAAACTT CCCTAGTGAA 2460
ATCCCGGAAA TCTGCCATTT TCTGGATGCT TACCAACAAG GAACAACTC AAAACCATGC 2520
TTCCAAAAGA AAGATGTGGA AGATGCAAGC CAATTTTTTA GGCAAAGCAT CAGGAATAGA 2580
TTAGCAACCT ATATACCTAT TTATAAGTCT TTGGGGTTTG ACTCATTGAA GATGTGTAGA 2640
60 GCGCTGAAA GCATTTTAGG GATTGTAGAT GGCATAAAG CAGTATTAAA ATTTGAGGAG 2700
CCAAGTCACA ATCTTTCTCC TGTTTAACAT GACAAAAATG ACTCACTTCA GTACTTCAGC 2760
TCTTCAAGAA AAAAAAATAA ACCTTAAAAA GCTACTTTTG TGGGAGTATT TCTATTATAT 2820
AACCAGCACT TACTACCTGT ACTCAAAATT CAGCACCTTG TACATATATC AGATAATTGT 2880
AGTCAATTGT ACAAACTGAT GGAGTCACCT GCAATCTCAT ATCTGGTGG AATGCCATGG 2940
65 TATTAAAGT GTGTTGTGA TAGTTGCTGT CAAAAAATAA AAAAAAATAA AAAAAAATAA 3000
AAAA

SEQ ID NO:286 PBQ9 Protein sequence

Protein Accession #: Q02108

1 11 21 31 41 51
70 MPCTKLKDLK ITGECFPLL APQGVNESS EBAAGSSESC KATVPICQDI FERNIQESLP 60
QRKTSRSRVY LFTLAESICK LIPFEFERLN VALQRTLAKE KIKESRKSLE REDFERTIAR 120
75 QAVAAAGVPVE VIKESLGEIV FKICYEEDEN ILGVVGGLTK DFLNSPSTLL KQSSHCQAG 180
KRGRLEDASI LCLDKEDDFL HVYFFPERKT TSLILPGILK AAHVLYETE VEVSLMPFPC 240
HNDCESEFVNQ PYLLYSVEMK STKPSLSPSK POSSLVPTS LFCRTFFEFH MFDKMTILQ 300
FGNGIRRLMN RRDPPQKPNP EHYFELLTFK INQTFSGIM MLRMQPVVRV RMDNSVKKK 360
SRVMDLKGQM IYIVRESSAL FLGSPCVDR L EDFTGRGLYL SDIPIHNAIR DVLVIGDAR 420
80 AQDGLKKRLG KLEATLEQAH QALEEKKKT VDLCSIFPC EVAQQLWQGO VVQAKFENV 480
THLFSDIIVG TAICSCQSFL QWITMLNLY TRFDQCCGEL DVYKVTIGD AYCVAAGLEK 540

ESDTHAVQIA LMALKMELS DEVMSPEGEP IKRIGLHSG SVFAGVGVK MPRYCLFGNN 600
 VTLANKFESC SVPRKINVSP TTYRLKDCP GFVFTFRSRE ELFPNFPSEI PGICHPDAY. 660
 QQGTNSKPCF QKQDVEDGNA NPLGKASGID

5

SEQ ID NO:287 PFD2 DNA SEQUENCE

Nucleic Acid Accession#: NM_000720

Coding sequence: 119-6664 (underlined sequence corresponds to start and stop codon)

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1	11	21	31	41	51	
AGAATAAGGG	CAGGGACCGC	GGCTCCTATC	TCTTGGTGAT	CCCTTCCCCC	ATTCCGCCCC	60
CGCCTCAACG	CCCAGCACAG	TGCCCTGCAC	ACAGTAGTCG	CTCAATAAAT	GTTCGTGGAT	120
GATGATGATG	ATGATGATGA	AAAAAATGCA	GCATCAACGG	CAGCAGCAAG	CGGACCACGC	180
GAACGAGGCA	AACTATGCAA	GAGGCACCAG	ACTTCTCTTT	TCTGGTGAAG	GACCAACTTC	240
TCAGCCGAAT	AGCTCCAAGC	AAACTGTCTT	GTCTTGGCAA	GCTGCAATCG	ATGCTGCTAG	300
ACAGGCCAAG	GCTGOCACAA	CTATGAGCAC	CTCTGCACCC	CCACCTGTAG	GATCTCTCTC	360
CCAAAGAAAA	CGTCAGCAAT	AGCCCAAGAG	CAAAAAACAG	GGTAACCTGT	CCAACAGCCG	420
ACCTGCCCGC	GCCTTTTCTT	GTTTATCACT	CAATAACCCC	ATCCGAAGAG	CCTGCATTAG	480
TATAGTGGAA	TGGAACCATC	TTGACATATT	TATATTATTG	GCTATTTTTG	CCAATTGTGT	540
GGCCTTAGCT	ATTACATCCC	CATTCCCTGA	AGATGATTCT	AATTCACAA	ATCATAACTT	600
GGAAAAAGTA	GAATATGCCCT	TCTTGATTAT	TTTTACAGTC	GAGACATTTT	TGAAGATTAT	660
AGCGTATGGA	TTATGTCTAC	ATCCTAATGC	TTATGTTAGG	AATGGATGGA	ATTTACTGGA	720
TTTTGTATTA	GTAAATAGTAG	GATTGTTTAG	TGTAATTTTG	GAACAATTAA	CCAAAGAAAC	780
AGAAGGGGGG	AACCACTCAA	GCGGCAAAATC	TGGAGGCTTT	GATGTCAAAG	CCCTCCGTGC	840
CTTTCGAGCT	TTGCGACCA	TTGCACTAGT	GTCAAGGGTG	CCCACTTTC	AAGTGTCTCT	900
GAACCTCATT	ATAAAAAGCCA	TGGTTCCTCT	CCTTCACATA	GCCTTTTGG	TATTATTTGT	960
AATCATTAAT	TATGTCTATT	TAGGATTGGA	ACTTTTATT	GGAAAAATGC	ACAAACATG	1020
TTTTTTTGGT	GACTCAGATA	TCGTAGCTGA	AGAGGACCCA	GCTCCATGTG	CGTTCCTAGG	1080
GAATGGAGCG	CAGTGTACTG	CCAATGGCAC	GGAATGTAGG	AGTGGCTGGG	TGGCCCGGAA	1140
CGGAGGCATC	ACCACTTTGC	ATAACTTTGC	CTTTGCCATG	CTTACTGTGT	TTCACTGCAT	1200
CACCATGGAG	GGCTGGACAG	ACGTGCTCTA	CTGGGTAAAT	GATGCGATAG	GATGGGAATG	1260
GCCATGAGTG	TATTTTGTTA	GTCTGATCAT	CCTTGGCTCA	TTTTTCGTCC	TTAACTCGGT	1320
CTTTGGTCTC	CTTCTGTGAG	AATTCCTCAA	GGAAAGAGAG	AAGGCAAAAG	CACGGGGAGA	1380
TTTCAGAGAG	CTCCGGGAGA	AGCAGCAGCT	GGAGGAGGAT	CTAAAGGGCT	ACTTGGATTG	1440
GATCAGCCAA	GCTAGGAGCA	TCGATCCGGA	GAATGAGGAA	GAAGGAGGAG	AGGAAGGCAG	1500
ACGAATAACT	AGCATGCCCA	CCAGCCGAGC	TGAGTCTGTG	AACACAGAGA	ACGTACGCGG	1560
TGAAGGGGAG	AACCGAGGCT	GCTGTGGAAG	TCTCTGGTGC	TGGTGGAGAC	GGAGGGCGC	1620
GGCCAGAGCG	GGGCCCTCTG	GGTGTGCGCG	GTGGGGTCAA	GCCATCTCAA	AATCCAAACT	1680
CAGCCGACGC	TGGCCTGCTC	GGAAACGATT	CAATCGCAGA	AGATGTAGGG	CCGCCGTGAA	1740
GTCTGTCACT	TTTTACTCGT	TGGTTATCGT	CCTGGTGTCT	CTGAACACCT	TAAACATTTC	1800
CTCTGAGCAC	TACAATCAGC	CAGATTGGTT	GACACAGATT	CAAGATATTG	CCAACAAAGT	1860
CCTCTTGGCT	CTGTTCACCT	GCGAGATGCT	GGTAAAATG	TACAGCTTGG	GCCTCCAAAG	1920
ATATTGTGTC	TCCTCTTTTC	ACCGGTTTGA	TTGCTTCTGT	GTGTGTGTGT	GAATCACTGA	1980
GACGATCTGT	GTGGAACATG	AAATCATGTC	TCCTCTGGGG	ATCTCTGTGT	TTGGTGTGTG	2040
GGCCCTCTTA	AGAACTCTCA	AAGTGACCAG	GCACTGGACT	TCCTGAGACA	ACTTAGTGGC	2100
ATCCTTATTA	AACTCCATGA	AGTCCATCGC	TTGCTGTGTG	CTTCTGCTTT	TTCTCTTCAT	2160
TATCATCTTT	TCCTTGTCTG	GGATGCAGCT	GTTTGGCGGC	AAGTTTAATT	TTGATGAAAC	2220
GCAACCAAGG	CGGAGCAACT	TTGACAATTT	CCCTCAAGCA	CTTCTCACAG	TGTTCCAGAT	2280
CCTGACAGGC	GAAAGCTGGA	ATGCTGTGAT	GTACGATGGC	ATCATGGCTT	ACGGGGGGCC	2340
ATCCTCTTCA	GGAATGATCG	CTCTCATCTA	CTTCTCATCT	CTCTTCATTT	GTGGTAACTA	2400
TATTTCTACTG	AATGTCTTCT	TGGCCATCGC	TGTAGACAA	TTGGCTGATG	CTGAAAGTCT	2460
GAACACTGCT	CAGAAAGAG	AAGCGGAAGA	AAGGAGAGG	AAAAAGATTG	CCAGAAAAGA	2520
GAGCCTAGAA	ATAAAAAGA	ACAACAACCC	AGAAGTCAAC	CAGATAGCCA	ACAGTGACAA	2580
CAAGGTTACA	ATTGATGACT	ATAGAGAAGA	GGAATGAAGC	AAGGACCCCT	ATCCGCCCTG	2640
CGATGTGCCA	GTAGGGGAAG	AGGAAGAGGA	AGAGGAGGAG	GATGAACCTG	AGGTTCCTGC	2700
CGGACCCCGT	CCTCAACAGG	TCTCGGAGTT	GAACATGAAG	GAATAAATTG	CCCCATCCC	2760
TGAAGGGAGC	GCTTTCTTCA	TTCTTAGCAA	GACCAACCCG	ATCCGCGTAG	GCTGCCACAA	2820
GCTCATCAAC	CACCACTACT	TCACCAACCT	CATCCTTGTG	TTCATCATGC	TGAGCAGCGC	2880
TGCCCTGGCC	GCAAGGAGCC	CCATCCGAG	CACTCCTCTT	CGGAACACGA	TACTGGGTTA	2940
CTTTGACTAT	GCCTTCACAG	CCATCTTTAC	TGTTGAGATC	CTGTGAAGA	TGACAACTTT	3000
TGGAGCTTTC	CTCCACAAAG	GGGCCCTCTG	CAGGAACCTAC	TTCAATTTGC	TGGATATGCT	3060
GGTGGTTGGG	GTGTCTCTGG	TGTCAATTGG	GATTCAATCC	AGTGCCATCT	CCGTGTGTAA	3120
GATTCTGAGG	GTCTTAAGGG	TCCTGCGTCC	CCTCAGGGCC	ATCAACAGAG	CAAAAGGACT	3180
TAAGCACGTC	GTCCAGTGGC	TCTTGGTGGC	CATCCGGACC	ATCGGCAACA	TCATGATCGT	3240
CACTACCCCTC	CTGCAATTCA	TGTTTGCCTG	TATCGGGGTC	CAGTTGTTC	AGGGGAAGTT	3300
CTATCGCTGT	ACGGATGAAG	CCAAAAGTAA	CCCTGAAGAA	TGCAGGGGAC	TTTTTCATCT	3360
CTACAAGGAT	GGGGATGTTG	ACAGTCTCTG	GGTCCGTGAA	CGGATCTGGC	AAAACAGTGA	3420
TTTCAACTTC	GACCAACGTC	TCTCTGCTAT	GATGGCGCTC	TTCAAGTCTC	CCACGTTTGA	3480
GGGCTGGCCT	GGGTGCTGCT	ATAAAGCCAT	CGACTCGAAT	GGAGAGAACA	TCCGCCCAAT	3540
CTACAAACAC	CGCGTGGAGA	TCTCCATCTT	CTTCAATCAT	TACATCATCA	TTGTAGCTTT	3600
CTTCAATGAT	AACATCTTTG	TGGGCTTTGT	CATCGTTACA	TTTCAGGAAC	AAGGAGAAAA	3660
AGAGTATAAG	AACTGTGAGC	TGGACAAAA	TCAGCGTCAG	TGTGTGAAT	ACGCTTTGAA	3720
AGCAGGCTCC	TTGCGGAGAT	ACATCCCAAA	AAACCCCTAC	CAGTACAAGT	TCTGGTACGT	3780
GGTGAACCTC	TGCCCTTTGG	AATACATGAT	GTTTGTCTCT	ATCATGCTCA	ACACACTCTG	3840
CPTGGCCATC	CAGCACTACG	AGCAGTCCAA	GATGTTCAAT	GATGCCATGG	ACATTCTGAA	3900
CATGCTCTTC	ACCGGGGTGT	TCACCGTCCA	GATGGTTTTC	AAAGTCAATG	CATTTAAGCC	3960
TAAGGGGTAT	TTTAGTGAGC	CCTGGAACAC	GTTTGAATCC	CTCATGTTAA	TCCGCAACAT	4020
TATAGACGTG	GCCTCAGCG	AAGCGGACCC	AACTGAAAGT	GAATAATGTC	CTGTCCCAAC	4080

5 TGCTACACCT GGGAACTCTG AAGAGAGCAA TAGAATCTCC ATCACCTTTT TCCGTCTTTT 4140
 CCGAGTGTATG CGATTGGTGA AGCTTCTCAG CAGGGGGGAA GGCATCCGGA CATGTCTGTG 4200
 GACTTTTATT AAGTCTCTTC AGGCGCTCCC GTATGTGGCC CTCTCATAG CCATGCTGTT 4260
 CTTTATCTAT GCGGTCAATG GCATGCAGAT GTTTGGGAAA GTTGCCATGA GAGATAACAA 4320
 CCAGATCAAT AGGAACAATA ACTTCCAGAC GTTTCCCCAG GCGGTGCTGC TGCTCTTCAG 4380
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 10 TGTATCATG GATAATTTCG ACTATCTGAC CCGGGACTGG TCTATTTTGG GGCTCACCAC 4620
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 ACACCTTGAT GTGTCACTC TGCTTCGACG CATCCAGCCT CCCCTGGCGT TTGGGAAGTT 4740
 ATGTCCACAC AGGCTAGCGT GCAAGAGATT AGTTGCCATG AACATGCCCT TCAACAGTGA 4800
 CGGGACATTC ATCTTTAATG CAACCTGTGT TGCTTTGGTT CGAACGGCTC TTAAGATCAA 4860
 15 GACCGAAGGG AACCTGGAGC AAGCTAATGA AGAACTTCGG GCTGTGTATA AGAAAAATTG 4920
 GAAGAAACCC CATCTAGAA TACTTGACCA AGTTGTCCCT CCAGCTGGTG ATGATGAGGT 4980
 AACCGTGGGG AGGTCTCATG CCACTTTCCCT GATACAGGAC TACTTTAGGA AATTCAAGAA 5040
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SEQ ID NO:288 PFD2 Protein sequence

Protein Accession #: A38198

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SEQ ID NO:289 OB16 DNA SEQUENCE

Nucleic Acid Accession#: NM_002812

Coding sequence: 150-3382 (underlined sequence corresponds to start and stop codon)

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SEQ ID NO:290 DB16 Protein sequence
Protein Accession #: NP_002812

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25	KERNLTLRPA	GPEHSGLYSC	CAHSAFGQAC	SSQNFTLSIA	DESFARVULA	PQDVVVARTE	240
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	CIGQGQGRFP	ILLEATLHLA	EIEDMLFEP	RVFTAGSEER	VTCLPKGLP	EPSVWMEHAG	360
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	SQLEBGRPGY	LDCLTQATPK	PTVWYRNQM	LISEDSEFV	FKNGTLRINS	VEYDGTWYR	480
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30	GSSLPFWYTD	NAGTLHFARV	TRDDAGNYTC	IASNGPQGOI	RAHVQLTVAV	FITFKVEPER	600
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35	KRHSTSDKMH	FFRSSLQPIIT	TLGKSEFGEV	FLAKAQGLEE	GVAETLVLVK	SLQTKDEQQQ	840
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	YHFRQAWVPL	KHMSPEALIE	GDPSTKSDVW	AFGVLMWEVP	THGENPHGGQ	ADDEVILADLQ	1020
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SEQ ID NO:291 AAB1 DNA SEQUENCE

Nucleic Acid Accession #: NM_002205
Coding sequence: 1-3150 (underlined sequences correspond to start and stop codons)

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SEQ ID NO:292 AAB1 Protein sequence:
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EVRGVVYVLQ HPAGIEPTPT LTLTGHEDFG RFGSSLTPLG DLDQDGYNDV AIGAPFGGET 420
QGGVVVFPFG GPGGLGSKPS QVLQPLNAAS HTPDPFGSAL RGGRLDNGG YPDLIVGSFG 480
VDKAVVYRGR FIVSASASLT IFFPAMFNPEE RSCSLGPNV ACINLSPCLN ASGKEVADSI 540
GFIVELQLWF QKQKGVVRA LFLASRQATL TQTLLIQNGA REDCREMKIY LRNESEPRDK 600
LSPIHIALNF SLDPQAPVDS HGLRPAHYQ SKSRIEDKQ ILLDCGEDNI CVPDLQLEVF 660
GEQNHVYLGQ KNAINLTFHA QNVGEGGAYE AELRVTAFFE AEYSGLVRHP GNFSSLSCDY 720
FAVNPRLV CDLGNPKAG ASLWGLRFT VPHLRDTKKT IQPDPQLSK NNNNSQSDVV 780
SFRLSVEAGA QVTLNGVSKP EAVLFPVSDW HPRDQPKKEE DLGPAVHVHY ELINQGFSSI 840
SQGVLEACP QALEGQQLLY VTRVTGLNCT TNPINPKGL ELDPGSLHH QKREAPSRs 900
SASSGPQILK CPEABCFRLR CELGPLHQBE SOSLQLHFRV WAKTFLOREH QPFSLQCEAV 960
YKALKMPYRI LPRQLPQKER QVATAVQWTK AEGSYGVFLW IILAILFLGL LLGLLLTYIL 1020
YKLGFPKRSL FYGTAMEKAQ LKFPATSDA
  
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50
 55
 60
 65
 70
 75

SEQ ID NO:293 LBH4 DNA SEQUENCE

Nucleic Acid Accession #: BC001291
 Coding sequence: 44-541 (start and stop codons are underlined)

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1 11 21 31 41 51
GGGGGGGCGG CGGCTGAACC CTCCCTGGGC AOCGCTGGGG ACGATGGCGC TGCTGCCTT 60
GCTGCTGGTC GTGGCCCTAC CGCGGGGTGT GACAGAAGCC AACTGACTG CGAGACAAAG 120
AGATCCAGAG GACTCCAGC GAACGGAGCA GGTGACAAT AGAGTGTGGT GTCATGTTG 180
TGAGAGAGAA AACACTTTG AGTGCCAGAA CCAAGGAGG TGCAAAATGA CAGAGCCATA 240
CTGCGTTATA GCGGCCGTGA AAATATTTCC ACGTTTTTC ATGTTTGGCA AGCAGTGCTC 300
CGCTGTTTGT GCAGCGATGG AGAGACCCAA GOCAGAGGAG AAGCGGTTTC TCTGGAAGA 360
GCCATGCCC TTCTTTTACC TCAAGTGTG TAAAATTGCG TACTGCAAT TAGAGGGGCG 420
ACCTATCAAC TCATCAGTGT TCAAAGAATA TGCTGGGAGC ATGGGTGAGA GCTGTGGTGG 480
GCTGTGGCTG GCCATCTCTC TGCTGCTGCC CTCCATGCA GCCGGCCTCA GCTGTCTTG 540
AGCCACGGGA CTGCCACAGA CTGAGCCTTC CGGAGCATGG ACTCGCTCCA GACCGTTGTC 600
ACCTGTGCA TTAACATTGT TTTCTGTTGA TTAOCTCTTG GTTTGACTTC CAGGGTCTT 660
GGGATGGGAG AGTGGGATC AGGTGCAATT GGCTCTTAAC CCTCAAGGT TCTTTAACTC 720
ACATTCAAGG GAAGTCCAGA TCTCCTGAGT AGTGATTTTG GTGACAAGTT TTTCTCTTG 780
AAATCAAGAC TTGTAACCTA TTTATTGCTG ATGGCCACTC TTTTCTTGA CTCOCTCTG 840
CCTCTGAGGG CTTCAGATT GATGGGGAGG GAGGCTAAG TACCACATCAT GGAGAGTATG 900
TGCTGAGATG CTCCGACCT TTCAGGTGAC GCAGGAACAC TGGGGGAGTC TGAATGATTG 960
GGGTGAAGAC ATCCCTGGAG TGAAGGACTC CTCAGCATGG GGGGCACTGG GGCACACGTT 1020
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CTACAGATT CCAAGGAGCA GAAGATAACT AATTGTGTTG AAGAACTTA GACTTCACCC 1140
ACCAGCTGGC ACAGGTGCAC AGATTCATAA ATTCCACAC GTGTGTGTTT AACATCTGAA 1200
ACTAGGCA AGTAGAGGC ATCAGGTAA ATGGCGTTCA TTTCTGTGTT AAGATGCAGC 1260
CATCCATGGG GAGCTGAGAA ATCAGACTCA AAGTTCACC AAAAACAAT ACAAGGGGAC 1320
TTCAAAAGTT CACGAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAA
  
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SEQ ID NO:294 LBH4 Protein sequence
 Protein Accession #: AAH01291

5 1 11 21 31 41 51
 | | | | | |
 MALLALLLVV ALPRVWTDAN LTARQDPED SQTDEGDNR VWCHVCEREN TFECQNPRRC 60
 KWTEPYCVIA AVKIFPRPFM VAKQCSAGCA AMERPKPEEK RFLLEPMPPF FYLKOCKIRY 120
 10 CNLEGPINS SVFKEYAGSM GESCGGLWLA ILLIASIAA GLSL

15 It is understood that the examples described above in no way serve to limit the
 true scope of this invention, but rather are presented for illustrative purposes. All
 publications, sequences of accession numbers, and patent applications cited in this
 specification are herein incorporated by reference as if each individual publication or patent
 20 application were specifically and individually indicated to be incorporated by reference.

WHAT IS CLAIMED IS:

- 1 1. A method of detecting a prostate cancer-associated transcript in a cell
2 from a patient, the method comprising contacting a biological sample from the patient with a
3 polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence
4 as shown in Tables 1-16.
- 1 2. The method of claim 1, wherein the polynucleotide selectively
2 hybridizes to a sequence at least 95% identical to a sequence as shown in Tables 1-16.
- 1 3. The method of claim 1, wherein the biological sample is a tissue
2 sample.
- 1 4. The method of claim 1, wherein the biological sample comprises
2 isolated nucleic acids.
- 1 5. The method of claim 4, wherein the nucleic acids are mRNA.
- 1 6. The method of claim 4, further comprising the step of amplifying
2 nucleic acids before the step of contacting the biological sample with the polynucleotide.
- 1 7. The method of claim 1, wherein the polynucleotide comprises a
2 sequence as shown in Tables 1-16.
- 1 8. The method of claim 1, wherein the polynucleotide is labeled.
- 1 9. The method of claim 8, wherein the label is a fluorescent label.
- 1 10. The method of claim 1, wherein the polynucleotide is immobilized on
2 a solid surface.
- 1 11. The method of claim 1, wherein the patient is undergoing a therapeutic
2 regimen to treat prostate cancer.
- 1 12. The method of claim 1, wherein the patient is suspected of having
2 prostate cancer.

- 1 13. A method of monitoring the efficacy of a therapeutic treatment of
2 prostate cancer, the method comprising the steps of:
3 (i) providing a biological sample from a patient undergoing the therapeutic
4 treatment; and
5 (ii) determining the level of a prostate cancer-associated transcript in the
6 biological sample by contacting the biological sample with a polynucleotide that selectively
7 hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1-16,
8 thereby monitoring the efficacy of the therapy.
- 1 14. The method of claim 13, further comprising the step of: (iii) comparing
2 the level of the prostate cancer-associated transcript to a level of the prostate cancer-
3 associated transcript in a biological sample from the patient prior to, or earlier in, the
4 therapeutic treatment.
- 1 15. The method of claim 13, wherein the patient is a human.
- 1 16. A method of monitoring the efficacy of a therapeutic treatment of
2 prostate cancer, the method comprising the steps of:
3 (i) providing a biological sample from a patient undergoing the therapeutic
4 treatment; and
5 (ii) determining the level of a prostate cancer-associated antibody in the
6 biological sample by contacting the biological sample with a polypeptide encoded by a
7 polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence
8 as shown in Tables 1-16, wherein the polypeptide specifically binds to the prostate cancer-
9 associated antibody, thereby monitoring the efficacy of the therapy.
- 1 17. The method of claim 16, further comprising the step of: (iii) comparing
2 the level of the prostate cancer-associated antibody to a level of the prostate cancer-
3 associated antibody in a biological sample from the patient prior to, or earlier in, the
4 therapeutic treatment.
- 1 18. The method of claim 16, wherein the patient is a human.

- 1 19. A method of monitoring the efficacy of a therapeutic treatment of
2 prostate cancer, the method comprising the steps of:
3 (i) providing a biological sample from a patient undergoing the therapeutic
4 treatment; and
5 (ii) determining the level of a prostate cancer-associated polypeptide in the
6 biological sample by contacting the biological sample with an antibody, wherein the antibody
7 specifically binds to a polypeptide encoded by a polynucleotide that selectively hybridizes to
8 a sequence at least 80% identical to a sequence as shown in Tables 1-16, thereby monitoring
9 the efficacy of the therapy.
- 1 20. The method of claim 19, further comprising the step of: (iii) comparing
2 the level of the prostate cancer-associated polypeptide to a level of the prostate cancer-
3 associated polypeptide in a biological sample from the patient prior to, or earlier in, the
4 therapeutic treatment.
- 1 21. The method of claim 19, wherein the patient is a human.
- 1 22. An isolated nucleic acid molecule consisting of a polynucleotide
2 sequence as shown in Tables 1-16.
- 1 23. The nucleic acid molecule of claim 22, which is labeled.
- 1 24. The nucleic acid of claim 23, wherein the label is a fluorescent label
- 1 25. An expression vector comprising the nucleic acid of claim 22.
- 1 26. A host cell comprising the expression vector of claim 25.
- 1 27. An isolated polypeptide which is encoded by a nucleic acid molecule
2 having polynucleotide sequence as shown in Tables 1-16.
- 1 28. An antibody that specifically binds a polypeptide of claim 27.
- 1 29. The antibody of claim 28, further conjugated to an effector component.

- 1 30. The antibody of claim 29, wherein the effector component is a
2 fluorescent label.
- 1 31. The antibody of claim 29, wherein the effector component is a
2 radioisotope or a cytotoxic chemical.
- 1 32. The antibody of claim 29, which is an antibody fragment.
- 1 33. The antibody of claim 29, which is a humanized antibody
- 1 34. A method of detecting a prostate cancer cell in a biological sample
2 from a patient, the method comprising contacting the biological sample with an antibody of
3 claim 28.
- 1 35. The method of claim 34, wherein the antibody is further conjugated to
2 an effector component.
- 1 36. The method of claim 35, wherein the effector component is a
2 fluorescent label.
- 1 37. A method of detecting antibodies specific to prostate cancer in a
2 patient, the method comprising contacting a biological sample from the patient with a
3 polypeptide encoded by a nucleic acid comprises a sequence from Tables 1-16.
- 1 38. A method for identifying a compound that modulates a prostate cancer-
2 associated polypeptide, the method comprising the steps of:
3 (i) contacting the compound with a prostate cancer-associated polypeptide, the
4 polypeptide encoded by a polynucleotide that selectively hybridizes to a sequence at least
5 80% identical to a sequence as shown in Tables 1-16; and
6 (ii) determining the functional effect of the compound upon the polypeptide.
- 1 39. The method of claim 38, wherein the functional effect is a physical
2 effect.

- 1 40. The method of claim 38, wherein the functional effect is a chemical
2 effect.
- 1 41. The method of claim 38, wherein the polypeptide is expressed in a
2 eukaryotic host cell or cell membrane.
- 1 42. The method of claim 38, wherein the functional effect is determined by
2 measuring ligand binding to the polypeptide.
- 1 43. The method of claim 38, wherein the polypeptide is recombinant.
- 1 44. A method of inhibiting proliferation of a prostate cancer-associated
2 cell to treat prostate cancer in a patient, the method comprising the step of administering to
3 the subject a therapeutically effective amount of a compound identified using the method of
4 claim 38.
- 1 45. The method of claim 44, wherein the compound is an antibody.
- 1 46. The method of claim 45, wherein the patient is a human.
- 1 47. A drug screening assay comprising the steps of
2 (i) administering a test compound to a mammal having prostate cancer or a
3 cell isolated therefrom;
4 (ii) comparing the level of gene expression of a polynucleotide that selectively
5 hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1-16 in a
6 treated cell or mammal with the level of gene expression of the polynucleotide in a control
7 cell or mammal, wherein a test compound that modulates the level of expression of the
8 polynucleotide is a candidate for the treatment of prostate cancer.
- 1 48. The assay of claim 47, wherein the control is a mammal with prostate
2 cancer or a cell therefrom that has not been treated with the test compound.
- 1 49. The assay of claim 47, wherein the control is a normal cell or mammal.

1 50. A method for treating a mammal having prostate cancer comprising
2 administering a compound identified by the assay of claim 47.

1 51. A pharmaceutical composition for treating a mammal having prostate
2 cancer, the composition comprising a compound identified by the assay of claim 47 and a
3 physiologically acceptable excipient.

1 52. The method according to claim 1, wherein said biological sample is
2 contacted with a plurality of polynucleotides comprising a first polynucleotide that
3 selectively hybridizes to a sequence at least 80% identical to a first sequence as shown in
4 Tables 1-16; and a second polynucleotide that selectively hybridizes to a second sequence at
5 least 80% identical to a second sequence as shown in Tables 1-16.

1 53. A method according to claim 52, wherein the plurality of
2 polynucleotides comprises a third polynucleotide that selectively hybridizes to a sequence at
3 least 80% identical to a third sequence as shown in Tables 1-16..

1 54. A method of detecting a prostate cancer associated transcript, the
2 method comprising contacting a biological sample from the patient with a plurality of
3 polynucleotides wherein at least two of said polynucleotides selectively hybridize to a
4 difference sequence at least 80% identical to a sequence as shown in Tables 1-16.

1 55. A method of detecting a prostate cancer, the method comprising the
2 steps of:
3 (i) providing a biological sample from a patient;
4 (ii) contacting the biological sample with a first polynucleotide that selectively
5 hybridizes to a sequence at least 80% identical to a first sequence as shown in Tables 1-16 to
6 determine the level of a prostate cancer-associated transcript in the biological sample; and
7 with a second polynucleotide that selectively hybridizes to a second sequence at least 80%
8 identical to a sequence not shown in Tables 1-16; wherein the expression of said second
9 sequence is not substantially changed in prostate cancer, to determine the level of expression
10 of a control transcript in the biological sample;

11 (iii) comparing the level of the prostate cancer-associated transcript to a level
12 of the normal tissue associated transcript in the biological sample.

1 56. A method of quantitating a prostate cancer-associated transcript in a
2 cell from a patient, the method comprising contacting a biological sample from the patient
3 with a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a
4 sequence as shown in Tables 1-16.

1 57. The method of claim 56, wherein the polynucleotide selectively
2 hybridizes to a sequence at least 95% identical to a sequence as shown in Tables 1-16.

1 58. The method of claim 56, wherein the biological sample is a tissue
2 sample.

1 59. The method of claim 56, wherein the biological sample comprises
2 isolated nucleic acids.

1 60. The method of claim 56, wherein the nucleic acids are mRNA.

1 61. The method of claim 59, further comprising the step of amplifying
2 nucleic acids before the step of contacting the biological sample with the polynucleotide.

1 62. The method of claim 56, wherein the polynucleotide comprises a
2 sequence as shown in Tables 1-16.

1 63. The method of claim 56, wherein the polynucleotide is labeled.

1 64. The method of claim 63, wherein the label is a fluorescent label.

1 65. The method of claim 56, wherein the polynucleotide is immobilized on
2 a solid surface.

1 66. The method of claim 56, wherein the patient is undergoing a
2 therapeutic regimen to treat metastatic prostate cancer.

1 67. The method of claim 56, wherein the patient is suspected of having
2 metastatic prostate cancer.

1 68. A biochip comprising a plurality of polynucleotides that selectively
2 hybridize to a sequence at least 80% identical to a sequence as shown in Tables 1-16.

1 69. A method of screening drug candidates comprising:
2 i) providing a cell that expresses an expression profile gene selected from the
3 group consisting of an expression profile gene set forth in Tables 1-16 or fragment thereof;
4 ii) adding a drug candidate to said cell; and
5 iii) determining the effect of said drug candidate on the expression of said
6 expression profile gene.

1 70. A method according to claim 59 wherein said determining comprises
2 comparing the level of expression in the absence of said drug candidate to the level of
3 expression in the presence of said drug candidate.

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